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Run
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
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                                                                                                                                                                                                                                                                                                     Pred. No.
score grea
and is der
                                                                                                                                                                                                             Score
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seq
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/SIDS1/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp/AA1981.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp/AA1982.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp/AA1983.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp/AA1986.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqp/AA1988.DAT:*
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2563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                    SIDS1/gcgdata/geneseq/geneseqp/AA199 DAT: *
/SIDS1/gcgdata/geneseq/geneseqp/AA199 DAT: *
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AAW37733
AAW44159
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                                                                                                                                                                                                                                                                       SUMMARIES
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332.928 Million cell updates/sec
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              Human cytochrome P
Human retinoid met
Cytochrome P450RAI
Mouse retinoid met
Human PSEC64 prote
Arabidopsis thalia
Arabidopsis thalia
                                                                                                                                                                                                                 Description
                                                                                                                                                            Cytochrome zP450RA zebrafish retinoid
 Arabidopsis
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Arabidopsis thalla	AAW26640	18	520	12.9	330.5	45
T	AAB48181	22	513	13.0	332	44
Amino acid sequenc	AAB31008	22	513	13.0	332	43
Human derived cyto	AAR81465	17	490		332	
Human cytochrome P	AAR93168	17	490	13.0	332	41
	AAR72361	16	490	•	332	40
thali	AAG20785	21	388	13.0	333	39
Arabidopsis thalia	AAG23014	21	469	•	339	38
Mammalian cytochro	AAY04127	20	490	•	339.5	37
Human cytochrome P	AAW64073	19	490	•	339.5	ω 6
O	AAW64070	19	490	•	339.5	ω G
Cytochrome P450 2C	AAR89865	17	490		339.5	34
	AAR89862	17	490	13.2	339.5	w w
Arabidopsis thalia	AAG23012	21	479		342	32
	AAG23013	21	471	13.3	342	31
Sweetgum coniferyl	AAB19694	21	511		343	30
A P450-2 protein i	AAY23341	20	511		343	29
	AAB07676	21	475	14.3	366	28
Arabidopsis thalia	AAG30050	21	433	•	366.5	27
	AAG30049	21	481	•	394	26
	AAG30048	21	489	•	394.5	25
0	AAB40557	21	163		397	24
	AAG20784	21	430	16.6	425.5	23
	AAG20783	21	468		470	22
	AAG11834	21	465	18.6	475.5	21
	AAG11835	21	462		475.5	20
	AAG11836	21	461		475.5	19
	AAG46491	21	465		481.5	18
	AAG46489	21	462	•	481.5	17
	AAG46490	21	6	•	481.5	16
A cytochrome P450	AAB07921	21	513	•	503	15
4	AAG45023	21	444	•	536	14
	AAG44572	21		20.9		13
Arabidopsis thalia	AAG44570	21	492	21.6	552.5	12

ALIGNMENTS

RESULT

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AAW37733 standard; Protein;

492

B

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Identifying DNA encoding inducible or suppressible cytochrome P450 - by screening for drugs which reduce the catabolism of retinoic acid useful in cancer chemotherapy and the treatment of acne and
                                                                                    01-OCT-1996;
21-JUN-1996;
                                                                                                                          31-DEC-1997.
                                                                                                                                         WO9749832-A2
                                                                                                                                                        Danio rerio.
                              WPI; 1998-077193/07.
N-PSDB; AAV09251.
                                                                   (TOOH ) UNIV QUEENS KINGSTON
                                                                                                           23-JUN-1997;
                                                      Petkovich
                                                                                   96US-0724466.
96US-0667546.
                                                                                                            97WO-CA00488
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oxidative metabolism; P450RAI; retinoic acid; RA; promoter.

Retinoid regulated gene; cytochrome P450 gene;

Cytochrome zP450RAI protein.

07-JUL-1998 AAW37733;

(first

entry)

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RESULT
AAW44159
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Best Local
     actinic
                    Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid; zebrafish; inhibitor; antibody; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is the amino acid for cytochrome zP450RAI of the zebra fish. Its expression is dependent on the presence of retinotc acid (RA). The retinoid-regulated genes such as the inducible cytochrome P450RAI gene specifically metabolises a derivative of the RA. The cytochrome P450 gene in general produces enzymes involved in the oxidative metabolism of endogenous and exogenous compounds. The cytochrome P450 nucleotide sequence can be used to induce or suppress the expression of its protein. P450RAI is highly induced by RA in cell lines and tissues. This allows for development of a drug screen using promoters and nucleotide sequences to identify drugs which are useful for reducing the catabolism of RA.
                                                                                                    Zebrafish
                                                                                                                                                   22-JUN-1998
                                                                                                                                                                                                       AAW44159;
                                                                                                                                                                                                                                                   AAW44159 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421
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     keratosis;
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                                                                                                    retinoid
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                                                                                                                                                (first entry)
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                                                                                               metabolising
                                                                                                                                                                                                                                                   Protein; 492
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h; inhibitor;
leukoplakia;
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Pred. No. 5.3e-227;
); Mismatches 0; Indels 0;
                                                                                             protein
                                                                                                                                                                                                                                                   Å
  antibody;
head tumo
                                                                                               zP450RAI.
tumour; neck tumour;
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                                                                                                                                                                                                                                                                                                                                                                                                   This protein comprises a novel zebrafish retinoid metabolising protein, designated zp450RAI. Its amino acid sequence was deduced from a CDNA clone (see AAVI2203) isolated from a 6-18 hr embryo library. It includes a haem-binding motif characteristic of cytochrome p450 proteins. zp450RAI is a retinoid oxidase that has the ability to hydroxylate retinoic acid at the 4 position of the beta-ionone ring, and is inducible in epithelial cells exposed to retinoic acid. Zebrafish, human and mouse p450RAIs (see AAW44159-61) are claimed. They can be expressed in host cells and used to metabolize retinoic acid in an organism or cell, in drug screening, and to raise antibodies useful for inhibiting retinoic acid hydroxylation for the treatment of cancer, actinic keratosis, oral leukoplakia, secondary tumours of the head and/or neck, non-small cell lung carcinomas, basal cell carcinomas, acute promyelocytic leukaemia, skin cancer, and premalignancy associated with actinic cell lung carcinomas, and/or ichthocsis.
                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-small cell lung carcinomá; basal cell carcinoma; acute promyelocytic leukaemia; skin cancer; acne; psoriasis; ichthyosis; therapy; diagnosis; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                              keratosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 50-51; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beckett BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996;
21-JUN-1996;
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    301
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                                                                                        181
                                                                                                                                                121
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                                                                                                                                                                                                                                                           TASTATSLVMFLGLNTEVVQKVREEVQEKVEMGMYTPGKGLSMELLDQLKYTGCVIKETL
                                              HSKIEENIRKKIQDDDNENEQKYKDALQLLIENSRRSDEPFSLQAMKEAATELLFGGHET
                                                                                                  KKLMFRIAMRILLGFEPEQIKTDEQELVEAFEEMIKNLFSLPIDVPFSGLYRGLRARNFI
                                                                                                                                                          GSDTLSNVHGVQHKNKKKAIMRAFSRDALEHYIPVIQQEVKSAIQEWLQKDSCVLVYPEM
                                                                                                                                                                                                    hskie enirkkiq dddnene qkykdalqlliens rrsdepfslqamke aatellf gghet\\
                                                                                    kklmfriamrillgfepeqiktdeqelveafeemiknlfslpidvpfsglyrglrarnfi
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                                                                                                                                                                                                                                                                                                                          492;
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                                                                                                                                                                                                                                                                                                                                                                                                                            acne, psoriasis and/or ichthyosis.
                                                                                                                                                                                                                                                                                                                                                                                                  492 AA;
                                                                                                                                                                                                                                                                                                                          Conservative
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96US-0667546.
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                                                                                                                                                                                                                                                                                                                          0;
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Pred. No. 5.3e-227;
                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful to develop oral leukoplakia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          White JA;
                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT
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        Query Match
Best Local Similarity
Matches 338; Conserv
                                                                      This is the amino acid sequence of the human cytochrome P450RAI. Its expression is dependent on the presence of retinoic acid (RA). The retinoid-regulated genes such as the inducible cytochrome P450RAI gene specifically metabolises a derivative of the RA. The cytochrome P450 gene in general produces enzymes involved in the oxidative metabolism of endogenous and exogenous compounds. The cytochrome P450 nucleotide sequence can be used to induce or suppress the expression of its protein. P450RAI is highly induced by RA in cell lines and tissues. This allows for development of a drug screen using promoters and nucleotide sequences to identify drugs which are useful for reducing the catabolism of RA.
                                                                                                                                                                                                           Identifying DNA encoding inducible or suppressible cytochrome P450 by screening for drugs which reduce the catabolism of retinoic acid useful in cancer chemotherapy and the treatment of acne and
                                                                                                                                                                                                                                                                                                               01-OCT-1996;
21-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                Retinoid regulated gene; cytochrome P450 gene; en; oxidative metabolism; P450RAI; retinoic acid; RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cytochrome P450RAI protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW37734 standard; Protein; 497
                                                                                                                                                                                                                                                                            Petkovich PM;
                                                                                                                                                                                                                                                                                                                                         23-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                      Sequence
                                                                                                                                                                                 Example 4; Pages 58-59; 113pp; English.
                                                                                                                                                                                                                                                           WPI;
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DB; AAV09247.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rinppvpggfrvalktfelngygipkgwnvlysicdthdvadvfpnkeefgperfmskgl
                                                       497
          Conservative
                                                                                                                                                                                                                                                                                             QUEENS KINGSTON
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                                                                                                                                                                                                                                                                                                               96US-0667546.
                                                                                                                                                                                                                                                                                                                                          97WO-CA00488
                  67.8%;
          63;
       Score 1738; DB 19;
Pred. No. 3.6e-151;
i3; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                        enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                promoter
                          Length 497;
         Indels
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         12;
        Gaps
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Retinoid metabolising
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                            WPI;
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Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid; human; inhibitor; antibody; cancer; actinic keratosis; oral leukoplakia; head tumour; neck tu
                                                                                                                                               01-OCT-1996;
21-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                non-small cell lung carcinoma;
acute promyelocytic leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human retinoid metabolising protein hP450RAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUN-1998
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                                                              Beckett BR,
                                                                                                                                                                                                            23-JUN-1997;
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                                                                                                       VIND ( HOOT)
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                                                                                                       QUEENS KINGSTON
                                                            Jones G,
                                                                                                                                             96US-0724466.
96US-0667546.
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                                                              Petkovich
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                                                                                                                                                                                                                                                                                                                                                                                                basal cell carcinoma;
skin cancer; acne; ps
                                                              PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                           head tumour; neck tumour;
                                                              White JA;
                                                                                                                                                                                                                                                                                                                                                                                                psoriasis;
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protein

useful to develop products to treat,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          designated hp450RAI. Its amino acid sequence was deduced from a cDNA clone (see AAV12204) isolated from a retinoic acid-treated NT2 cDNA clone (see AAV12204) isolated from a retinoic acid-treated NT2 cell library. It includes a haem-binding motif characteristic of cytochrome P450 proteins. hp450RAI is a retinoid oxidase that has the ability to hydroxylate retinoic acid at the 4 position of the beta-ionone ring, and is inducible in epithelial cells exposed to retinoic acid. Zebrafish, human and mouse P450RAIs (see AAW4159-61) are claimed. They can be expressed in host cells and used to metabolize retinoic acid in an organism or cell, in drug screening, and to raise antibodies useful for inhibiting retinoic acid hydroxylation for the treatment of cancer, actinic keratosis, oral leukoplakia, secondary tumours of the head and/or neck, non-small cell loung carcinomas, basal cell carcinomas, acute promyelocytic leukaemia, skin cancer, and premalignancy associated with actinic keratosis, acne, psoriasis and/or ichthyosis.
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Best Local :
     07-JUL-1998
                                                  AAW37735;
                                                                                                  AAW37735 standard;
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(first entry)
                                                                                                  Protein;
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68.0%;
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21-JUN-1996;
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Identifying DNA encoding inducible or suppressible cytochrome P450 by screening for drugs which reduce the catabolism of retinoic acid. useful in cancer chemotherapy and the treatment of acne and
                                                                                                                                                                                                     WPI; 1998-077193/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Retinoid regulated gene; cytochrome P450 gene; enzyme; oxidative metabolism; P450RAI; retinoic acid; RA; promoter; isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytochrome P450RAI isoform.
                                                                                                                                                                                                                                                                                                                                                         (TOOH ) UNIV QUEENS KINGSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0724466
96US-0667546
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This amino acid sequence is of an isoform of cytochrome zP450RAI. Its expression is dependent on the presence of retinoic acid (RA). The retinoid-regulated genes such as the inducible cytochrome P450RII gene specifically metabolises a derivative of the RA. The cytochrome P450 gene in general produces enzymes involved in the oxidative metabolism of endogenous and exogenous compounds. The cytochrome P450 nucleotide sequence can be used to induce or suppress the expression of its protein. P450RAI is highly induced by RA in cell lines and tissues. This allows for development of a drug screen using promoters and nucleotide sequences to identify drugs which are useful for reducing the catabolism of RA.

Similarity Conservative 67.78; 67.78; 61; Mismatches Score 1734; DB 19; Pred. No. 8.4e-151; Indels Length 497; 10;

4.

294 LFGGHETTASTATSLVMFLGLNTEVVQKVREEVQEKVEMGMYTPGKGLSMELLDQLKYTG 121 gagclsnlhdsshkqrkkvimqafsrealqcyvlviaeevsscleqwl---scgergllv 61 vlqrrkflqmkrrkygflykthlfgrptvrvmgadnvrrillgehrlvsvhwpasvrtil 61 ILQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVRTIL 120 1 MGLYTLMVTFLCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQL lfgghettasaatslitylglyphvlqkvreeikskgllcksnqdnkldmetleqlkyig YPEMKKLMFRIAMRILLGFEPEQI--KTDEQELVEAFEEMIKNLFSLPIDVPFSGLYRGL GSDTLSNVHGVQHKNKKKAIMRAFSRDALEHYIPVIQQEVKSAIQEWLQKDSC----VLV ${\tt mglpallasalctfvlplllflaalklwdlycvssrdrscalplppgtmgfpffgetlqm}$ karnliharieenirakirrlqatepdggckdalqlliehswergerldmqalkqsstel RARNFIHSKIEENIRKKIQD-DDNENEQKYKDALQLLIENSRRSDEPFSLQAMKEAATEL ypevkrlmfriamrillgcepgpagggedeqqlveafeemtrnlfslpidvpfsglyrgv Gaps 357 234 120 60 60 293 177 297 237

Length 497;

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                                      designated mp450RAI. Its amino acid sequence was deduced from a colona clone (see AAV12205) isolated from a retinoic acid-treated p19 teratocarcinoma library. It includes a haem-binding motif characteristic of cytochrome P450 proteins. mp450RAI is a retinoid coxidase that has the ability to hydroxylate retinoic acid at the 4 position of the beta-ionone ring, and is inducible in epithelial cells exposed to retinoic acid. Zebrafish, human and mouse P450RAIs (see AAW44159-61) are claimed. They can be expressed in host cells and used to metabolize retinoic acid in an organism or cell, in drug screening, and to raise antibodies useful for inhibiting retinoic acid hydroxylation for the treatment of cancer, actinic keratosis, coral leukoplakia, secondary tumours of the head and/or neck, non-small cell lung carcinomas, basal cell carcinomas, acute with activic because a secondary tumours of the head and/or associated with a coral carcinomas, skin cancer, and premalignancy associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid; mouse; inhibitor; antibody; cancer; actinic keratosis; oral leukoplakia; head tumour; neck tumour; non-small cell lung carcinoma; basal cell carcinoma; acute promyelocytic leukaemia; skin cancer; acne; psoriasis;
                                                                                                                                                                                                                                                                                                  Claim 1; Page 65-66; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                Retinoid metabolising protein - useful to develop products to treat, e.g. cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-077178/07
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21-JUN-1996;
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                             actinic keratosis, acne, psoriasis and/or ichthyosis
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                                                                                                                                                         mouse P450RAIs
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Best Local
                    A protein related protein -
                                                                                                     N-PSDB;
                                                                                                                                                                                                                                        19-NOV-1998;
                                                                                                                                                                                                                                                                                                                                              06-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; PSEC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuron
                                                                                                                                                                                                                                                                                             98JP-0329989
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67.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            growth; nerve disease
                                              growth of neuron and
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 150;
The present sequence is Arabidopsis thaliana cytochrome P450 type hydroxylase. The hydroxylase can be used to identify brassinosteroids or brassinosteroid inhibitors, useful to produce plants with modified physiological and/or phenotypic characteristics. The modified plants may show, e.g. stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                    Cytochrome P450-type hydroxylase; identification; brassinosteroid; brassinosteroid inhibitor; modified plant; recombinant production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a human protein, designated PSEC64, which is related to neuron growth. The PSEC64 protein and its gene can be used for the development of a preventive agent for use in the treatment of diseases in which nerves are involved.
                                                                               Claim 1; Pages 44-46; 77pp; English.
                                                                                                          New isolated plant cytochrome P450-type hydroxylase gene - used to identify substances acting as brassino-steroid(s) or brassinosteroid inhibitors for the production of modified plants
                                                                                                                                                                                                       Altmann T,
                                                                                                                                                                                                                                                                                     27-MAR-1997;
                                                                                                                                                                                                                                                                                                                02-OCT-1997
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                                                                                                                                                              1997-489649/45.
DB; AAT85306, AAT85307.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gsgclsnlhdsshkqrkkvimrafsrealecyvpviteevgssleqwl---scgergllv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSDTLSNVHGVQHKNKKKAIMRAFSRDALEHYIPVIQQEVKSAIQEWLQKDSC----VLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \verb|mglpallasalctfvlplllflaaiklwdlycvsgrdrscalplppgtmgfpffgetlqm|
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                                                                                                                                                                                                       Koncz C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                       Mathur J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               accelerated seed germination at low temperatures, an increase in dry weight, repressed anthocyanin production during growth in light and/or inhibited de-eticlation which is induced, e.g. by cytokinin, in the dark or an increase in stress tolerance. The hydroxylase or its coding sequence can also be used for the recombinant production of compounds, e.g. teasterone.
                                                                                                                                                  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 55847.
                                                                                                                                                                                                                                           18-OCT-2000
                                                                                                                                                                                                                                                                              AAG44571;
                                                                                                                                                                                                                                                                                                             AAG44571 standard; Protein; 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLYMFLGINTEVVQKVREEVQEKVEMGMYTPGKGLSMELLDQLKYTGCVIKETLRINPPV 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggvfrramtdveikgykipkgwkvfssfravhldpnhfkdartfnpwrwqsnsvttgpsn
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25-FEB-2000; 2000EP-0301439

06-SEP-2000. EP1033405-A2 Arabidopsis thaliana

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-1999; -1999; -1999; -1999;	-1999; -1999; -1999;	1999;	1999;	1999;	.1999;	1999;	1999;	1999;	.1999; .1999;	1999;	.1999;	.1999;	1999;	1999;	1999;	; 666T.	1999;	1999;	1999;	.1999; .1999;	1999;	1999;	.1999; .1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999,	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;
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US-014 US-014 US-014 US-014	03-01 03-01 03-01	US-01	US-01	10-SD	US-01	US-01	05-01	us-01	US-01	US-01	US-01	0S-01	US-01	US-01	TO-SD	0S-01	08-01	US-01	TO-SD	us-01	TO-SD	US-01	us-01	US-01	TO-SD	US-01	US-01	US-01	TO-SD	US-01	TO-SD	0S-01:	us-01	US-01	T0-SD	0S-01:	0S-01	TO-SU	us-01:
42154 42055 42390 42803 42920	40991 40991 41287 41842	40354	9899 9899 7	9763	9462	39461	39459	39457	39455	39454	39453	39452	38847	38540	37724	37502	37222	36392	35629	35124 35353	34941	34370	34219 34221	34218	32863	32486	32485	32407	32048	30891	0120)077)449	29845.	3234	27462	26264 26785	25788	23180.	21825.
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23-JUL-1999; 23-JUL-1999;

99US-0145218. 99US-0145224. 99US-0145276. 99US-0145913. 99US-0145918. 99US-0145919.

27-JUL-1999

99US-0145951 99US-0146386

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06-SEP-2000
                                                EP1033405-A2
                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 55846.
                                                                                                                                                                                                                                                                                                                                         AAG44570;
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                                                                                            Arabidopsis thaliana
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29.9%; Pred. No. 3.2e-42;
Live 98; Mismatches 205;
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01-SEP-1999; 07-SEP-1999; 10-SEP-1999;

13-OCT-1999; 13-OCT-1999; 13-OCT-1999;

14 OCT 1999 18 OCT 1999 21 OCT 1999

99US-0160980

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10-AUG-1999; 11-AUG-1999; 12-AUG-1999;

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99US-0148565

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08-OCT-1999;
12-OCT-1999;
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rygsvfmthlfgeptifsadpetnrfvlqnegklfecsypasicnllgkhslllmkgslh
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                                                                                                                                                                                    SLYMFLGLNTEVVQKVREEVQEKVEMGMYTPGKGLSMELLDQLKYTGCVIKETLRINPPV
                                                                                                                                                                                                                                                                                                                                                                                                         KNKKKAIMRAFSRDAL--EHYIPVIQQEVKSAIQEWLQKDSCVLVYPEMKKLMFRIAMRI 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KYGCIYKTHLEGNPTVRVMGADNVRQILLGEHKLVSVQWPASVRTILGSDTLSNVHGVQH 133
                       PGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADVFPNKEEFQPERFMSKGLEDGSRF
                                                                                                                                                            lavkfltetplalaqlkee-hekir-amksdsyslewsdyksmpftqcvvnetlrvanii
                                                                                                                                                                                                                                                                                                                                                                  LLGFEP----EQIKTDEQELVEAFEEMIKNLFSLPIDVPFSGLYR-GLRARNFIHSKIEE 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     llllssiaagfllllrrtryr-rmglppgslglpligetfqligayktenpepfiderva
                                                                                ggvfrramtdveikgykipkgwkvfssfravhldpnhfkdartfnpwrwqsnsvttgpsn
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99US-0161405.
99US-0161406.
99US-0161359.
99US-0161360.
99US-0161361.
99US-0161920.
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28-JUL-1999 02-AUG-1999 02-AUG-1999 02-AUG-1999 03-AUG-1999 04-AUG-1999 05-AUG-1999 06-AUG-1999 06-AUG-1999 06-AUG-1999 06-AUG-1999 09-AUG-1999

> 99US-0147302. 99US-0147192. 99US-0147260.

99US-0147303. 99US-0147416. 99US-0147493.

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11-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                         DWF4; cytochrome P450 enzyme; brassinosteroid; 22alpha-hydroxylation; plant phenotype; cell elongation.
                                                                                                                                                                                                                                                                                                                                                                                                                  A cytochrome P450 enzyme designated DWF4.
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(ARIZ-) ARIZONA BOARD OF REGENTS
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; Pred. No. 9.1e-41;
92; Mismatches 194;
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10-SEP-1999

990S-0147935.
990S-0148119.
990S-0148841.
990S-0148844.
990S-0148968.
990S-014975.
990S-014975.
990S-0149929.
990S-015066.
990S-015066.
990S-0151066.
990S-015106.
990S-015106.
990S-0151263.
990S-015126.

16-AUG-1999 17-AUG-1999 18-AUG-1999 20-AUG-1999 20-AUG-1999 20-AUG-1999 23-AUG-1999 23-AUG-1999 25-AUG-1999 26-AUG-1999 27-AUG-1999 27-AUG-1999 27-AUG-1999 31-AUG-1999 31-AUG-1999 31-AUG-1999 31-AUG-1999 31-AUG-1999 31-AUG-1999

28-SEP-1999; 29-SEP-1999; 04-OCT-1999; 05-OCT-1999; 06-OCT-1999; 07-OCT-1999;

08-OCT-1999; 12-OCT-1999; 13-OCT-1999;

18-OCT-1999; 21-OCT-1999; 21-OCT-1999; 21-OCT-1999; 21-OCT-1999; 21-OCT-1999;

> 99US-0159638. 99US-0159584. 99US-0160741.

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99US-01607768.
99US-0160770.
99US-0160814.
99US-0160815.
99US-0160981.
99US-0160989.

13-0CT 1999; 13-0CT 1999; 14-0CT 1999; 14-0CT 1999; 14-0CT 1999; 14-0CT 1999;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated \text{dw} f4 polynucleotide useful for altering the phenotype of plants, for diagnostic assays and in the production of antibodies –
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N-PSDB; AAA59599.
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                                                                                                             392 YSICDTHDVADVFPNKEEFQPERFM-----SKGLEDGSRF--NYIPFGGGSRMCVGKE 442
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                                   FAKVLLKIFLVELTQHCNWILSNGPPTMKTGPTIYPVDNLP 483
laklemavfihhlvlkfnwelaeddg----pfafpfvdfp 502
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Maximum Match 100%
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US-08-882-166A-4
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US-08-201-118-13
US-08-201-118-7
US-08-31-075A-50
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Sequence 6, Appl1	·φ	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 14, Appl		Sequence 11, Appl		: =	Sequence 70, Appl		4.	Sequence by, Appl	•		Sequence 25, Appl	7, A

ALIGNMENTS

RESULT 1 US-08-724-466B-2

; Sequence 2, Application US/08724466B; Patent No. 6063606

GENERAL INFORMATION:

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; STRANDEDNESS: ; TOPOLOGY: lir US-08-724-466B-2
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                                                                                 Matches
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Best Local S
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PRIOR APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767,
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1050863-4344
                                                                                                                                                                                                                                                               TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett.
COMPUTER: COMPAQ, IB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
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ZIP: M5L 1A9
Connery: Canada
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                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                  Local Similarity
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                   1 MGLYTLMVTFLCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQL 60
MGLYTLMVTFLCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQL 60
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                                                                             100.0%; Score 2563; DB 3; ilarity 100.0%; Pred. No. 1.8e-246; Conservative 0; Mismatches 0;
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SYSTEM: MS-DOS 5.1
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                                                                                                           FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
                                   TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    ZIP: M5L 1A9
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
                                                               REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: June 21
                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481
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CITY: Toronto
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RESULT 3
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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-882-164D-2

                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08724466B Patent No. 6063606
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,466B
FILING DATE: October 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 492;
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Best Local
                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                APPLICANT: Petkovich, P. Martin. APPLICANT: Beckett, Barbara R., TITLE OF INVENTION: Retinoid Meinumber of Sequences: 30
                                                                                                                                                                                                                                                                                                                                                                                                    481
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                                                                                                         MEDIUM TYPE: Diskette, 3
COMPUTER: COMPAQ, IBM PC
OPERATING SYSTEM: MS-DOS
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                                                                                                                                                                  CITY: Toronto
ZIP: M5L 1A9
COUNTRY: Canada
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STREET: Bo
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Pred. No. 1.8e-246;
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US-08-882-164D-4
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 67.8%; Score 1738; DB 3; Best Local Similarity 68.0%; Pred. No. 2.2e-164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                   Sequence 4, Application US/08882164D Patent No. 6306624
                                                                                                                                                                       GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
                                                                                              APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                            297
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                                        STREET: Box 25
CITY: Toronto
STATE: Ontario
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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             COUNTRY: Canada ZIP: M5L 1A9
                                                                                   ADDRESSEE: Blake,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWPASVRTIL
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                                                                                                                                                                                                                                                                                    GPTIYPVDNLPTKFTSY 489
                                                                                                                                                                                                                                                                                                                                                                                   YPEMKKLMFRIAMRIILIGFEPEQIKTD---EQELVEAFEEMIKNLFSLPIDVPFSGLYRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVRTIL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                            LLFGGHETTASAATSLITYLGLYPHYLQKVREELKSKGLLCKSNQDNKLDMEILEQLKYI 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLFGGHETTASTATSLVMFLGLNTEVVQKVREEVQEKVEMGMYTPGKGLSMELLDQLKYT 352
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                                                                                                                                                                                                                                                                        SPTVYPVDNLPARFTHF
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                                        Ontario
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TOPOLOGY: US-08-882-164D-4
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage COMPUTER: COMPAQ, IBM PC compatible OPERATING SYSTEM: MS-DOS 5.1 SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/
FILING DATE: June 25, 1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                        417
                                                                    413 ERFMSKGLEDGSRFNYIPFGGGSRMCVGKEFAKVLLKIFLVELTQHCNWILSNGPPTMKT 472
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477 SPTVYPVDNLPARFTHF 493
                          473 GPTIYPVDNLPTKFTSY 489
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                                                                                                              GCVIKETLRINPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADVFPNKEEEFQP
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                                                                                                                                                                      LLFGGHETTASAATSLITYLGLYPHVLQKVREELKSKGLLCKSNQDNKLDMEILEQLKYI
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(416) 863-26E
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US-08-882-164D-32

Sequence 32, Application US/08882164D Patent No. 6306624

RESULT

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Best Local Similarity
Matches 336; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: Canada
COUNTRY: Canada
ZIP: M5L 1A9
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/
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NAME: Hunt, John C.

REGISTRATION NUMBER: 36,424

REFERENCE/DOCKET NUMBER: 5076

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 863-4344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/882,160
FILING DATE: June 25, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein
                         354 CVIKETLRINPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADVFPNKEEFQPE 413
                                                                                                              294 LFGGHETTASTATSLVMFLGLNTEVVQKVREEVQEKVEMGMYTPGKGLSMELLDQLKYTG 353
                                                                                                                                                                        238 KARNLIHARIEENIRAKIRRLQATEPDGGCKDALQLLIEHSWERGERLDMQALKQSSTEL
                                                                                                                                                                                                      235 RARNFIHSKIEENIRKKIQD-DDNENEQKYKDALQLLIENSRRSDEPFSLQAMKEAATEL 293
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CORRESPONDENCE ADDRESS:
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TOPOLOGY: linear
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CVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADIFTNKEEFNPD
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                                                                                                                                                                                                                                                                                       YPEMKKLMFRIAMRILLGFEPEQI--KTDEQELVEAFEEMIKNLFSLPIDVPFSGLYRGL 234
                                                                                                                                                                                                                                                                                                                                                   GAGCLSNLHDSSHKQRKKVIMQAFSREALQCYVLVIAEEVSSCLEQWL---SCGERGLLV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVRTIL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGLYTLMVTELCTIVLPVLLELAAVKLWEMLMIRRVDDNCRSPLPPGTMGLPFIGETLQL 60
                                                                                     LFGGHETTASAATSLITYLGLYPHVLQKVREEIKSKGLLCKSNQDNKLDMETLEQLKYIG
                                                                                                                                                                                                                                                                                                                                                                                                                                          VLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVHWPASVRTIL 120
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Commerce Court West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.7%; Score 1734; DB 4; Length 497; 67.7%; Pred. No. 5.4e-164; tive 61; Mismatches 89; Indels 1
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                                                                                                                                                                                                                                                                                      Best Local Similarity Matches 145; Conserv
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22040 V...
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 27-MAR-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SZEKERES, MIKLOS
APPLICANT: ALTMANN, THOMAS
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING CYTOCHROME
TITLE OF INVENTION: P450-TYPE PROTEINS INVOLVED IN THE BRASSINOSTEROID SYNTHESI
 182 LMSFDPGEWSESLRKEYLLVIEGF--
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                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 472 amino acids
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                                                                                                                                                             74 KYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVRTILGSDTLSNVHGVQH 133
                                                                                                                                                                                                                                               19 LLFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQLI-----LQRRKFLRMKRQ 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     478 PTVYPVDNLPARFTYF 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: SVENSSON, LEONARD R. REGISTRATION NUMBER: 30,330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
SOFTWARE: Patenti
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                               LLGFEP----EQIKTDEQELVEAFEEMIKNLFSLPIDVPFSGLYR-GLRARNFIHSKIEE 246
                                                                 K-RMHSLTMSFANSSIIKDHLMLDIDRLVRFNLDSW----SSRVLLMEEAKKITFELTVKQ 181
                                                                                                   KNKKKAIMRAFSRDAL--EHYIPVIQQEVKSAIQEWLQKDSCVLVYPEMKKLMFRIAMRI 191
                                                                                                                                      RYGSVFMTHLFGEPTIFSADPETNRFVLQNEGKLFECSYPASICNLLGKHSLLLMKGSLH 125
                                                                                                                                                                                                            LLLLSSIAAGFLLLLRRTRYR-RMGLPPGSLGLPLIGETFQLIGAYKTENPEPFIDERVA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFIVPHPEDASRFSFIPFGGGLRSCVGKEFAKILLKIFTVELARHCDWQLLNGPPTMKTS 477
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5. 5952545
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SZEKERES, MIKLOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/622,166A
                                                                                                                                                                                                                                                                                     98;
                                                                                                                                                                                                                                                                                 Score 552.5; DB 2;
Pred. No. 1.7e-46;
98; Mismatches 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0147-0153P
-FSLPL-FSTTYRKAIQARRKVAEALTV
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                                                                                                                                                                                                                                                                                                                    Length 472;
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                                                 Query Match 21.6%; Score 552.5; DB 2; Best Local Similarity 29.9%; Pred. No. 1.7e-46; Matches 145; Conservative 98; Mismatches 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: KONCZ,
APPLICANT: MATHUR
                                                                                                                                                                                                                                          TELEFAX: (703) 205-80 TELEX: 248345 INFORMATION FOR SEQ ID NO:
                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING CYTOCHROME
TITLE OF INVENTION: P450-TYPE PROTEINS INVOLVED IN THE BRASSINOSTEROID SYNTHESIS
NUMBER OF SEQUENCES: 4
CORRESSPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         462 PIFVK 466
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ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: P.O. Box 7. CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0
FILING DATE: 27-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
              19 LLFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQLI-----LQRRKFLRMKRQ 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSYVR 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VFTPFGGGPRLCPGYELARVALSVFLHRLVTGFSWV-----PAEQDKLVFFPTTRTQKRY 461
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ALTMANN, THOMAS
                                                                                                                                                                                                                                                                     (703) 205-8050
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Length
                                                      Indels
                                                      37;
                                                    Gaps
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                                                                                                                                                                                                              Matches 123;
                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Carraway, Daniel T
APPLICANT: Smeltzer, Richard H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chiang, Vincent L APPLICANT: Carraway, Daniel
                                                                                                                                                                                                                                                                                                                                    LENGTH: 511
TYPE: PRT
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                                                                                                                                           19 IIPLLLLLGLVS-----RLRQ-----RLPYPPGPKGLPVIGNMLMMDQLTHRGLAKLAKQ 68
                                                                                                                                                                          15 VLPVLLFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQLILQRRKFLRMKRQK 74
     PFWRQMRKLCVMKLFSRKRAESW-ESVRDEVDSAVRVVASNIGSTVNIGELVFALTKNIT 186
                                                                                                       YGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVR----TILGSDTLSNVHG 130
                                      -VQHKNKKKAIMRAFSRDALEHYIPVIQQEVKSAIQEWLQK-DSCV----LVYPEMKKLM 184
                                                                        YGGLFHLKMGFLHMVAVSTPDMARQVLQVQDNIFSNR-PATIAISYLTYDRADMAFAHYG
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                91;
                                                                                                                                                                                                                  Mismatches
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TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
FILE REFERENCE: 50617
CURRENT PAPLICATION NUMBER: US/08/991,677A
CURRENT FILING DATE: 1997-12-16
EARLIER APPLICATION NUMBER: US 60/033,381
EARLIER FILING DATE: 1996-12-16
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 K-RMHSLTMSFANSSIIKDHLMLDIDRLVRFNLDSW---SSRVLLMEEAKKITFELTVKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VFTPFGGGPRLCPGYELARVALSVFLHRLVTGFSWV-----PAEQDKLVFFPTTRTQKRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLVMFLGLNTEVVQKVREEVQEKVEMGMYTPGKGLSMELLDQLKYTGCVIKETLRINPPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLGFEP----EQIKTDEQELVEAFEEMIKNLFSLPIDVPFSGLYR-GLRARNFIHSKIEE 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RYGSVFMTHLFGEPTIFSADPETNRFVLQNEGKLFECSYPASICNLLGKHSLLLMKGSLH
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                13.4%; Score 343; DB 4;
25.5%; Pred. No. 1.4e-25;
                                               Length 511;
Indels
56;
Gaps
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; TOPOLOGY: 1; MOLECULE TYPE: US-08-201-118-3
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US-08-201-118-3
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                                                                                                                    TELEFAX: (415) 326-24 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: CLO
TITLE OF INVENTION: DNA.
TITLE OF INVENTION: SUB-
TITLE OF INVENTION: SUB-
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                             NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   474 PDG
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                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0
FILING DATE: 22-FEB-1994
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CITY: Palo Alto
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                              (415) 326-2422
(415) 326-2422
TD NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GOLDSTEIN, JOYCE A.
ROMKES-SPARKS, Marjorie
PONTION: CLONING AND EXPRESSION OF COMPLEMENTARY
VENTION: DNAS FOR MULTIPLE MEMBERS OF THE HUMAN (
                              SS: single
linear
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US-08-201-118-9
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Best Local
APPLICATION NUMBER: US/08/
FILING DATE: 22-FEB-1994
CCLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                              ZIP: 94301
COMPUTER READABLE FORM:
TYPE: Floppy disk
                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: GOLDSTEIN, JOYC APPLICANT: ROMKES-SPARKS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
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                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                               STREET: 379 Lytton Avenue CITY: Palo Alto
                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 9, AFE
No. 5786191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YSICDT-HDVADVFPNKEEFQPERFMSKGLEDGSRFN----YIPFGGGSRMCVGKEFAKV 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISKSLTNLSKVYGPVFTLYFGLKPIVVLHGYEAVKEALIDLGEEFSGRGIFPLAERANRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISLTSVLHDNKE-FPNPEMFDPHHF----LDEGGNFKKSKYFMPFSAGKRICVGEALAGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HNQPSEFTIESLENTAVDLFGAGTETTSTTLRYALLLLKHPEVTAKVQEEIERVI----
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                                                                                                                                                                                                                                                                              California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08201118
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CLONING AND EXPRESSION OF COMPLEMENTARY
DNAS FOR MULTIPLE MEMBERS OF THE HUMAN
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                                                    US 07/864,962
                                                                                                                    US/08/201,118
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Pred. No. 2.9e-25;
                                                                                                                                                        Version #1.25
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US-08-338-821B-3
; Sequence 3, Application US/08238821B
; Patent No. 5912120
; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
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                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                         APPLICANT: GOLDSTEIN, JOYCE A.
APPLICANT: ROMKES-SPARKS, MATJORIE
APPLICANT: DE MORAIS, SONIA M.F.
TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF
TITLE OF INVENTION: CTFOCHROME P450 2C19: THE PRINCIPAL
TITLE OF INVENTION: MEPHENYTOIN METABOLISM
NUMBER OF SEQUENCES: 61
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Local Similarity 26.9%; Pred. No. 2.9e-25;
No. 2.9e-25; Mismatches 218;
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US-08-238-821B-3
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Best Local Similarity
Matches 139; Conserv
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INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
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REGISTRATION NUMBER: 37,505
REFERENCE, DOCKET NUMBER: 155
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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447 LLKIFLYELTQHCNWILSNGPPTMKTGPTIYPVDNLP 483
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                                            ISLTSVLHDNKE-FPNPEMFDPHHF----LDEGGNFKKSKYFMPFSAGKRICVGEALAGM
                                                                                   YSICDT-HDVADVFPNKEEFQPERFMSKGLEDGSRFN----YIPFGGGSRMCVGKEFAKV 446
                                                                                                                                    ---GRNRSPCMQDRSHMPYTDAVVHEVQRYLDLLPTSLPHAVTCDIKFRNYLIPKGTTIL
                                                                                                                                                                    YTPGKGLS--MELLDQLKYTGCVIKETLRINPPVPGGFRVALK-TFELNGYQIPKGWNVI 391
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Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (650) 326-2422 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATA:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,962
APPLICATION NUMBER: 1992
APR-1992
APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 1
MOLECULE TYPE:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 0
FILING DATE: 22-FEB-1994
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181 KKLMFRIAMRILLGFEPEQI------KTDEQ--ELVEAFEEMIK------N 217
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                                                         110 -----FGIVFSNGKKWKEIRRFSLMTLRNF-----GMGKRSIEDRVQEEARCLVEELR 157
                                                                                               122 SDTLSNVHGVQHKNKKK-AIMRAFSRDALEHYIPVIQQEVKSAIQEWLQKDSCVLVYPEM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 06-MAY-1994
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                           64 RRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQIL--LGEHKLVSVQWPASVRTILG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE:
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                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                      5 TLMVTFLCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQL-ILQ 63
                                                                                                                                      ISKSLTNLSKYYGPVFTLYFGLKPIVVLHGYEAVKEALIDLGEEFSGRGIFPLAERANRG 109
                                                                                                                                                                                                                   SLVVLVLC---LSCLLLLS---LWR-----QSSGRGKLPPGPTPLPVIGNILQIGIKD 49
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5. 5912120
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amino acid
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ROMKES-SPARKS, MARJORIE
DE MORAIS, SONIA M.F.
JENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
JENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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Pred. No. 2.9e-25;
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                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ROMKES-SPARKS, Marjorie
APPLICANT: DE MORAIS, SONIA M.F.
TITLE OF INVENTION: CLOUING, EXPRESSION AND DIAGNOSIS OF HUMAN
TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT
TITLE OF INVENTION: OF S-MEPHYNYTOIN METABOLISM
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 06-MAY-1
PRIOR APPLICATION DATA:
                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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    MOLECULE TYPE:
                                                                                                                                                                                                                                                      FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                              REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM:
                    TOPOLOGY:
                                       STRANDEDNESS:
                                                                                                                                                         TELEPHONE:
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                    linear
                                                                                                                                                         (415) 326-2400
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                     APPLICANT: DE MORAIS, SONIA M.F.
TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT
TITLE OF INVENTION: OF S-MEPHYNYTOIN METABOLISM
NUMBER OF SEQUENCES: 61
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: 9C-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                          FILING DATE
                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISKSLTNLSKVYGPVFTLYFGLKPIVVLHGYEAVKEALIDLGEEFSGRGIFPLAERANRG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLVVLVLC---LSCLLLLS---LWR-----QSSGRGKLPPGPTPLPVIGNILQIGIKD 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLKIFLVELTQHCNWILSNGPPTMKTGPTIYPVDNLP 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NFSPIIDY-FPGTHNKL-LKNVAFMKSYILEKVKEHQESMDMNNPQDFIDCFLMKMEKEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELFLFLTSILQNFNLKSLVDPKNLDTTPVVNGFASVP 480
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                                                                                                                                                                    Floppy disk
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 US 08/238,821
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; Pred. No. 2.9e-25;
83; Mismatches 218;
                                                                                                                 Version
                                                                                                                 #1.25
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US-09-091-432-2
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REFERENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 490 amino acids
  GENERAL INFORMATION:
APPLICANT: Chapple, Clint
TITLE OF INVENTION: A Method For Regulation
FILE REFERENCE: 7024-325
                                                                             Sequence 2, Application US/09091432 Patent No. 5981837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 139;
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Best Local Similarity
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 06-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0)
FILING DATE: 22-FEB-1994
PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                              332 ---GRNRSPCMQDRSHMPYTDAVVHEVQRYIDLLPTSLPHAVTCDIKFRNYLIPKGTTIL
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                        YSICDT-HDVADVFPNKEEFQPERFMSKGLEDGSRFN----YIPFGGGSRMCVGKEFAKV 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                             HNQPSEFTIESLENTAVDLFGAGTETTSTTLRYALLLLKHPEVTAKVQEEIERVI----
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CURRENT APPLICATION NUMBER: US/09/091,432
CURRENT FILING DATE: 1998-06-18
EARLIER APPLICATION NUMBER: PCT/US96/20094
EARLIER FILING DATE: 1996-12-19
EARLIER FILING DATE: 1996-12-19
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: US 60/003,119
EARLIER APPLICATION NUMBER: US 60/013,388
EARLIER FILING DATE: 1995-03-14
UNMBER OF SEQ ID NOS: 3
SOFTWARE: Microsoft Word 2.0C
SEQ ID NO 2
LENGTH: 520
TYPE: PRT
ORGANISM: Artificial
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Best Local Similarity
Matches 125; Conserv
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                                                                                  178
466 YALDLAVAHIL-HCFTWKLPDG 486
                                         446 VLLKIFLVELTQHC-NWILSNG 466
                                                                                                                                                                                                      332 MGMYTPGKGLSMEL----LDQLKYTGCVIKETLRINPPVPGGFRVALKTFELNGYQIPKG 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 MAFAHYGPFWRQMRKVCVMKVFSRKRAESW-----ASVRDEVDKMVRSVSCNVGKPINVG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124
                                                                                                                                                                                                                                                                     295 TADLQNSIKLTRDNIKAIIMDVMFGGTETVASAIEWALTELLRSPEDLKRVQQELAEVV-
                                                                                                                                                                                                                                                                                                280 PFSLQ------AMKEAATELLFGGHETTASTATSLYMFLGLNTEVVQKVREEVQEKVE 331
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                                                                                                                                                                                                                                                                                                                                                                                                           232 ---RGLRARN----FIHSKIEENIRKK-----IQDDDNENEQKYKDALQLLIENSRRSDE 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 KKYGGLCHLRMGFLHMYA-----VSSPEVARQVLQVQDSVFSNR-PATIAISYLTYDRAD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 QKYG--CIYK---THLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVR----TILGSD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 SLVIVVSLF-----IFISFITRRRRPPYPPGPRGWPIIGNMLMMDQLTHRGLANLA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 TIVLPVLLFLAAVKLWEMIMIRRVDPNCRSPLPPGTMGLPFIGETLQLILQRRKFLRMKR 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQIFALTRNITYRAAFGSACEK----GQDEFIRILQEFSKLFGAFNVADFIPYFGWIDPQG 234
                                                                                                                                                                              -----GLDRRVEESDIEKLTYLKCTLKETLRMHPPIPLLLHETAEDTSIDGFFIPKK
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Search completed: November 6, 2001, 13:27:04 Job time: 9917 sec

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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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1: pir1:*
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ALIGNMENTS

cytochrome P450 - Synechocystis sp. (st N;Alternate names: protein slr0574 N;Contains: oxidoreductase (BC 1.-.-)

(strain

PCC 6803)

RESULT S75761

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C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 c;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase F;251-413/Domain: cytochrome P450 homology <P45> F;391/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: $75761
R;Kaneko, T.; Sato,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
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                                                                             IDVPFSGLYRGLRARNFIHSKIEENIRKKIQDDDNENEQKYKDALQLLIENSRRSDEPFS
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submitted to the EMBL Data Library, May 1995
A; Reference number: S55379
A; Reference number: S55379
A; Rocession: S579
A; Cross-references: EMBL:X87367; NID:g853718; PIDN:CAA60793.1; PID:g853719
C; Genetics:
A; Gene: CYP90
C; Genetics: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology
C; Keywords: Chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase; F; 275-440/Domain: cytochrome P450 homology <P45>
F; 418/Binding site: heme iron (Cys) (axial ligand) #status predicted
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N;Contains: oxidoreductase (EC 1.-.-)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: S55379
R;Szekeres, M; Nemeth, K.; Koncz, Z.; Nagy, F.; Koncz, C.
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                                                         VFTPFGGGPRLCPGYELARVALSVFLHRLVTGFSWV-----PAEQDKLVFFPTTRTQKRY
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                                                                                                                                                                                                                                                                                                                                                                                    SLVMFLGLNTEVVQKVREEVQEKVEMGMYTPGKGLSMELLDQLKYTGCVIKETLRINPPV | ! ! | | | | | | | ; ; | | | ; | | | ; ; | | ; | ; | | ; | ; | | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVMKR-REEEEGAERKKDMLAALL----AADDGFSDEEIVDFLVALLVAGYETTSTIMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K-RMHSLTMSFANSSIIKDHLMLDIDRLVRFNLDSW---SSRVLLMEEAKKITFELTVKQ
TSYVR
                                                                                                                              NYIPFGGGSRMCVGKEFAKVLLKIFLVELTQHCNWILSNGPPTMKTGPTIYPVDNLPTKF
                                                                                                                                                                                                   GGVFRRAMTDVEIKGYKIPKGWKVFSSFRAVHLDPNHFKDARTFNPWRWQSNSVTTGPSN
                                                                                                                                                                                                                                                                                                                                        LAVKFLTETPLALAQLKEE-HEKIR-AMKSDSYSLEWSDYKSMPFTQCVVNETLRVANII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIRKKIQDDDNENEQKYKDALQLLIENSRRSDEPFSLQAMKEAATELLFGGHETTASTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LMSFDPGEWSESLRKEYLLVIEGF-----FSLPLPL-FSTTYRKAIQARRKVAEALTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RYGSVFMTHLFGEPTIFSADPETNRFVLQNEGKLFECSYPASICNLLGKHSLLLMKGSLH 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVRTILGSDTLSNVHGVQH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQLI-----LQRRKFLRMKRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KNKKKAIMRAFSRDAL--EHYIPVIQQEVKSAIQEWLQKDSCVLVYPEMKKLMFRIAMRI 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLLLSSIAAGFLLLLRRTRYR-RMGLPPGSLGLPLIGETFQLIGAYKTENPEPFIDERVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VFPNKEEFQPERFMSKGLEDGSR-----FNYIPFGGGSRMCVGKEFAKVLLKIFLYELTQ 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QFDWTLLPGQNLELVVTPSPRPKDNLRVKLHS 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HCNWILSNGPP-TMKTGPTIYPVDNLPTKFTS
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491
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e EMBL Data Library, May 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 552.5; DB 1;
Pred. No. 2e-29;
8; Mismatches 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             488
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C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 C;Keywords: heme; iron; metalloprotein F;432/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-485 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shea, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999 White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter N;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID:20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable cytochrome P450 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change C;Accession: A84859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: At2g42850
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Best Local
  458
                                                                                                                                                                                                                                                                                                                                                                             236 KARLEIETFLVGKVREKRREMEKEGAEKPNTTLFSRLVE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 SLYRSAKVLTFTVVFECLYG-----IKV-EIGMLEVFERVLEGVFALPVEFPCSKFARAK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 VRTILGSDTLSNVHGVQHKNKKKAIMRAFSRDALEHYIPVIQQEVKSAIQ-EWLQKDSCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 KAQKSNRVFEDFVNPRIIKHGNIFKTRIMGSPTIVVNGAEANRLILSNEFSLVVSSWPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
mes 143; Conserv
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VYPDETISMDPLPFPSLGMPIKISPKV
                                            SNGPPTMKTGPTIYPVDNLPTKFTSYV 490
                                                                                         FQDPMSFDPTRF-DKPIQ---AYTYLPFGGGPRLCAGHQLAKISILVFMHFVVTGFDWSL
                                                                                                                                      FPNKEEFQPERFMSKGLEDGSRFNYIPFGGGSRMCVGKEFAKVLLKIFLVELTQHCNWIL
                                                                                                                                                                                  EDVKKMKYSWQVVRETMRLSPPIFGSFRKAVADIDYGGYTIPKGWKILWTTYGTHYNPEI
                                                                                                                                                                                                                                 ELLDQLKYTGCVIKETLRINPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADV 403
                                                                                                                                                                                                                                                                                 EVVDNMVLLVFAAHDTTSYAMSMTFKMLAQHPTCRDTLLQEHAQIKANKG----EGEYLTV
                                                                                                                                                                                                                                                                                                                           ------LLFGGHETTASTATSLVMFLGLNTEVVQK-VREEVQEKVEMGMYTPGKGLSM 343
                                                                                                                                                                                                                                                                                                                                                                                                                       RARNFIHSKIEENIRKKIODDDNENEOKYKDAL-OLLIENSRRSDEPFSLQAMKEAATE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVYPEMKKLMFRIAMRILLGFEPEQIKTDEQELVEAFEEMIKNLFSLPIDVPFSGLYRGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.8%; Score 532.5; DB 2; ilarity 28.2%; Pred. No. 4.5e-28; Conservative 101; Mismatches 214;
484
                                                                                                                                                                                                                                                                                                                                                                             -----ELIKGVITEE
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RESULT T02739

probable

cytochrome

P450

At2g29090 [imported] -

Arabidopsis thaliana

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K;KOUNSLEY, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC T9I4 genomic sequence.
A;Reference number: Z14710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: cytochrome P450 homolog T914.17 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 C;Accession: T02739; D84692 R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:AC005315; NID:g3461834; PID:g3461849
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fuji
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; T
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.;
Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 2
A;Introns: 80/2; 187/3; 238/3; 321/3; 351/3; 413/3; 453/2
C;Superfamily: Synechocystis cytochrome P450 slr0574; cyto
F;291-453/Domain: cytochrome P450 homology <P45>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-482 <R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487 A;Accession: D84692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: translated from GB/EMBL/DDBL
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A; Residues: 1-482 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNVHGVQHKNKKKAIMRAFSRDALEHYIPVIQQEVKSAIQEWL-QKDSCVLVYPEMKKLM 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt MVTFLCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQLILQR-R}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVRTILGSDTL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LITLTIVVVVVVLLF----KWWLHWKEQRL-----RLPPGSMGLPYIGETLRLYTENPN
IRVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FFHQGPYHSTLKRLVQSSFMPSALRPTVSHIELLVLQTLSSWTSQKSINTLEY--MKRYA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFFATRONKYGDIFKTHILGCPCVMISSPEAARMVLVSKAHLFKPTYPPSKERMIGPEAL
                                        TKFT 487
                                                                                                                                                            VLSFTFREAVQDVEYDGYLIPKGWKVLPLFRRIHHSSEFFPDPEKFDPSRF----
                                                                                                                                                                               PVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADVFPNKEEFQPERFMSKGLEDGS 424
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                                                                                 KPYTYMPFGNGVHSCPGSELAKLEMLILLHHLTTSFRWEVIGDEEGIQYGPFPVPKKGLP
                                                                                                                   R-FNYIPFGGGSRMCVGKEFAKVLLKIFLVELTQHCNWILSNGPPTMKTGPTIYPVDNLP 483
                                                                                                                                                                                                                                             LTWLLKYLHDHPNLLQEVSRE-QFSIRQKIKKENRRISWEDTRKMPLTTRVIQETLRAAS
                                                                                                                                                                                                                                                                                    ATSLVMFLGLNTEVVQKVREEVQEKVEMGMYTPGKGLSMELLDQLKYTGCVIKETLRINP
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Pred. No. 4.1e-26;
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steroid 22-alpha-hydroxylase (DWF4) - Arabidopsis thaliana N;Alternate names: protein T3A5.40 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 16-Feb-2001 C;Accession: T46143 C;Accession: T46143 R;Bloecker, H.; Mewes, H.W.; Mayer, K.F.X.; Lemcke, K.; Schueller, C.; Quet: submitted to the Protein Sequence Database, December 1999
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T46143
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A; Experimental source: Cultivar Columbia; BAC clone T3A5
C; Genetics:
A; Map position: 3
A; Map position: 3
A; Note: T3A5.40
C; Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome C; Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome C; Keywords: heme; iron; metalloprotein
F; 462/Binding site: heme iron (Cys) (axial ligand) #status predic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-513 <BLO>
A; Cross references: EMBL: AL132979
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A; Accession: T46143
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                                                                              467
                                                                                                                                                                                                                                                                                                                  291 LKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---LQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVRT 118
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                                                                                                                                                                                                                                   LG----ESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVL
                                                                                                                                                                                                                                                                         MGMYTPGKGLSMELLDQLKYTGCVIKETLRINPPVPGGFRVALKTFELNGYQIPKGWNVI
                                                                                                                                                                                                                                                                                                                                                   ----PFSLQAMKEAATELLFGGHETTASTATSLVMFLGLNTEVVQKVREE----VQEKVE
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                                                                              LAKLEMAVFIHHLVLKFNWELAEDDK--
                                                                                                                 FAKVLLKIFLVELTQHCNWILSNGPPTMKTGPTIYPVDNLP 483
                                                                                                                                                                                              YSICDTHDVADVFPNKEEFQPERFM-----
                                                                                                                                                       PVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSGSGSFSTWGNNYMPFGGGPRLCAGSE
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Pred. No. 4.5e-26;
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1999
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cytochrome P450 - Arabidops N; Alternate names: protein N; Contains: oxidoreductase

Arabidopsis thaliana : protein T18B16.200; reductase (EC 1.-.-.-)

protein T5K18.

th

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A;Molecule type: DNA
A;Residues: 131-457 <BBW>
A;Cross-references: EMBL:ALIO22580
A;Cross-references: cultivar Columbia; BAC clone T5K18
C;Genetics:
A;Map position: 4
A;Introns: 67/2; 173/3; 302/3; 358/1; 393/3
A;Note: T18B16.200; T5K18.10
C;Superfamily: Synechocystis cytochrome P450 slr0574; cyt
C;Keywords: chromoprotein; electron transfer; heme; iron;
F;272-433/Domain: cytochrome P450 homology <P45>
C;Accession: T07859
R;Bishop, G.J.; Harrisc
Plant Cell 8, 959-969,
                                        cytochrome P450 homolog - tomato
c;Species: Lycopersicon esculentum (tomato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999
C;Accession: T07859
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A; Cross references: EMBL:AL021687
A; Experimental source: cultivar Columbia; BAC clone T18B16
R; Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.;
submitted to the Protein Sequence Database, April 1998
A; Reference number: Z15453
A; Accession: T05806
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A; Accession: T04444
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                         GGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADVFPNKEEFQPERFMSKGLEDGSRFN 427
                                                                                                                                                                                                                                                                                                                                                  LAENPNVLEAVTEEQMAIRKDKEE-----GESLTWGDTKKMPLTSRVIQETLRVASILS
                                                                                                                                                                                                                                    -YIPFGGGSRMCVGKEFAKVLLKIFLVELT 456
                                                                                                                                                                                                                                                                                                                                                                                          LGLNTEVVQKVREEV----QEKVEMGMYTPGKGLSMELLDQLKYTGCVIKETLRINPPVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----KDEVLYREDLKRCYYILEKGYNSMPVNLPGTLFHKSMKAR----KELSQILARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127;
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Harrison, K.; Jones, J.D.
59-969, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 489.5; DB Pred. No. 3e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S.; Borkova, D.; Ansorge, W.; Bancroft, I.; Database, April 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                 429
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heme; iron; monooxygenase; oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183;
                                                    #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T5K18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 457;
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                                                                                                                                                                                                                                                                          -EVAPKPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
        A;Map position: 4
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 C;Keywords: heme; iron; metalloprotein
E;396/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                    C;Accession: D85429
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                 cytochrome P450 like protein [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) Copate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Apr-2001
                                                                                       A; Gene: AT4g36380
                                                                                                             C; Genetics
                                                                                                                              A; Cross-references:
                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-457 <STO>
                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                         A; Title: Sequence and analysis of chromosome A; Reference number: A85001; MUID: 20083488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Дb
                                                                                                                                                                                                           A; Accession: D85429
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GB:NC_001268; NID:g7270586; PIDN:CAB80304.1; GSPDB:GN00140

homology

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of

the plant Arabidopsis thaliana

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A:Gene: dwarf
C:Superfamily: Synechocystis cytochrome P450 slr0574;
F;273-436/Domain: cytochrome P450 homology <P45>
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A;Molecule type: mRNA
A;Residues: 1-464 <BISS
A;Cross-references: EMBL:U54770; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U54770; NID:g1421740; A;Experimental source: strain GCR758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: The tomato Dwarf gene isolated by heterologous A; Reference number: Z16181; MUID:96266705 A; Accession: T07859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
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                                                                                                                                                                                                                                                                                                          251 KIQDD-----DNENEQKYKDALQLLIENSRRSDEPFSLQAMKEAATELLFGGHETTASTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 LFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQLILQRRKFLRMKRQKYGCIY
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QNSF--LVFGGGTRQCPGKELGVAEISTFLHYFVTKYRWEEIGGDKLMK
                                            GSRFNYIPFGGGSRMCVGKEFAKVLLKIFLVELTQHCNWILSNGPPTMK 471
                                                                                                                                                                                                                      TSLVMFLGLNTEVVQKVREE----VQEKVEMGMYTPGKGLSMELLDQLKYTGCVIKETLRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMRAFS----RDALEHYIPVIQQEVKSAIQEWLQKDSCVLVYPEMKKLMFRIAMRILLGF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVRTILGSDTLSNVHGVQHKNKKKA
                                                                                      ATIVNGVLRKTTQDMEINGYIIPKGWRIYVYTRELNYDPRLYPDPYSFNPWRWMDKSLEH
                                                                                                                                  NPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADVFPNKEEFQPERFMSKGLED
                                                                                                                                                                              MMAVKYLHDHPKVLEELRKEHMAIREKKK-----PEDPIDYNDYRSMRFTRAVILETSRL
                                                                                                                                                                                                                                                                  EIQHDMLGYLMNEEATRFK-----LTDDE-----MIDLITILYSGYETVSTTS
                                                                                                                                                                                                                                                                                                                                                         ESTSL----AQEFMSEFFNLVLGTLSLPINLPNTNYHRGFQARKIIVNLLRTLIEERRASK
                                                                                                                                                                                                                                                                                                                                                                                              EPEQIKTDEQELVEAFEEMIKNLFSLPIDVPFSGLYRGLRAR----NFIHSKIEE-NIRK
                                                                                                                                                                                                                                                                                                                                                                                                                                             LLSLISPTMIRDQL---LPKIDEFMRSHLTNWDNK--VIDIQEKTNKMAFLSSLKQIAGI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSHILGCPTIVSMDSELNRYILVNEAKGLVPGYPQSMIDILGKCNIAAVNGSAHKYMRGA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133;
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Pred. No. 1.1e-
90; Mismatches
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, X.; Liu, S.X.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719

A; Residues: 1-490 <STO>
A; Map position: 1
C; Genetics: GB:AE005172; NID:g2388581; PIDN:AAB71462.1; GSPDB:GN00141
C; Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIKNLFSLPIDVPFSGLYRGLRARNFIHSKIEENIRKKIQDDD--NENEQKYKDALQLLI 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QILLGEHKLVSV-QWPASVRTILGSDTLSNVHGVQHKNKKKAIMRAFSRDALEHYIPVIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIKGLICIPIKFPGTRLYKSLKAK----ERLIKMVKKVVEERQVAMTTTSPANDVVDVLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QEVKSAI----QEWLQKDSCVLVYPEMKKLMFRIAMRILLGFEPEQIKTDEQELVEAFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVEMGMYTPGKGLSMELLDQLKYTGC-----VIKETLRINPPVPGGFRVALKTFELN 380
                                                       RSPLPPGTMGLPFIGETLQLILQRR-----KFLRMKRQKYG--CIYKTHLFGNPTVRVMG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEFAKVLLKIFLVELTQHCNWILSNGP----PTMK 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt GYLIPKGWCVLASFISVHMDEDIYDNPYQFDPWRWDRINGSANSSICFTPFGGGQRLCPG}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NMEM-----KRRKLELGEEYKWTDYMSLSFTQNVINETLRMANIINGVWRKALKDVEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RDGGDSEKQSQPSDFVSGK--IVEMMIPGEETMPTAMTLAVKFLSDNPVALAKL---VEE
  RHYLPPGDLGWPFIGNMLSFLRAFKTSDPDSFTRTLIKRYGPKGIYKAHMFGNPSIIVTT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.8%;
Similarity 28.6%;
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                                                                                                               Conservative
                                                                                                                                       17.6%;
27.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90; Mismatches
                                                                                                               84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 455; DB 2;
Pred. No. 6.1e-23;
                                                                                                               Score 450; DB 2;
Pred. No. 1.4e-22;
4; Mismatches 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185;
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                                                                                                                                                                    Length 490
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-489 <STO>
A;Cross-references: GB:AE002093; NID:g3831452; PIDN:AAC69934.1;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Talleuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ven Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable cytochrome P450 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
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A;Map position: 2
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome
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Best Local Similarity
Matches 130; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450 SIFLHHFLLKYQVKRSNPECPVMYLPHTRPTDN 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               449 KIFLVELTQHCNWILSNGPPTMKTGPTIYPVDN 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392 KVLTWFRDVHIDPEVFPDPRKFDPARWDNGFVPKAGAF--LPFGAGSHLCPGNDLAKLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389 NYIYSICDTHDVADVFPNKEEFQPERFMSKGLEDGSRFNYIPFGGGSRMCVGKEFAKVLL
  229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MILKSRPEGOKGLSLKETRKMEFLSOVVDETLRVITFSLTAFREAKTDVEMNGYLIPKGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLIENSRRSDEPFSLQAMKEAATELLFGGHETTASTATSLVMFLGLNTEVVQKVREEVQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALNYGVRAMAVNIPGFAYHRALKARKTLVAAFQSIVTER----RNQRKQNILSNKKDMLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMIKNLFSLPIDVPFSGLYRGLRARNFIHSKIEENIRKKIQDDDNENEQKY----KDALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPVIQQEVKSAIQEWLQKDSCVLVYPEMKKLMFRIAMRILLGFEPEQIKTDEQELVEAFE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDTCRRVLTDDDAF-KPGWPTSTMELIGRKSFVGISFEEHKRLRRLTAAPVNGHEALSTY 160
                                                                                        CVLVYPEMKKLMFRIAMRILLGFEPEQIKTDEQELVEAFEEMIKNL----FSLPIDVPFS
                                                                                                                                                                               ASVRTILGSDTLSNVHGVQHKNKKKAIMRAFS-RDALEHYIPVIQQEVKSAIQEWLQKDS 172
GLYRGLRARNFIHSKIEENIRKKIQDDDNENEQKYKDALQLLI----ENSRRSDEPFSLQ
                                                                                                                                                                                                                              LRAFKTSDPESFIQSYITRYGRTGIYKAHMFGYPCVLVTTPETCRRVLTDDDAF-HIGWP
                                               EIEFLSHLRKLTFKVIMYIFLSSESEHV-----MDSLEREYTNLNYGVRAMGINLPGF
                                                                                                                                   KSTMKLIGRKSFYGISFEEHKRLRRLTSAPVNGPEALSVYIQFIEETVNTDLEKW-SKMG
                                                                                                                                                                                                                                                                          I----LQRRKFLRMKRQKYG--CIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWP
                                                                                                                                                                                                                                                                                                                       TGLILMWFPLIILGLFVLKW---VLKRVNVWIYVSKLGEKKHYLPPGDLGWPVIGNMWSF
                                                                                                                                                                                                                                                                                                                                                                     TFLCTIVLPVLLFLAAVKLWEMLMIRRVD-----PNCRSPLPPGTMGLPFIGETLQL
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        15.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                       96; Mismatches 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 394.5; DB 2
Pred. No. 7.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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C.Y

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A;Molecule type: DNA
A;Residues: 1-512 <STO>
A;Cross-references: GB:A;
C;Genetics:
A;Gene: T9L24.44
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID: 21016719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
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IPVIQQEVKSAIQEWLQKDSCVLVYPEMKKLMFRIAMRILLGFEPEQIKTDEQELVEAFE
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSP--LPPGTMGLPFIGET------
                                                             DFVDGCLSVPIDLPGFTYNKAMKARKEIIRKINKTIEKRLQ-NKAASDTAGNGVLGRLLE
                                                                                                     EMIKNLFSLPIDVPFSGLYRGLRARNFIHSKIEENIRKKIQDDDNENEQKYKDALQLLIE
                                                                                                                                                                                                                                NRFIMQNEGKLFQSSYPKSFRDLVGKDGVITVHGDQQRRLHSIASSMMRHDQLKTHFLEV 185
                                                                                                                                                                                                                                                              VRQILLGEHKLVSVQWPASVRTILGSDTLSNVHGVQHKNKKKAIMRAFSRDALE-HY----
                                                                                                                                                                                                                                                                                                                   SHPSSFVEKQIKKFVSLLCSVLLLILKRPDNSGFNEIRYGRIFSCSLFGKWAVVSADPDF
                                                                                                                                                                                                                                                                                                                                                                                                    TFLAFIIIFLLAGIARRKR-------RAPHRLPPGSRGWPLIGDTFAWLNAVAG
                                                                                                                                              IPVVMLQTLSNFKD----GEVVLLQDICRKVAIHLMVNQLLGVSSE---SEVDEMSQLFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADVFPNKEEFQPERFMSKGLEDGSRFNYIPFGGGSRMCVGKEFAKVLLKIFLVELTQHCN 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSMELLDQLKYTGCVIKETLRINPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AYHRALKARKKLVAAFQSIVTNRRNQRKQNISSNRKDMLDNLIDVKDENGRVLDD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WILSN-GPPTMKTGPTIYPVDNLPTKFT 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEIYPDPKKFDPSRWEGYTPKAGT---FLPFGLGSHLCPGNDLAKLEISIFLHHFLLKYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTLKETREMVYLSQVIDETLRVITFSLTAFREAKSDVQMDGYIIPKGWKVLTWFRNVHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---EETIDLLLMYLNAGHESSGHLTMWATILMQEHPMILQKAKEE-QERI-VKKRAPGQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          il Similarity
130; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB:AE005173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.9%; score 382.5; DB 2; 26.6%; Pred. No. 4.9e-18; tive 76; Mismatches 200;
                                                                                                                                                                                                                                                                                                                                                           ----LQLILQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NID:g11120803; PIDN:AAG30983.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Winkler, R.G.; Helentjaris, T.
Plant Cell 7, 1307-1317, 1995
A;Title: The maize dwarf3 gene encodes a cytochrome A; Reference number: Z14648; MUID:96004534
A; Accession: T02263
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вb
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A;Experimental source: strain B73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-519 <WIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
C;Accession: T02263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Contains: oxidoreductase (EC 1.-.-.)
C;Species: Zea mays (maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytochrome P450 DWARF3 - maize
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 RSPLPPGTMGLPFIGETLQLILQRRK-----FLRMKRQKYG--CIYKTHLFGNPTVRVMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                          FEEMIKNLFSLPIDVPFSGLYRG-LRARNFIHSKIEENIRKKIQDDDNENEQKYK-----
LIPKGWKVQLWYRSVHMDPQVYPDPTKFDPSRWEGHSPRAGT---FLAFGLGARLCPGND
                                    QIPKGWNVIYSICDTHDVADVFPNKEEFQPERFMSKGLEDGSRFNYIPFGGGSRMCVGKE
                                                                                KAE-QEAIMRSIPSSQRGLTLRDFRKMEYLSQVIDETLRLVNISFVSFRQATRDVFVNGY
                                                                                                                       REEVQEKVEMGMYTPGKGLSMELLDQLKYTGCVIKETLRINPPVPGGFRVALKTFELNGY
                                                                                                                                                                GVDMMDRLIEAQDERGRHLDDDEIIDVLVMYLNAGHESSGHITMWATVFLQENPDMFARA
                                                                                                                                                                                                       --DALQLLIENSRRSDEPFSLQAMKEAATELLFGGHETTASTATSLVMFLGLNTEVVQKV
                                                                                                                                                                                                                                                  YTELNYGMRAMAINLP-GFAYRGALRARRLVAVLQGVL-----
                                                                                                                                                                                                                                                                                                                                GYLPFIDRTVTSSLRAWADHGGSVEFLTELRRMTFKIIVQIFLG-GADQATT--RALERS
                                                                                                                                                                                                                                                                                                                                                                       HYIPVIQQEVKSAIQEWLQKDSCVLVYPEMKKLMFRIAMRILLGFEPEQIKTDEQELVEA
                                                                                                                                                                                                                                                                                                                                                                                                                AEGCKQVLMDDDAFVT-GWPKATVALVGPRSFVAMPYDEHRRIRKLTAAPINGF--DALT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADNVRQILLGEHKLVSVQWPASVRTILGSDTLSNVHGVQHKNKKK---AIMRAFSRDALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RARLPPGEMGWPLVGGMWAFLRAFKSGKPDAFIASFVRRFGRTGVYRSFMFSSPTVLVTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARLQIALFL 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CFVVPFLSAVHLDESYYKESLSFNPWRWLDPETQQKRNWRTSPFYCPFGGGTRFCPGAEL 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WNVIYSICDTHDVADVFPNKEEFQPERFMSKGLEDGSRFN----YIPFGGGSRMCVGKEF 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GMYTPGKGLSMELLDQLKYTGCVIKETLRINPPVPGG-----FRVALKTFELNGYQIPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----EESLPNESMADFIINLLFAGNETTSKTMLFAVYFLTHCPKAMTQLLEE-HDRLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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25.6%;
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1; Mismatches
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Pred. No. 1.6e-17;
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gc; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: D70649
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N;Contains: oxidoreductase (EC 1.-.-)

C;Species: Mycobacterium tuberculosis

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Ju1-2000

C;Accession: D70649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: Mycobacterium cytochrome P450 Rv3059; cytochrome P450 homology C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase F;300-461/Domain: cytochrome P450 homology <P45> F;439/Binding site: heme iron (Cys) (axial ligand) #status predicted
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A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-492 <COL>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                 YRGLRARNFIHSKIEENIRKKIQDDDNENEQKYKDALQLLIENSRRSDEPFSLQAMKEAA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSLVEHMLLNTKFPEKKLAEPPPGSGLKPVVGDAGLPILGHMIEMLRGGPDYLMF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTLDIASMVFMGHEP----GTDHELVTKVNKAFTITTRAGNAVIRT--SVP---PFT-W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLMFRIAMRILLGFEPEQIKTDEQELV------EAFEEMIKNLFSLPIDVPFSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt DF-----EEHMFHRRIMQEAFVRSRLAGYLEQMDRVVSRVVADDWVVNDARFLVYPAMK}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DTLSNVHGVQHKNKKKAIMRAFSRDALEHYIPVIQQEVKSAI-QEWLQKDSCVLVYPEMK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --LYKTKGPVVFGDSAVLPGVAALGPDAAQVIYSNRNKDYSQQGWVPVIGPFFHRGLMLL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCIYKTH---LFGN----PTVRVMGADNVRQILLGEHKLVSVQ-W-----PASVRTILGS
                                                                                                                                                                                                                                     KYTGCVIKETLRINPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADVFPNKEE
                                                                                                                                                                                                                                                                                                                                    TELLFGGHETTASTATSLVMFLGLNTEVVQKVREEVQEKVEMGMYTPGKG-LSMELLDQL 349
QPRWDYSAMP I PMDGMP
                                             PPTMKTGPTIYPVDNLP
                                                                                          FDPERFTEPRNEHKRHRYAFTPFGGGVHKCIGMVFDQLEIKTILHRLLRRYRLELSRPDY 469
                                                                                                                                                                                          ESLDLVMNESIRLVTPVQWAMRQTVRDTELLGYYLPKGTNVIAYPGMNHRLPEIWTDPLT
                                                                                                                                                                                                                                                                                         IFLMMAAHDTSTSTATTMAYQLAAHPEWQQRCRDESDRH----
                                                                                                                                                                                                                                                                                                                                                                                    WRGLRARELLENYFTARVKERREASGN------DLLTVLCQTEDDDGNRFSDADIVNHM
                                                                                                                                            FQPERFMS-KGLEDGSRFNYIPFGGGSRMCVGKEFAKVLLKIFLVELTQHCNWILS--NG
  486
                                             483
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                                                                                                                                                                                                                                                                                         --GDGPLDIESLEQL
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probable cytochrome P450 T9E8.50 - Arabidopsis thaliana
N;Alternate names: protein T9E8.50
N;Contains: oxidoreductase (EC 1----)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 13-Aug-1999
C;Accession: T06288
R;Bevan, M; Pohl, T; Weizenegger, T; Bancroft, I; Mewes, H.W.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 1999
A;Reference number: Z15588
A;Accession: T06288
A;Accession: T06288
A;Accession: T06288
A;Accession: E06286
A;Accession: T06286
A;Accession:
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                                                                455 LTQHCNWILSNGPP-----
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                                                                                                                                                                                                                                                                                                    GKGLSMELLDQLKYTGCVIKETLRINPPVPGGF-RVALKTFELNGYQIPKGWNVIYSI-C
                                                                                                                                                                                                                                                                                                                                                                                               QFELEKSALKLIIWDMFLAGTATTLSFLEWAMTELMRNPKVMKKLQEEIRSSSPQDLFVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEPFSLQAMKEAATELLFGGHETTASTATSLVMFLGLNTEVVQKVREEVQEKVEMGMYTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSLSWIDRIRGLDH-KMEVVDKRFDEFLERVVKEHEEADKETRSDLVDKL-LTIQSDKTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGLYRGLRARNFIHSKIE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPSPVNLSQILMTLTNDIICRVALGRKYSGKKDGIDVENIVRTFAAL---LGEFPVGEYI 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----VLVYPEMKKLMFRIAMRILLG--FEPEQIKTDEQELVEAFEEMIKNLFSLPIDVPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILSGGRDVAFAPYGEYWRQMKSICIQNLLNNKMVRSYEKIREEEIKRMIEK-LEKASCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IL--GSDTLSNVHGVQHKNKKK-AIMRAFSRDALEHYIPVIQQEVKSAIQEWLQKDSC-- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLHTHRSLRSLSLRYGPLMLLH-FGRTPVLIVSSADVAHDVMKTHDLVCANRPKTKVVDK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPAS--VRT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MILITLCLTTLLALLLKSILKRTATKNFN----
IVKRFNWRMDVEPQRVQHDLTEATGLVVFRKFPLIAIPS
                                                                                                                                 IQRDTTTWGTDAEEFKPERHLDTNLDFQGQDFKFIPFGSGKRICPGIGFTSALIGVTLAN
                                                                                                                                                                                              DTHDVADVFPNKEEFQPERFMSKGLE-DGSRFNYIPFGGGSRMCVGKEFAKVLLKIFLVE
                                                                                                                                                                                                                                                                  EKE----AEKMNYLQAVIKEALRLRPPAPLLVPRVLSEDVKLKGYNIPAGTQVIVNAWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.9%; Score 356.5;
26.2%; Pred. No. 2.56
ative 80; Mismatches
                                                                       -TMKTGPTI---YPVDNLPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -ENIRKKIQDDDNENEQKYKDALQLLIENSRRS
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nes 242;
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                                                                       484
             493
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probable cytochrome P450 T9E8.30 N;Alternate names: protein T9E8.30

Arabidopsis

thaliana

N; Contains:

oxidoreductase

OH)

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Search completed: November Job time: 597 sec
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C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 13-Aug-1999
C:Accession: T06286
R:Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schuelsubmitted to the Protein Sequence Database, April 1999
A:Deferonce protein: 715686
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A;Cross-references: EMBL:AL049608
A;Experimental source: cultivar Columbia; BAC clone T9E8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 4
A;Introns: 129/3; 288/3; 382/3
A;Note: T9E8.30
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A; Accession: T06286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.6%; Score 349; DB 2; Length 490; Best Local Similarity 25.0%; Pred. No. 8e-16; Matches 127; Conservative 91; Mismatches 239; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics:
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                                                                                                            462
                                                                                                                                                        467
                                                                                                                                                                                                 402
                                                                                                                                                                                                                                                                             342 DYLQAVIKEALRLRPPAPLMVPRVFSEDVTLKGYNIPAGTQVIINAWAIQRDTTTWGIDA 401
                                                                                                                                                                                                                                                                                                                                                                            287
                                                                                                                                                                                                                                                                                                                                                                                                            290 ATELLFGGHETTASTATSLVMFLGLNTEVVQKVREEVQEKVEMGMYTPGKGLSMELLDQL 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 LSQLFMTLTNDIICRAALGRKYSSKEDGIDVENIVRAFSALVGE-FPIGEYIPSLSWIDK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 RDVAFAPYGEYWKQMKSICIQNLLSNKMYRSYKKIREDEIKLMIEKVENASSCSPPSPVN 173
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                                                                                                                                                 PP----TMKTGPTI---YPVDNLPT 484
                                                                                                                                                                                                                        EEFQPERFMSKGLE-DGSRFNYIPFGGGSRMCVGKEFAKVLLKIFLVELTQHCNWILSNG 466
                                                                                                                                                                                                                                                                                                           KYTGCVIKETLRINPPVPGGF-RVALKTFELNGYQIPKGWNVIYSI-CDTHDVADVFPNK 407
                                                                                                                                                                                                                                                                                                                                                                   IWDMFLAGTATSLSFLEWAMTELMRNPKVMKKLQEEIRSSSRQGLFVTEKE-----AEKM 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDTLSNVHGVQHKNKKK-AIMRAFSRDALEHYIPVIQQEVKSAIQEWLQKDSCVLVYPEM 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILVT-LCLTTLLALLLLKSI------LKRTTTN-NLNLPPSPWRLPVIGNLHQLSLNTH 54
                                                                                                                                                                                          EEFRPERHLDSILDFQGQDFKFIPFGSGKRICPGIGFTSALIGVTLANIVKRFNWRMDVE 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKLMFR-----IAMRILLG--FEPEQIKTDEQELVEAFEEMIKNLFSLPIDVPFSGLYRG
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                    σ,
                    2001, 13:35:29
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM protein -
    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  1816.5
11646.5
11034.5
11034.5
199.5
598.5
598.5
539.5
523
515.5
503
503
489.5
481.5
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481.5
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                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein search, using sw model
                                                                                                                                                                                                                                                                                                                                 SPTREMBL_16:*

1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organe1:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
12: sp_unclass
13: sp_vertebr
14: sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length: 0
length: 2000000000
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   70.9
667.8
39.9.9
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220.4
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119.1
118.8
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Gapop 10.0 , Gapext 0.5
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2563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 4.5 Copyright (c) 1993 ~ 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                     sp_virus:*
                                                                                                                                                                                                                                                                                                                                              sp_unclassified:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                     sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                sp_plant:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search time 115.92 Seconds (without alignments) 561.543 Million cell updates/sec
O9nr63 homo sapien
O9np41 homo sapien
O9990 synechocyst
O91vy7 arabidopsis
O9sih2 arabidopsis
O9sih7 phaseolus a
O81077 arabidopsis
O64989 arabidopsis
O64989 arabidopsis
O65624 arabidopsis
O65624 arabidopsis
O9scq9 arabidopsis
                                                                                                                                                                                                                                Description
                                                                                                                                                                                  Q9pub4 gallus gall
Q9r1f4 mus musculu
Q93323 xenopus lae
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ALIGNMENTS

MONOOXYGENASE AS SEQUENCE 492 AA; 55264 MW; 7F28B72E75C232FB C	DR PROSITE; PS00086; P430; DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.	Pfam; P	EMBL; AF199462; AAF09250.1;	SIMILARITY):- SIMILARITY: BELONGS TO THE CYTOCHROME P450	-!- SUBCELLULAR LOCATION:	-	<pre>"Complementary Domains of Retinoic Acid Production the Early Chick Embryo.";</pre>	Eichele G.;	Swindell		OX NCBI TaxID=9031:	Archosauria; Aves; Neognathae; Galliformes;	Eukaryota; Met	DE CYTOCHROME) (P450RAI) (RETINOIC ACID 4-HYDROXYLASE) GN CYP26A1.	CYTOCHROME P450 26 (EC 1.14)	01-MAR-2001 (TrEMBLrel. 16, Last	01-MAY-2000 (TrEMBLrel. 13,	DT 01-MAY-2000 (TrEMBLrel. 13, Created)	ID Q9PUB4 PRELIMINARY; PRT; 492 AA.	RESULT 1 Q9PUB4
	Membrane: Microsome:			FAMILY.	ASMIC RETICULUM (BY		on and Degradation in		vich M., Jessell T.M.,			Phasianidae; Phasianinae;	ta; Euteleostomi;	SE).	METABOLIZING	te)				

δÃ

Query Match 70.9%; Score 1816.5; DB 13 Best Local Similarity 70.4%; Pred. No. 1.5e-112; Matches 345; Conservative. 63; Mismatches 79;

DB 13; Length 492; :-112; 79; Indels 3;

3; Gaps

2

1 MGLYTLMVTFLCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQL 60

Matches

337;

Conservative

60;

Mismatches

89;

Indels

10;

Gaps

4

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Дb
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Query Match
Best Local Similarity
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Q9R1F4;
                                                                                                                                                                                                                                            "Identification of tuftelin- and amelogenin-interacting proteins the yeast two-hybrid system.";
Connect. Tissue Res. 38:257-267(1998).
-:- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + OXIDIZED FLAVOPROTEIN + H(2)O (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLRel. 16, Last annotation update)
CYTOCHROME P450 RETINOIC ACID METABOLIZING ENZYME P450RA.
                                                                                                               PRINTS; PR00385; P450.

PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.

Electron transport; Endoplasmic reticulum; Heme; Membrane; Monooxygenase; Oxidoreductase.

SEQUENCE 497 AA; 56191 MW; 67CB167A997842C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=11063033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Paine C.T., Paine M.L., Snead M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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VLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGAENVRHILLGEHRLVSVQWPASVRTIL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
67.8%;
67.9%;
Score 1738; DB 11; Pred. No. 2.4e-107;
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                      Length 497;
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 Matches
              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                  O93323 PRELIMINARY; PRT; 492 AA.
O93323;
O1-NOV-1998 (TrEMBLrel. 08, Created)
O1-NOV-1998 (TrEMBLrel. 08, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CYTOCHROME P450 26 (EC 1.14...) (RETINOIC ACID-METABOLIZING CYTOCHROME) (P450RAI) (RETINOIC ACID 4-HYDROXYLASE).
                                                                                                                                                                    InterPro; IPR001128; -.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450; 1.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 492 AA; 55459 MW; DID4BB7651BF2E
                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
                                                                                                                                                                                                                                                                                  Xenopodinae;
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIXSICDTHDVADIFTNKEEENPD
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 Conservative
                                                                                                                                                                                                                                                                                Xenopus.
              64.2%;
; Score 1646.5; DB 13; Lengt
; Pred. No. 2.8e-101;
84; Mismatches 87; Indels
                                                                              D1D4BB7651BF2D3E CRC64;
                             Length 492;
   11;
 Gaps
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1 MGLYTLMVTFLCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQL

60

Best Local Similarity

42.38;

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Indels

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-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 F
EMBL; AF252297; AAF76003.1; -.
InterPro; IPR001128; -.
Pfam; PF00067; p450; 2.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Electron transport; Endoplasmic reticulum; Heme;
Monooxygenase; Oxidoreductase.
SEQUENCE 512 AA; 57512 MW; A06D1D9944E6726F
                                                                                                                                                                                                                                                                                                                                                                              Q9NR63;
Q9NR63;
Q1-OCT-2000
                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-MAR-2001 (TrEMBLrel. 16, Last annotation
CYTOCHROME P450 RETINOID METABOLIZING PROTEI
                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE=20300913; PubMed=10823918;
White J.A., Ramshaw H., Taimi M., Stangle W., Zhang A., E

Creighton S., Tam S.-P., Jones G., Petkovich M.;

"Identification of the human cytochrome P450, P450RAI-2,

predominantly expressed in the adult cerabellum and is re
all-transretingic acid metabolism."

all-transretingic acid metabolism."
                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
Eukaryota; Metazoa; (
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                                                                                                                        C. Natl. Acad. Sci. U.S.A. 97:6403-6408(2000).

CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = OXIDIZED FLAVOPROTEIN + H(2)O (BY SIMILARITY).

SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICE
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Primates;
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                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
     A06D1D9944E6726F
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                                                                                                                               ENDOPLASMIC RETICULUM
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                                                                                                      P450 FAMILY
                              Heme;
      CRC64
                              Membrane;
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01-OCT-2000
01-MAR-2001
                                                             Waterston
Submitted
                                                                                              [2]
SEQUENCE FROM N.A.
SEQUENCE S., Bauer C., Pape K., Jones T.;
Bourne S., Bauer C., Pape K., Jones T.;
"The sequence of Homo sapiens BAC clone RP11-493L16.";
"The sequence of Homo sapiens BAC clone RP11-493L16.";
                                                                                                                                                                                                                                                                 01-OCT-2000 (TrembLrel. 15, 01-OCT-2000 (TrembLrel. 15, 01-MAR-2001 (TrembLrel. 16, WUGSC:H_NH0493L16.1 PROTEIN
                                                                                                                                                                                                                                                                                                                       Q9NP41
                                                                                                                                                                                                                                             Homo sapiens (Human)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                              Q9NP41;
                                                                                                                                                          Sulston J.E., Waterston R.; "Toward a complete human genome sequence."; Genome Res. 8:1097-1108(1998).
                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=99063792; PubMed=9847074;
                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                     Mammalia; Eutheria;
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                             SEQUENCE FROM N.A.
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SIMILARITY).
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BL; AC007002;
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 BELONGS TO THE CYTOCHROME AAF65576.1; -.
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10; Mismatches 168;
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Last annotation updat
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                                                                                                                                                                                                                                      Catarrhini;
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Best Local
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE CYTOCHROME P450 120.
CYP120 OR CYP OR SLR0574.
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PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.

Electron transport; Endoplasmic reticulum; Heme; Membrane; Microsome; Monooxygenase; Oxidoreductase.

SEQUENCE 525 AA; 59124 MW; 71D47B6752A60315 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q59990
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N., Sugiura M., Tabata S.; "Sequence analysis of the genome of the unicellular cyanobacteriu
                                                                                             SEQUENCE FROM N.A. MEDLINE-96127529;
                                                                                                                                                                                    Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                 STRAIN-PCC6803;
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                 Synechocystis sp. (strain PCC 6803). Bacteria; Cyanobacteria; Chroococcales;
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      unicellular cyanobacterium
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Best Local Similarity
Matches 156; Conserv
                           CYTOCHROME P450-LIKE.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Sp.
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                     Q9LVY7;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
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pfam; pF00067; p450; 1.
prosiTE; pS00086; CYTOCHROME_P450; UNKNOWN_1.
Hypothetical protein; Heme; Monooxygenase; Oxidoreductase
SEQUENCE 444 AA; 50578 MW; 8F62A9EED3B54BDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.
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      Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                          Q9LVY7
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-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; D64003; BAA10496.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLPPGTMGLPFIGETLQLILQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                          PRELIMINARY;
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34.5%; Pred. No. 6e-3
tive 99; Mismatches
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15,
                                                                                                                                                                Last sequence update)
                                                                                                                                                                                                                                Created)
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                                                                                                                                                            update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regions.";
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RESULT
Q9SJH2
ID Q9
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DT 01
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Best Local
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  Q9SJH2;
01-MAY-2000
01-MAY-2000
                                                                 Q9SJH2
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PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.

Electron transport; Endoplasmic reticulum; Heme; Membrane; Microsome;
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1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = OXIDIZED FLAVOPROTEIN + H(2)O (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20181125; PubMed=10718197; Sato S., Nakamura Y., Kaneko T., K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB018112; BAA96885.1; -. InterPro; IPR001128; -. Pfam; PF00067; p450; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              294
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SEQUENCE 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structural analysis of Arabidopsis thaliana chromosome 5. x. Se features of the regions of 3,076,755 bp covered by sixty Pl and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                MKTGPTIYP----
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                                                                                                                                                                        ----EKVFPNENKIVVDPLP
                                                                                                                                                                                                                                                                                                                                         RYSWNVACEVMRIVPPLSGTFREAIDHFSFKGFYIPKGWKLYWSATATHMNPDYFPEPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFGGHETTASTATSLVMFLGLNTEVVQKVREE-----VQEKVEMGMYTPGKGLSMELLDQL 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSKIEENIRKKIQDDDNENEQKYKDALQ------LLIENSRRSDEPFSLQAMKEAATEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLMFRIAMRILLGFE-PEQIKTDEQELVEAFEEMIKNLFSLPIDVPFSGLYRGLRARNFI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MQTS--SKEEARKLRMLLSQFMKPEALRRYVGVMDEIAQRHFETEWANQDQ-VIVFPLTK 179
                                                                                                                                                                                                                                                         FEPNRFEGSGPKP---YTYVPFGGGPRMCPGKEYARLEILIFMHNLVNRFKW---
                                                                                                                                                                                                                                                                                            FQPERFMSKGLEDGSRENYIPFGGGSRMCVGKEFAKVLLKIFLVELTQHCNWILSNGPPT 469
                                                                                                                                                                                                                                                                                                                                                                                  KYTGCVIKETLRINPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADVFPNKEE 409
                                                                                                                                                                                                                                                                                                                                                                                                                          LIGGHDTASIVCTFVVNYLAEFPHVYQRVLQEQKEILKEKKEK-----EGLRWEDIEKM
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  (TrEMBLrel.
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                                                                 PRELIMINARY;
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                                                                                                                                                                                                                -VDNLP 483
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  13,
13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94; Mismatches 182;
                      Created)
    Last sequence
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Pred. No. 7.1
                                                                 PRT;
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Best Local :
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.
Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.
Adams M.D., Carzera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome II of Arabidopsis thaliana.";
Nature 402:761-788(1999).
-1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
OXIDIZED FLAVOPROTEIN + H(2)O (BY SIMILARITY).
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Pfam; PF00067; P450; 2.

PRINTS; PR00385; P450;

PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.

Electron transport; Endoplasmic reticulum; Heme; Membrane;

Monooxygenase; Oxidoreductase.

SEQUENCE 485 AA; 55405 MW; 08B0B16474620F82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AC006931; AAD21724.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Last annotation update) PUTATIVE CYTOCHROME P450.
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                                                                                                                                                      ELLDQLKYTGCVIKETLRINPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVQLMGMNCIMAKQGEKHRVLRGIVANSLSYIGLESLIPKLCDTVKFHHETEWRGKEE-I
  SNGPPTMKTGPTIYPVDNLPTKFTSYV
                                                                                   FPNKEEFQPERFMSKGLEDGSRFNYIPFGGGSRMCVGKEFAKVLLKIFLVELTQHCNWIL
                                                                                                                                                                                                              EVVDNMVLLVFAAHDTTSYAMSMTFKMLAQHPTCRDTLLQEHAQIKANKG----EGEYLTV
                                                                                                                                                                                                                                                                                                                                                                                  SLYRSAKVLTFTVVFECLYG-----IKV-EIGMLEVFERVLEGVFALPVEFPCSKFARAK
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                                          FQDPMSFDPTRF-DKPIQ----AYTYLPFGGGPRLCAGHQLAKISILVFMHFVVTGFDWSL
                                                                                                                             EDVKKMKYSWQVVRETMRLSPPIFGSFRKAVADIDYGGYTIPKGWKILWTTYGTHYNPEI
                                                                                                                                                                                                                                                                                                 KARLETETFLYGKVREKRREMEKEGAEKPNTTLFSRLVE
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                                                                                                                                                                                                                                                      -----LLFGGHETTASTATSLVMFLGLNTEVVQK-VREEVQEKVEMGMYTPGKGLSM
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143; Conser
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28.2%; Pred. No. 1.76
tive 101; Mismatches
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Gaps

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VYPDETISMDPLPFPSLGMPIKISPKV

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Q9FH76;
01-MAR-2001 (TrEN
01-MAR-2001 (TrEN
01-MAR-2001 (TrEN
CYTOCHROME P450.
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clones.";
clones.";
7:31-63(2000)
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MEDLINE=20181125;
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sato S.,
Tabata S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty P1 and TAC
                                                                                                                                                    471
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                                                                                         444 QYGPFALPQNGLP 456
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                                                                                                                                                    KTGPTIYPVDNLP 483
                                                                                                                                                                                                                                                                                                                                       TYRVIQETLRAATILSFTFREAVEDVEYEGYLIPKGWKVLPLFRNIHHNADIFSDPGKFD
                                                                                                                                                                                                                                                                                                                                                                           TGCVIKETLRINPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADVFPNKEEFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AARDTTASVLTWILKYLADNPTVLEAVTEEQMAIRKDKKE-----GESLTWEDTKKMPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNFIHSKIEENIRKKIODDDNENEOKYKDALOLLIEN-SRRSDEPFSLOAMKEAATELLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YQEMKTYTFNVALISILGKDEVYYRED----LKRCYYILEKGYNSMPINLPGTLFHKAMKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YPEMKKLMFRIAMRILLGFEPEQIKTDEQELVEAFEEMIKNLFSLPIDVPFSGLYRGLRA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RMLGKQAIFFHQGDYHSKLRKLVLRAFMPDAIRNMVPHIESIAQESLNSW---DGTQLNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TILGSDTLSNVHGVQHKNKKKAIMRAFSRDALEHYIPVIQQEVKSAIQEWLQKDSCVL-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLYSQDPNVFFAAKQRRYGSVFKTHVLGCPCVMISSPEAAKFVLVTKSHLFKPTFPASKE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLYTLM----VTFLCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETL
                                                                                                                                                                                                                PSRF-----EVAPKPNTFMPFGSGIHSCPGNELAKLEISVLIHHLTTKYRWSIVGPSDGI
                                                                                                                                                                                                                                                                        PERFMSKGLEDGSRFN-YIPFGGGSRMCVGKEFAKVLLKIFLVELTQHCNWILSNGPPTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGHETTASTATSLVMFLGLNTEVVQKVREEV----QEKVEMGMYTPGKGLSMELLDQLKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKEL-AQILANILSK----RRQNPSSHTDLLGSFMEDKAGLTDEQIA-----DNIIGVIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLILQ-RRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLFLTLSAAALFLC-----LLRFIAGV-----RRSSSTKLPLPPGTMGYPYVGETF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               463 AA; 52366 MW;
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 523; DB 10;
Pred. No. 6.8e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    463
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Best Local
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00385; P450.

PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_Electron transport; Endoplasmic reticulum; Monooxygenase; Oxidoreductase.

SEQUENCE 474 AA; 54037 MW; A2542A809C5B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phaseolus aureus (Mung bean) (Vigna radiata),
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sp
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Fabales; Fabaceae; Papilionoideae; Vigna.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH - OXIDIZED FLAVOPROTEIN + H(2)O (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=CV. 2937; Yang M.T., Chen Y.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY EMBL; AF279252; AAF89209.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and sequencing
P450.";
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406 ANVYTPFGGGPRLCPGYELARVVLSVFLHRIVTRFSWVPAEEDKLVFFPTTRTQKR-YPI
                                                                                                                                                                                                                                                                                                187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
                              FN-YIPFGGGSRMCVGKEFAKVLLKIFLVELTQHCNWILSNGP-----PTMKTGPTIYPV
                                                             IGGIFRRATTDIDIKGYTIPKGWKVFASFRAVHLNPEYYKDARTFNPWRWQSNSSEAANP
                                                                                             VPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADVFPNKEEFQPERFMSKGLEDGSR
                                                                                                                               TLAVKFLTETPLALAQLKEE-HDQIR-ARSDPGAPLEWTDYKSMVFTQHVVNETLRVANI
                                                                                                                                                               TSLVMFLGLNTEVVQKVREEVQEKVEMGMYTPGKGLSMELLDQLKYTGCVIKETLRINPP
                                                                                                                                                                                               LVVRQR-REEYNQGKEKKSDMLGALL----ASGDHFSDDQIVDFLLALLVAGYETTSTIM
                                                                                                                                                                                                                               ENIRKKIQDDDNENEQKYKDALQLLIENSRRSDEPFSLQAMKEAATELLFGGHETTASTA
                                                                                                                                                                                                                                                             IAMRILLGFEPEQIKTDEQELVEAFEEMIKNLFSLPIDVPFSGLY-RGLRARNFIHSKIE
                                                                                                                                                                                                                                                                                                                                KGALHK-RMHSLTMSFANSSIIKDHLLHHIDRLIGLNLDTWSDR----VTLMDQAKKITFE
                                                                                                                                                                                                                                                                                                                                                              HGVQHKNKKKAIMRAFSRDAL--EHYIPVIQQEVKSAIQEWLQKDSCVLVYPEMKKLMFR 186
                                                                                                                                                                                                                                                                                                                                                                                                DERVRRYGSIFMTHVFGEPTVFSADPELNRFILQNEGKLLDCSYPGSISNLLGKHSLLLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSLPTLLLLFAASA-AAIFLHRAFSRRKFRLPPGSYGLPFIGETLQLISAYKSSNPEPFM
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16,
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Last sequence update)
Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 515.5;
Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A2542A809C5BAC6D CRC64;
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081077;
01-NOV-1998 (TrEMBLre
01-NOV-1998 (TrEMBLre
01-MAR-2001 (TrEMBLre
PUTATIVE CYTOCHROME F
T914.17.
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-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AC005315; AAC33235.1; -.
Interpro; IPR001128; -.
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
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064989
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PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Heme; Monooxygenase; Oxidoreductase.
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(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
TOCHROME P450.
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Pred. No. 1
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Best Local
Q9SCQ9;
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01-MAY-2000
01-MAY-2000
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE CYTOCHROME P4:
EMBL; AF044216; AAC05093.1; -.
InterPro; IPR001128; -.
Pfam; PF00067; p450; 1.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 513 AA; 58867 MW; B1639BDD9A4DA6
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eddicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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Plant Cell 10:0-0(1998).
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                                                                                                                  LAKLEMAVFIHHLVLKFNWELAEDDQ----
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Pred. No. 1.7e-25;
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Best Local S
Matches 144
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065624;
01-AUG-1998
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ database
-i- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AL132979; CAB62435.1; -.
InterPro; IPR001128; -.
Pfam; PF00067; p450; 1.
PRINTS; PR00085; P450; 1.
PRINTS; PR00085; CYTOCHROME_P450; UNKNOWN_1.
Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 513 AA; 58867 MW; B1639BDD9A5D7C93 CRC64;
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NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.6%; Score 503; DB 10; 27.6%; Pred. No. 1.7e-25; tive 95; Mismatches 216;
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Best Local
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ c
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450
EMBL; AL021687; CAA16713.1; -.
EMBL; AL161550; CAB78925.1; -.
HSSP; P33006; 1CPT.
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Van Der Schueren J., Chuang Y.J., Aert R., Defoor
Volckaert G., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ data
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T18B16.200 OR AT4G19230.
Trabidopsis thaliana (Mouse-ear Arabidopsis thalia
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PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
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Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Bevan M., Benes V., Rechmann S., Borkova
Mewes H.W., Mayer K., Schueller C.;
Submitted (JAN-1998) to the EMBL/GenBank,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracher
Magnoliophyta; eudicotyledons; core eudicots;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                              GGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADVFPNKEEFQPERFMSKGLEDGSRFN
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FTFREAVEDVEYEGYLIPKGWKVLPLFRNIHHSADIFSNPGKFDPSRF---
                                                                                                    LAENPNVLEAVTEEQMAIRKDKEE-----GESLTWGDTKKMPLTSRVIQETLRVASILS
                                                                                                                                                LGLNTEVVQKVREEV----QEKVEMGMYTPGKGLSMELLDQLKYTGCVIKETLRINPPVP
                                                                                                                                                                                                          LSERRQNGSSHNDLLGSFMGDKEELTDEQIA----DNIIGVIFAARDTTASVMSWILKY
                                                                                                                                                                                                                                                            QDDDNENEQKYKDAL-QLLIENSRRSDEPFSLQAMKEAATELLFGGHETTASTATSLVMF
                                                                                                                                                                                                                                                                                                                    ----KDEVLYREDLKRCYYILEKGYNSMPVNLPGTLFHKSMKAR----
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NCE 457 AA; 52436 MW; 6105F
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28.2%;
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Last annotation updat
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Pred. No. 1.1e-24;
7; Mismatches 183;
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bugnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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O9FMA5;

01-MAR-2001 (TrEMBLrel. 16,

01-MAR-2001 (TrEMBLrel. 16,

01-MAR-2001 (TrEMBLrel. 16,
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Tabata S.;
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Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
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                                                                                           FMSKGLEDGSRFNYIPFGGGSRMCVGKEFAKVLLKIFLVELTQHCNWILSNGPPTMKTGP 474
                                                                                                                                                                                   VIKETLRINPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADVFPNKEEFQPER 414
                                                                                                                                                                                                                                                                                                                                   IHSKIEENIRKKIQDDDNENEQKYKDALQLLI--ENSRRSDEPFSLQAMKEAATELLFGG 297
                                     TIYP 478
                                                                         WMKKSLE--SQNSCFVFGGGTRLCPGKELGIVEISSFLHYFVTRYRWEEIGGDELM----
                                                                                                                                                 VIYETSRLATIVNGVLRKTTRDLEINGYLIPKGWRIYVYTREINYDANLYEDPLIFNPWR 393
                                                                                                                                                                                                                           YETVSTTSMMALKYLHDHPKALQELRAEHLAFRERKRQ-----DEPLGLEDVKSMKFTRA 333
                                                                                                                                                                                                                                                                                                   I-----DRILRELMQERRDSGETFTDMLGYLMKKEGNR---YPLTDEEIRDQVVTILYSG
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NCE 465 AA; 53767 MW; 0C00459C9C866D1F CRC64;
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Last annotation update)
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Search completed: November 6, 2001, 13:38:25 Job time: 253 sec

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gb_p12:AF318501
gb_p12:AF326277
gb_p11:AB020744
gb_p14:ZM032579
gb_p14:ZM032579
gb_ba3:MXTAH
gb_p13:ATT18B16
gb_p12:ATCHRIV50
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9b_p12: AF318212
9b_p11: AC006931
9b_p14: SLU54770
9b_p14: SLU54770
9b_p12: AF318500
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9b_p12: AF326277
9b_p11: AB020744
9b_p11: AB020744
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gb_in2:AF251548
gb_ov:OMU96077
gb_ro1:AF166266
gb_p12:AF139532
gb_pr2:AC007002
gb_pat2:E02279
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gb_pr5:AF319634
gb_ov:GGA250337
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Database length: -856060004
Search time (sec): 5019.990000
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Query length: 492
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gb_pat1:AR074363
gb_p12:ATCYP450R
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gb_ro1:AF115769
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gb_pr5:AF252297
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gb_ov:AF251272
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1.8e-22
2.8e-22
3.2e-21
7.4e-19
2.1e-17
2.4e-15
4.4e-17
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8.6e-17
3.7e-14
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4.7e-16

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5.8e-104
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11364 | D64003 Synechocystis sp. PCC
1608 | AR074363 Sequence 1 from pateri
1608 | X87367 A.thaliana mRNA for cyt
1494 | AF318211 Taxus cuspidata 5-alp
1649 | AF279222 Vigna radiata cytochr
116205 | AC006931 Arabidopsis thaliana
11395 | U54770 Solanum lycopersicum cy
322 | AF3185266 Gallus gallus CYP26 (C
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1743 | AF005418 Homo sapiens retinoid
1726 | AF115769 Mus musculus cytochro-
1756 | Y12657 M.musculus mRNA for P45
1479 | AF057566 Xenopus laevis retino
166337 | AL358613 Homo sapiens chromo
                                                                                                                                                                                                                                                                                        4 i AB00807 Arabidopsis thaliana
7 i AF318500 Arabidopsis thaliana
8 i AF212991 Cucurbita maxima ent
75 i AB018112 Arabidopsis thaliana
0 i AF318501 Arabidopsis thaliana
4 i AF318277 Hordeum vulgare ent-k
52 i AB020744 Arabidopsis thaliana
4 i AF32527 Bordeum vulgare ent-k
52 i AB020745 Arabidopsis thaliana
53 i AL021687 Arabidopsis thaliana
11 i AJ232955 Myxococcus xanthus cy
174 i AL021687 Arabidopsis thaliana
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178 i AL021687 Arabidopsis thaliana
178 i AL021687 Arabidopsis thaliana
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                                                             AF280108 Homo sapiens clone 15
AF319634 Homo sapiens cytochrc
AJ250337 Gallus gallus mRNA fc
AB017785 Mus musculus cyp4A10
AL359214 Streptomyces coelicc
J05034 Rabbit CYP3A6 gene ence
AF251272 Oryzias latipes cytoc
AF251272 Oryzias latipes cytoc
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| AF251548 Tribolium castaneum
| U96077 Oncorhynchus mykiss cyt
| AF280108 Homo sapiens clone 15
| AF319634 Homo sapiens cytochro
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gb_p11:AB037245
gb_om:RABP4503C
gb_pr10:HUMCYP2C9A
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VERSION
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LOCUS DRU68234
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from:

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to: 1479

50

Percent Identity: 100.000

Length:

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DRU68334 1479 bp mRNA VRT 22-NOV-1996 Danio rerio all-trans-retinoic acid 4-hydroxylase (p450RAI) mRNA,
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J. Biol. Chem. 271
97094702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-AUG-1996) Cancer Research Labs, Queen's University, Botterell Hall, Kingston, ON K7L 3N6, Canada Location/Qualifiers
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White, J.A., Guo, Y.,
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E., Dilworth,F.J., Jones,G. and Petkovich,M.
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SICDTHDVADVFPNKEEFOPEREMSKGLEDGSRRNVIPFGGGSRMCVGKEFAKVLLKI
FLVELTGHCNMILSNGPPTMKTGPTIYPVDNLPTKFTSYVRN"
25 a 331 c 379 g 344 t
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AB037245 Asparagus officina
M19139 Rabbit cytochrome P4
M61857 Human cytochrome P45
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                                     Submitted (28-OCT-1999) Max Planck Institute Endocrinology, Feodor-Lynen Strasse 7, Hannov Location/Qualifiers
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                                                                                                                                                                              Jessell, T.M. and Eichele
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s retinoic
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                                                                                                         Sockanathan, S.,
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                                                  Hannover 30625, German
                                                                                                          Petkovich, M
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| CCTGCAGATGAAGCGCAGGAAATACGGCTTCATCTACAAGACTCACCTCT
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|CTGCCCTTCTTCGGGGAGACGCTGCAGATGGTGCTGCAGCGGCGGAAATT
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etPheArgIleAlaMetArgIleLeuLeuGlyPheGluProGluGlnIle
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|||||||||||:::|||||||||||:::
ACCACGGCCAGTGCTGCTACATCACTGATTGCCTTCCTAGGGCTCCACCA
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                                                                                                                                                                                                                                                                           lproGlyClyPheArgValAlaLeuLysThrPheGluLeuAsnGlyTyrG
||||||||||||||||||
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                                                                                                                                        lyGlySerArgMetCysValGlyLysGluPheAlaLysValLeuLeuLys 449
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                                                                                                                                                                             GTCTCCGTCTCCGGAGGACTCCTCTAGGTTCAGTTTCATTCCTTTCGGTG
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ORIGIN
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MEDLINE
REFERENCE
AUTHORS
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VERSION
KEYWORDS
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ORGANISM
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Ratio: 4.087
Percent Similarity: 85.714
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LOCUS AF005418
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                                          139 GCGGCCGCGACCGCAGTTGTGCCCTCCCATTGCCCCCCGGGACTATGGGC 188
34
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                                                                                                                                                          rgArgValAspProAsnCysArgSerProLeuProProGlyThrMetGly 50
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Direct Submission
Submitted (26-MAY-1997) Cancer Research Labs, Queen's University,
Botterell Hall, Rm 355, Kingston, Ont K7L 3N6, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1743)

White,J.A. Beckett-Jones,B., Guo,Y.D., Dilworth,F.J., Bonasoro,J., Jones,G. and Petkovich,M.

CDNA Cloning of human retinoic acid-metabolizing enzyme (hP450RAI) identifies a novel family of cytochromes P450

J. Biol. Chem. 272 (30), 18538-18541 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens retinoic acid hydroxylase mRNA, complete cds. AF005418
AF005418.1 GI:2688845
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                     Identification of amelogenin- and tufte using the yeast two-hybrid system Connect. Tissue Res. 38, 257-267 (1998) 2 (bases 1 to 1726) 2 (bases 1 to 1726) Paine, C.T., Paine, M.L. and Snead, M.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 1726)
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AF115769
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                                                                                                                                                                                                                                                                                                                                                             Submitted (21-DEC-1998) CCMB, University of Southern California, 2250 Alcazar Street, CSA103, Los Angeles, CA 90033, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paine, C.T., Paine, M.L. and Snead, M.L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse.
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REFERENCE AUTHORS TITLE

JOURNAL

JOURNAL

FEATURES

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SOURCE

ORGANISM

KEYWORDS

VERSION ACCESSION DEFINITION

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REFERENCE

AUTHORS TITLE

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alignment_scores:
 Quality: alignment_block: US-09-668-482-2 x AF115769 Percent Similarity: 134 327 277 227 177 477 427 377 117 101 127 527 167 151 197 568 180 84 67 51 34 77 27 ATGGGGCTCCCGGCGCTGCTGCCCACTGCGCTCTGCACCTTCGTGCTGCC oValLeuLeuPheLeuAlaAlaValLysLeuTrpGluMetLeuMetIleA |:::||||||||||||||||||:::||||||||::::: MetGlyLeuTyrThrLeuMetValThrPheLeuCysThrIleValLeuPr |||||||| GCTGCTGCTCTTCCTGGCGCGCGCTCAAGCTCTGGGACCTGTACTGTGA eLeuArgMetLysArgGlnLysTyrGlyCysIleTyrLysThrHisLeuP ||||:::||||||||:::||||||||| HisTyrIleProValIleGlnGlnGluValLysSerAlaIleGlnGluTr ysAsnLysLysLysAlaIleMetArgAlaPheSerArgAspAlaLeuGlu ||::::::||||||:::|||||:::|||||||||::: CACCATCCTGGGCGCTGGCTGCCTCTCCAACCTGCACGATTCCTCGCACA gThrIleLeuGlySerAspThrLeuSerAsnValHisGlyValGlnHisL 134 TTGCTGGGAGAGCACCGGTTGGTGTCGGTGCACTGGCCCGCGTCGGTGCG LeuLeuGlyGluHisLysLeuValSerValGlnTrpProAlaSerValAr 117 TTGGGCGGCCCACGGTGCGGGTGATGGGCGCGGATAATGTGCGGCGCATC heGlyAsnProThrValArgValMetGlyAlaAspAsnValArgGlnIle 100 TCTGCAGATGAAGCGCAGGAAATACGGCTTCATCTACAAGACGCATCTGT GCAGCCGCGATCGCAGCTGCGCCCTTGCCCCCCGGTACCATGGGC rgArgValAspProAsnCysArgSerProLeuProProGlyThrMetGly pLeuGlnLysAspSerCys......ValLeuValTyrProGluM AGCAGCGAAAGAAGGTGATTATGCAGGCCTTCAGCCGCGAGGCACTCCAG eGluGluMetIleLysAsnLeuPheSerLeuProIleAspValProPheS ProGluGlnIle.....LysThrAspGluGlnGluLeuValGluAlaPh ||| GCTA....AGCTGCGGCGAGCGCGCCTCCTGGTCTACCCCGAGG TGCTACGTGCTCGTGATCGCTGAGGAAGTCAGCAGTTGTCTGGAGCAGTG Ratio: ţo: AF115769 1738.00 4.080 85.887 .080 from: Percent ţo: Identity: 67 Length: 496 4 . 944 84 67 34 176 126 76 326 276 226 50 196 180 167 476 150 426 526 228 667 211 617 567

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DEFINITION ACCESSION
                                                            seq_documentation_block:
                                                                                           seq_name: gb_rol:MMP450RA
 ERSION
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                                                                                                                                             TTGGCAGCTTCTAAATGGACCTCCTACAATGAAGACAAGCCCCCACTGTGT
                                                                                                                                                                                                        nTrpIleLeuSerAsnGlyProProThrMetLysThrGlyProThrIleT 477
                                                                                                                                                                                                                                                    AlaLysValLeuLeuLysIlePheLeuValGluLeuThrGlnHisCysAs 460
                                                                                                                                                                                                                                                                                                                  GCTTCATTCCATTTGGAGGAGGCCTTCGGAGCTGTAGGCAAAGAGTTT 1367
                                                                                                                                                                                                                                                                                                                                       snTyrIleProPheGlyGlyGlySerArgMetCysValGlyLysGluPhe 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                IleCysAspThrHisAspValAlaAspValPheProAsnLysGluGluPh 410
                                                                                                                           ACCCTGTGGACAATCTCCCTGCAAGATTCACCTACTTC 1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGATTGAATCCTCCGGTCCCAGGAGGGTTTCGGGTTGCTCTGAAGACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heGluLeuAsnGlyTyrGlnIleProLysGlyTrpAsnValIleTyrSer 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAGCAAGGGCTTACTTTGCAAGAGCAATCAAGACAACAAGTTAGACATG
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Y12657
Y12657.1
                            M.musculus mRNA for
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GI:2765213
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alignment_block:
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                             OValLeuleuPheLeuAlaAlaValLysLeuTrpGluMetLeuMetIleA 34
eLeuArgMetLysArgGlnLysTyrGlyCysIleTyrLysThrHisLeuP
||||:::||||||||:::||||||||
                                                             TTCCCATTCTTTGGGGAAACATTGCAGATGGTGCTTCAGCGGAGGAAGTT
                                                                                   LeuProPheIleGlyGluThrLeuGlnLeuIleLeuGlnArgArgLysPh
                                                                                                                                            GCAGCCGCATCGCAGCTGCGCCCTCCCCTTGCCCCGGTACCATGGGC
                                                                                                                                                                                    rgArgValAspProAsnCysArgSerProLeuProProGlyThrMetGly
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1756)

Fujii,H., Sato,T., Kaneko,S., Gotoh,O., Fujii-Kuriyama,Y.,

Osawa,K., Kato,S. and Hamada,H.

Metabolic inactivation of retinoic acid by a novel p450

differentially expressed in developing mouse embryos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 1734.00
Ratio: 4.070
nilarity: 85.887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P450RA gene. house mouse.
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57
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LLKIFTVELARHCDWQLLNGPPTMKTSPTVYPVDNLPARFTYFQGDI"
a 434 c 494 g 420 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mglpallasalctfylpllleflaakklwdlycvssrdrscalpl
ppgTwofpffcettlowvlorrkeldykrrkycofiykfyllferpfyrvygaddwrrill
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RNLFSLPIDVpfsGlYrgvkannlihariebwirakilrloayphylokyrbliks
RNLFSLPIDVpfSGlYrgvkannlihariebwirakilrloayphylokyrbliks
RNLFSLPIDVpfSGLYRGVKANNLIHARIEBWIRAKIRLOAYPHYLOKYRBIKSK
BLCKSNODNKLDMETCLEOLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGW
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57. 1550
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/db_xref="GI:2765214"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="P450RA protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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|ACCATCCTGGGCGCTGGCTGCCTCTCCAACCTGCACGATTCCTCGCACA
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|GCGCCTGTACCGCGCGTGAAGGCGCGGAACCTTATACACGCGCGCATC
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                           uArgIleAsnProProValProGlyGlyPheArgValAlaLeuLysThrP 377
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Regionalized metabolic activity establishes boundaries acid signalling
EMBO J. 17 (24), 7361-7372 (1998)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                            Chen, J.L., Grunz, H., Panitz, F., Pieler, T. and Hollemann, T
                                                                                                                                                                                                                                                                                                                                            Submitted (05-APR-1998) Developmental Biochemistry, University of Goettingen, Humboldtallee 23, Goettingen, Lower Saxony 37073,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          African clawed frog
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             lyLeuArgAlaArgAsnPheIleHisSerLysIleGluGluAsnIleArg 249
                                                                                                       GACCGCGAACAGGAAAACGCTGCTCGAAGCCTTCGAGGAAATGAGCCG
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|||:::||||||||||:::||||||:::
CTTCAACAGTTAAAGTATACTAGCTGTGTGTATTAAGGAGACTCTGCGGCT 1082
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                                                                                                             AL358613 166337 bp DNA HTG
Homo sapiens chromosome 10 clone RP11-348J12,
PROGRESS ***, 14 unordered pieces.
Homo sapiens
Eukaryota; M
                                                        AL358613.8 GI:13660841
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                            human.
                                                                                                       AL358613
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
------ Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (13-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1, (bases 1 to 166337)
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------ Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: XGAP4; version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it
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32410 32509; gap of
32510 52913; contig of 20404 bp in length
52914 53013; gap of
52914 53013; gap of
53014 55817; contig of 2804 bp in length
55818 55917; gap of
55918 74512; contig of 18595 bp in length
74513 74612; gap of
74613 83833; contig of 9221 bp in length
81834 83931; gap of
81934 87001; contig of 3068 bp in length
81934 87002 87101; gap of
8100 bp
8100 87101; gap of
8100 87101; gap of
8100 bp
8100 87101; gap of
8100 bp
8100 87101; gap of
8100 87101;
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129703 139802: gap of 100 bp
132463 132562: gap of 100 bp
132563 137099: contig of 4537 bp in length
132563 137099: gap of 100 bp
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100684 10529!
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fragment_chain:1
clone_end:T7
                                                                               /note="assembly_fragment:02593
                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/chromosome="10"
                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                              clone_lib="RPCI-11.2"
                                                                                                                                                                                                   /clone="RP11-348J12"
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100 bp
124/02: contig of 24307 bp
129802: gap of 100 100 1132462: cont',
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100583: contig of 2995 bp in length
100583: gap of 100 bp
105295: contig of 4612 bp in length
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alignment_block:
US-09-668-482-2 x AL358613
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                                                           LeuProPheIleGlyGluThrLeuGlnLeuIleLeu.Gln.....
                                                                                                                       GCGGCCGCGACCGCAGTTGTGCCCCCATTGCCCCCGGGACTATGGGC
                                                                                                                                                   rgArgValAspProAsnCysArgSerProLeuProProGlyThrMetGly 50
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97589. .1
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/note="assembly_fragment:02258
fragment_chain:2"
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fragment_chain:2"
100684..105295
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/note="assembly_fragment:02028.0"
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| 33577 c 34990 g
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132563. .137099
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fragment_chain:2"
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fragment_chain:2"
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fragment_chain:2"
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37.393
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fragment_chain:3
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22
29.931
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56	151 .HisTyrIleProVallleGlnGlnGluValLysSerAlaIleGlnGluT 167 ::: :::
56	NININININININININININININININININININI
	150 150
56	GGA MANANANANANANANANANANANANANANANANANANA
S6	140 eMetargAlaPheSerargAspAlaLeuglu
56	139Ala.Il 140 :::
56	>
	138 138
56	138 138 55614 AGGACCCTCTGCCAGCTCCAGGTTAGCTATACCCAGCTCGGAGAGTGCCA 55663
	GAATTCCGGCTGATGGATGCTAGGCGCGGGCTAGCAGCTTGAGGTGGGCT
л	138 138
56	GGGGGCAGGAGGCGACGGCTGGACAGGGAGGGGGGACCCCCATTTATGAGCG
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56	106 ysLeuValSerValGlnTrpProAlaSerValArgThrIleLeuGlySer 122 ::
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56	64ArgargLysPheLeuargMetLysArg 72
9	55214 CAGGGCTGGCGGGAGCGCGCGCGCCCCCCCCCCCCCATGCCCACTTC 55263
	63 63
56	63
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11 30	GluThrThrAlaSerThrAlaThrSerLeuVa	293
1L 29	AlametLysGlualaalaThrGluL ::: ::::::: AATGTGGGTCTCACTCTATTCTTAGGCACTAAAGCAATCTTCAACCGAAC	285 56901
4G 56	CAGTTCGATTCTGAGTAATCCTTCTGTCAAACCGCAGGCAG	56851
. 28		284
T 56	CTTTCTGTCAGCAAAACATTTAGCCCTTCTAGTCTTCCCTCCAGAACTCT	56801
28		284
3A 56	 GCTGAACTAAAGGGACGTTGCATTTTGTTTAAAGATATTGCTTTCCTTGA	56751
28	B	284
31 28 11 CA 56	ACTCAGGAGTTTCCGGTAGAGCGGGGTCGTACTCGCCTTACTG.CTCC	280 56702
PT 56	TGCAAAAATGTTAATAAAGAACCTTGCGATTTTAATAAAACTAAGACTTT	56652
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PT 56	ACTGGGAGCATCCCCTAGCCTTTCCAGGTTTCAAAGGGAAAGTTGGAATT	56602
27		279
3A 56	AGCTGCGGAAGGGGCTGCGGCGG	56552
27	rgArgSe	275
1A 56	AGCTTTCTGGAGTGGGCGGCCGGCTCAGACTACAGCTATGGAATCCCGAA	56502
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C 56	GGCTTTCCAAGCGCTGTTCCTGGGGCCCCCAAAGCGCGCGC	56452
. 27		274
TT 56	ATGCAGGTGAGTAGCAGCTTCAGACCAGGCACTGCGGAGTTTGGTCCCC	56402
27		274
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OG 56	SLYSI1eClnAspAspAspAsnGluAsnGluGlnLySTyrLySAsp CAAGATCTGCGGGCTGCGGGCATCCGAGGCGGGCCAGGGCTGCAAAGAC	250 56302
LY 25	LeuArgAlaArgAsnPheIleHisSerLysIleGluGluAsnIleArgL :::::: ::: ATGAAGGCGCGAACCTCATTCACGCGCCATCGAGCAGAACATTCGCG	234 56252
7. 23 GC 56	GCGCGGGACCTGGGCTCTGCTCTACCGCCGCGCGCTCTCTGCGCTCAGGG	233 56202
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FO 22	laPheGluGluMetIleLysAsnLeuPheSerLeuProIleAspValPr 	210 56102
3G 56		56055

57900	51 TCTTCCCTATGCTGTGGCTGCAATTCTTATGCTTTTGATAATTGTTCTGC	5785
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365 57750	49 LeuLysTyrThrGlyCysVallleLysGluThrLeuArgIleAsnProPr 	34 5770
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348	LeuSe	341
57650)1 GAGCACAAAATAACTGTTCACCTCTGTATGACTGTTTTGATAGGGTTTAC	57601
340	10	34
57600	51 GTTTAGTCTCCACTTAAGCCCTGTTTACGTCTGCTGGGCTGATTTTATTG	5755
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57500	5 TyrThrProGlyLyS.Gly :::::: :::::: CATTCTCCTGGGATTGTAAATAGATAGTGGATTTGGGCAGGCA	335 57451
7	TGGTGAGC	57401
334	4	334
57400	1 GGGCATACATAGTGTGAATAGCTGATTAGTGTGGGTGGTGGTGAGTG	57351
334		334
57350	1 ACCGTGGAGATTCTCAGATAGGTTCCACTTTCTTGAATTGGTGTGTCCAA	57301
334		334
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334		334
7	GAAGAGTAAGGTAGGAACTGGGTCTGGGGGGTGTCCTTATTAGCTTAGG	57051
334	IGInGINI.veVal GliMetGlyMet	ມ ວ
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) 7	TCCTCTTTGGAGGACACGAAACCACGGCCAGTGCAGCCACATCTCTGATC	56951

TyrGln1leProLysGlyTrpAsnVallleTyrSe 393	ATCTTTTGCAGGGA ATCTTTTGCAGGGA 	58051 AA7 58051 AA7 393 rI: 410 het 410 het 410 het 158151 TY: 427 As; 58251 TG 443 eA 443 eA 446 sn 58251 TG 460 sn 58351 TA 583
TCAGCCCTTGGGGTTTCAT 58050	TTTTGTTGTTGAAAGTTAAATTCCAGTTTGTCAGCCCTTGGGGTTTCAT	380 . 58001 T
	TCTCCCTTGCTTTAGCTCATAATTTCCCCCAAAGATATCAGTGACTGC	380 . 57951 C
. பா	CTATATGGAGATATGTTTCAGCAACCTGGATCCACCTCTCTCT	a
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alignment_block:
US-09-668-482-2 x AF252297
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ORIGIN
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                                                                                                                                                                                                                                                                                                          134 ysAsnLysLysAlaIleMetArgAlaPheSerArgAspAlaLeuGlu 150 ::!!!!!!::::!!!!!!!!!
                                                                                                                                                                                                                                                                                                                                                                                                           366 CATGTTGCTGGGCCCCAACACGGTGTCCAATTCCATTGGCGACATCCACC 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            416 GCAACAAGCGCAAGGTCTTCTCCAAGATCTTCAGCCACGAGGCCCTGGAG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 TICCCGCTCATCGGAGAGACCGGCCACTGGCTGCTGCAGGGTTCTGGCTT 215
516 GAGCAGCCACCCCGAGGCCATCAACGTGTACCAGGAGGCGCAGAAGCTGA 565
                                                     167 pLeuGlnLysAspSerCysValLeuValTyrProGluMetLysLysLeuM 184
                                                                                                                                    466 AGTTACCTGCCCAAGATCCAGCTGGTGATCCAGGACACACTGCGCGCCTG
                                                                                                                                                                                                 151 HisTyrIleProValIleGlnGlnGluValLysSerAlaIleGlnGluTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 TGGGGCGGCCGCTGATACGCGTGACCGGCGCGCGAGAACGTGCGCAAGATC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 CCAGTCGTCGCGGAGGGAGAAGTATGGCAACGTGTTCAAGACGCATTTGT 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 CCACTCGCGACAAGAGCTGCAAGCTGCCCATCCCCAAGGGATCCATGGGC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 heGlyAsnProThrValArgValMetGlyAlaAspAsnValArgGlnIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 eLeuArgMetLysArgGlnLysTyrGlyCysIleTyrLysThrHisLeuP 84 ::::||||:::||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 LeuProPheIleGlyGluThrLeuGlnLeuIleLeuGlnArgArgLysPh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 rgArgValAspProAsnCysArgSerProLeuProProGlyThrMetGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 GACGCTGCTGCCGCGTGTCGCAGCAGCTGTGGCAGCTGCGCTGCGCCCG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 oValLeuLeuPheLeuAlaAlaValLysLeuTrpGluMetLeuMetIleA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 TIGGATCIGGTGGCGCGCGCGCGCGCGTGCCTGGTGTCCGT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetGlyLeuTyrThrLeuMetValThrPheLeuCysThrIleValLeuPr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gThrIleLeuGlySerAspThrLeuSerAsnValHisGlyValGlnHisL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 1034.50
Ratio: 2.811
milarity: 74.494
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WSIRDTHDTAPVFKDVNVEDDDRFSQARSENKDRRHYLPFGGGVRTVGIKHLAKLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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P450RAI-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {	t LKVLAVELASTSRFELATRTFPRITLVPVLHPVDGLSVKFFGLDSNQNEILPETEAML}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAF76003.1"
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476 1438	nTrpIleLeuSerAsnGlyProProThrMetLySThrGlyProThrI::::	460 1389
460 1388	AlaLysValLeuLeuLysIlePheLeuValGluLeuThrGlnHisCysAs	444 1339
443 1338	<pre>snTyrIleProPheGlyGlyGlySerArgMetCysValGlyLysGluPhe :: ::: </pre>	427 1289
427 1288	nProGluArgPheMetSerLysGlyLeuGluAspGlySerArgPheA: ::: ::: ::: ::: 	411 1239
411 1238	CysaspThrHisAspValAlaAspValPheProAsnLysGluGluPheGl	395
394 1188	luLeuAsnGlyTyrGlnIleProLysGlyTrpAsnValIleTyrSerIle ::: ::: ::: :::	378 1139
378 1138	gIleAsnProProValProGlyGlyPheArgValAlaLeuLysThrPheG ::: ::: :::: :::: ::: CTGTTCACGCCCATTTCCGGCGGCTACCGCACTGTGCTGCAGACCTTCG	361 1089
361 1088	LeuLeuAspGlnLeuLysTyrThrGlyCysVallleLysGluThrLeuAr	345 1039
344 1038	lyMetTyrThrProGlyLysGlyLeuSerMetGlu	333 989
333 988	rGluValValGlnLysValArgGluGluValGlnGluLysValGluMetG ::::: ::: ::: CACTGTGCTGGAGAAGCTGCGGGATGAGCTGCGGGCTCAT	316 948
316 947	ThrThrAlaSerThrAlaThrSerLeuValMetPheLeuGlyLeuAsnTh	300
299 897	euGlnAlaMetLysGluAlaAlaThrGluLeuLeuPheGlyGlyHisGlu:: ::: :::::::::::::::::::::::::	283
283 847	aLeuGlnLeuLeuIleGluAsnSerArgArgSerAspGluProPheSerL ::: ::: ::::::::::::::	266 798
266 797	LysTysTleGlnAspAspAspAsnGluAsnGluGlnLysTyrLysAspAl:::: :::	250 757
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216 656	IleLysThrAspGluGlnGluLeuValGluAlaPheGluGluMetIleLy	200 616
199 615	etPheArgIleAlaMetArgIleLeuLeuGlyPheGluProGluGln ::: :::	184 566

476 leTyrProValAspAsnLeuProThrLysPhe 486

REFERENCE AUTHORS SOURCE seq_name: gb_ba3:SYCSLLE COMMENT REFERENCE REFERENCE KEYWORDS DEFINITION seq_documentation_block: FEATURES VERSION ACCESSION AUTHORS TITLE TITLE ORGANISM JOURNAL MEDLINE JOURNAL TITLE MEDLINE JOURNAL AUTHORS 1439 TGCACCCCGTGGATGGCCTCAGCGTCAAGTTC 1470 source synthetase; acyl-CoA desaturase 1; alanine racemase; aspartate 1-decarboxylase; cyanate lyase; cytochrome P450; dTDP-glucose 4,6-debydratase; elongation factor EF-G; endo-1,4-beta-glucnase; ferredoxin-nitrite reductase; ferredoxin-thioredoxin reductase; ferredoxin-thioredoxin reductase; catalytic chain; ferrochelatase; favoprotein; low affinity sulfate transporter; methionine aminopeptidase; methyltransferase; molybdenum cofactor biosynthesis protein A; molybdenum cofactor biosynthesis protein A; molybdenum cofactor subunit 2; molybdopterin (MPT) converting factor, subunit 1; molybdopterin biosynthesis MoeA; oligopeptide transport subunit 1; molybdopterin biosynthesis MoeA; oligopeptide transport system permease protein; peptidyl-tRNA hydrolase; phosphoribosyl formylglycinamidine cyclo-ligase; photosystem II p680 chlorophyll A apoprotein; polyA polymerase; endonuclease; replicative DNA helicase; succinate dehydrogenase iron-sulfur protein; tRNA-Cys; tRNA-fMet(exon1); tRNA-fMet(exon2); Ycf34. Synechocystis sp. (strain:PCC6803) DNA. Synechocystis sp. (strain:PCC6803) DNA. 2 (bases 1 to 113064) 2 (bases 1 to 113064) 2 (bases 1 to 113064) 3 (bases 1 to 113064) 4 (bases 1 to 113064) 5 (bases 1 to 113064) 6 (bases 1 to 113064) 7 (bases 1 to 113064) 7 (bases 1 to 113064) 8 (bases 1 to 113064) Kaneko,T., Tanaka,A., Sato,S., Kotani,H., Sazuka,T., Miyajima,N., Sugiura,M. and Tabata,S. Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome DNA Res. 2 (4), 153-166 (1995) D64003.1 GI:1001200 trNA-fMet; 2-ketcacid dehydrogenase (malate dehydrogenase, lactat dehydrogenase); 30S ribosomal protein S18; 50S ribosomal protein L33; 6-aminohexanoate-cycllc-dimer hydrolase; 7-ketc-8-aminopelargonic acid synthetase; KdtB; Mg-protoporphyrin IX monomethyl ester oxidative cyclase 66 kD subunit; MoxR protein; NADH dehydrogenase subunit 5; MoxR; Plab; acetyl-coenzyme A Tabata, Kazusa DNA Research Institute, Gene Structure 2; 1532-3 Yanauchino, Kisarazu, Chiba 292, Japan (E-mail:tabata@kazusa.or.jp, Tel:0438-52-3933, Fax:0438-52-3934) Yamada, M., Yasuda, M. and Tabata, S. Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC8803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions SYNCSLIE 113064 bp DNA BCT 13-FEB-1999 Synehocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766. Potential protein coding regions were assigned on the basis of similarity search of the ORFs and GeneMark analysis. D64003 AB001339 D64003.1 GI:10 Submitted (30-AUG-1995) to the DDBJ/EMBL/GenBank databases. Satoshi Direct Submission Tabata, S DNA Res. 3 (3), 109-136 (1996) teria; Cyanobacteria; Chroococcales; Synechocystis. (bases 1 to 113064) (bases 1 to 113064) complement(1. .3960) /note="ORF_ID:s110178" /product="hypothetical protein" /protein_id="BAA10440.1" /db_xref="GT:1001201" /organism="Synechocystis sp." /strain="PCC6803" 1. .113064 /db_xref="taxon:1143" transl_table=11 /codon_start=: ocation/Qualifiers Tanaka, A., Asamizu, E., Nakamura, Y., protein; Lactate

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LTQLPGWKEAEQATKKRIIQGAIQYIQQQTNIDYSWIGTNTYNFSELYGCKALQLILT
EAPRTLDNFSTDIWKRWTPIILSVPNSFIDSNPRKNCRKLVSLSYHHSPDEFLTTLLK
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NNQKRYALIENLVESIAEKDEDEDFYFLTSSMTEPIISSNDVDWMLEKLQDSNHEKIQ
RAWAKIIEEVFDRRDTKQISEIIKATQNNSILSDVFSYYFTPIELDSEEVTQLRDHYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (6412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVNKGEKQSIDAATVAGDFLEVLKTIVYLEPEAEVTPGGVCPLVWVEGLAITGE"
complement(6412...7251)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSK ITVGAHFYHVYSEKTAEKSYSLDQAENVVY IDKLQALHAGVNSLQGSFSLPFDGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CVSDDALHPGNISAERFDGEGTPTRRVDIIKNGVLTGLLHSAGTAKRFDTQPTGHANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLDYRPIPTGKYTVVFSARAFLSLLGAFSNLYNAQSILDKQSLATKETLGTAIASELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEASNRASVIVRVWNEKGLYGYTSTTDLDQAGISLALETAAEASAFGITDNIPDFSPE
AQVPIGGAENDVAEDAPMGDLITTLVKAEQDLLASHPAITGVPYNGLSEQTTERFYLN
SAGAKRYECRSYASIYLYSRAEQEGKKPRSAGEMKISRDLASLDIDGCLQTVKEKTLS
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/protein_id="BAA10442.1"
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/protein_id="BAA10441.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEKQKRFNWEILFGVIGIIGVIATVVGIFFNGIFNDVLKDSLNGSPSKIEQQAMPKN
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LIIPEPSNLDLSNQLSTIDKRTEKMEDEÞKIINNISDSTINAÞVGTSGVTSNNVTCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIDKENQDNNIFVIDRLEMCWDEKLENNLTEKYKDSQLKPNVFRKLLEKLIEQGAVQA
KDIALSTIRNYTNSEFDSERQKALFAIKALITYSDPDSWNVIWEKITADVQFGREAFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLIPQLHETAVWLASMRDNVFQEIIKTDPDVLLQTDIPTDSELRATIVANLLMQYEEE
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EVIQEVLDTGLFSSRGLHRMGWAHQTYAEFFAAWYLTQRNIDLSKIKTLLYSSADSTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLAIKPISLGFLLNTYRRHNSQFPPEQKRYESYLEGCKCLCEEVSKCRHALKETGNLD
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/note="ORF_ID:s1r0895"

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alignment_block:
US-09-668-482-2
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GGLSRGWTHNWDDASYGVAVILAQDTGNQAIKQDVTRWLDAWVKGTDGYQITDGGLRF
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QARPIMLIVIAATLFNILGNYGLGFGKWGFPALGITGLAIASIGSHWIMFISLLVYML
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SLTSALLFTDVNANTGGTGGEHQHPDD1PPTDPVVDPTPNPGTGRVFAANPAAADIVG
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AAHQYVSQTVLVLFMVPLAMSYAATVRVGQWFGQQHWPQIRQAALVSIGLAVLFMLTA
GIALLAYPQQIIGLYLDLNDPANGEALNVGISIMKIAAFGLVLDGLQRTANGVLQGLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="ferredoxin-nitrite reductase"
/protein_id="BAA10448.1"
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/db_xref="GI:1001207"
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/note="ORF_ID:slr0897"
/codon_start=1
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TTTTGTCTATTGTTGGGACAACATTCTGACATTCGAGAAAGGGTCAGACA 63004
                                       LeuValMetPheLeuGlyLeuAsnThrGluValValGlnLysValArgGl 324
                                                                                        TATTGCTATTGTTTGCCGGACATGAAACTTTAACTTCCGCATTATCTTCT
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                                                                                                                                                                                                                                 rArgArgSerAspGluProPheSerLeuGlnAlaMetLysGluAlaAlaT
                                                                                                                                                                                                                                                                                                                         {\tt GluAsnGluGlnLysTyrLysAspAlaLeuGlnLeuLeuIleGluAsnSe}
                                                                                                                                                                                                                                                                                                                                                                        TGGCTGAGCTTGAAAAATTATTAAAGCTCGACAACAGCAACCCCCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTACCTAATACCCTATTTGGTAAATCCCAACGAGCAAGGGCTTTGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValGluAlaPheGluGluMetIleLysAsnLeuPheSerLeuProIleAs 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATTTGGTATCCCCAATTAAGACGAATGACTTTTGATGTGGCGGCAACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTCCCTGGTTTGAAACTTATATTCAAGGGCTATTTAGTCTGCCAATTCC
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 Similarity:
                                                                                                                                                                                                                                                                                                                                                                           Sequence 1 from patent US
AR074363
                                                                                                                                                                                               1 (bases 1 to 1608)
Koncz,C., Mathur,J., Szekeres,M. and Altmann,T.
Nucleic acid molecules encoding cytochrome P450-type proteins
involved in the brassinosteroid synthesis in plants
Patent: US 5952545-A 1 14-SEP-1999;
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                                                                                                                                             TGGCGGAGGCGTTGACGGTGGTGGTGAAAAGG...AGGGAGGAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lyLysGluPheAlaLysValLeuLeuLysIlePheLeuValGluLeuThr 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCTTCTAATGTGTTCACACCGTTTGGTGGAGGGCCAAGGCTATGTCCCG
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                                                                                         thale cress.
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; viridiplantae; Embryophyta; Rosidae; eurosids II;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1608)
1 (bases 1 to 1608)
                               Szekeres, M., Nemeth, K., Koncz-Kalman, Z., Mathur, J., Kauschmann, A., Altmann, T., Redel, G.P., Nagy, F., Schell, J. and Koncz, C.

Brassinosteroids rescue the deficiency of CYP90, a cytochrome P450, controlling cell elongation and de-etiolation in Arabidopsis Cell 85 (2), 171-182 (1996)
                                                                                                                                                                                                                                                          Cytochrome P450.
                   96200769
                                                                                                                                                                                                                                                                                 X87367.1 GI:853718
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(bases 1 to 1608)
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alignment_block:
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TITLE
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313 ACCGGTTTGTTCTTCAGAACGAAGGGAAGCTTTTTGAGTGTTCTTATCCT
                                                                                         263
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                                                                                                                                                                                                                                                                                                                                               116 TACACGTTACCGT...CGGATGGGTCTGCCTCCGGGAAGCCTTGGTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                             66 CTCCTCCTCTCTCTCCATCGCCGCCGCCTCCTCCTCCTACTCCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 LeuLeuPheLeuAlaAlaValLysLeuTrpGluMetLeuMetIleArgAr
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                                                                                   GACGCATCTTTTGGTGAACCGACGATTTTCTCAGCTGACCCGGAAACGA 312
                                                                                                              sThrHisLeuPheGlyAsnProThrValArgValMetGlyAlaAspAsnV 97
                                                                                                                                                                                                              ArgArgLysPheLeuArgMetLysArgGlnLysTyrGlyCysIleTyrLy 80
                                          alArgGlnIleLeuLeuGlyGluHisLysLeuValSerValGlnTrpPro 113
                                                                                                                                                                        CCTGAGCCTTTCATCGACGAGAGAGTAGCCCGGTACGGTTCGGTTTTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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374 c 374 g 478 t
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48. .1466
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/db_xref="GI:853719"
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/cultivar="columbia"
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                                                                                   390 alIleTyrSerIleCysAspThrHisAspValAlaAspValPheProAsn 406
407 LysGluGluPheGlnProGluArgPheMetSerLysGlyLeuGluAspGl 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTCAATCATTAAAGACCATCTCATGCTTGATATTGACCGGTTAGTCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pValProPheSerGlyLeuTyrArg...GlyLeuArgAlaArgAsnPheI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValGluAlaPheGluGluMetIleLysAsnLeuPheSerLeuProIleAs 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGATCCAGGGGAATGGAGTGAGAGTTTAAGGAAAGAGTATCTTCTTGTC
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Length: Gaps:

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      511 ATAGGACACCATTTCAATGAAAAATGGAAGGGTAAAGATGAA...GTGAA 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 ATGGAAGGGCCCAAGTCTTTCATGAAACTGATTGGGGAAGATTCCATTGT 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 ValGlnTrpProAlaSerValArgThrIleLeuGlySerAspThrLeuSe 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 TCCTGTTTACATGACTTCCCTAATTGGGCATCCCACAGTTGTACTCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 CGATCAGAAACACCTCAAAAGTTTTTTGATGATAGATTGAAGAAATTCGG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 lProPheSerGlyLeuTyrArgGlyLeuArgAlaArg....... A 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 euLeuGlyPheGluProGluGlnIleLysThrAspGluGlnGluLeuVal 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 rAsnValHisGlyValGlnHisLysAsnLysLysLysAlaIleMetArgA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 yCysIleTyrLysThrHisLeuPheGlyAsnProThrValArgValMetG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 hrMetGlyLeuProPheIleGlyGluThrLeuGlnLeuIleLeuGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 eArgArgValAspProAsnCysArgSer.....ProLeuProProGlyT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CCTGCTATTCTTTCCCTTACCCTCGCACCTATTCTCGCCATTATTCTTCT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 ProValLeuLeuPheLeuAlaAlaValLysLeuTrpGluMetLeuMetIl 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCTAAAAGAGGCGAGGATCATCGCATCTTACGCACTGCACTTGCTCGGT 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCCTGCGGGAAACAATTAGTTCTTTCGAACGAGACAAGCTGGTAGAG 360
nLeuLeuIleGluAsnSerArgArgSerAspGluProPheSerLeuGlnA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lyAlaAspAsnValArgGlnIleLeuLeuGlyGluHisLysLeuValSer 109
                                                                                                           ATAGCTTCTGATGAT....
                                                                                                                                                                                 IleGlnAspAspAspAsnGluAsnGluGlnLysTyrLysAspAlaLeuGl 268
                                                                                                                                                                                                                                                                                                                                                                                                TCCAGGAACTCGTTATCGTAAAGGGCTTCAGGCGCGGCTGAAGCTTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluAlaPheGluGluMetIleLysAsnLeuPheSerLeuProIleAspVa 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTGCTTCCTTTGGTAAGAGGGCTTATCTTCTCCATTGCAAGCACCCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arg.....LysPheLeuArgMetLysArgGlnLysTyrGl 76
                                                                                                                                                                                                                                                          AAATTCTCTCTCTCTAATAAAACGCAGAAGAAGAGATCTGCGTTCAGGC
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                                                FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1219 GAAGAGTACTTCCCTGAGCCTGAAGAATTCAGGCCTTCAAGATTTGAGGA 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1069 TATACATGGCAAGCAGTTCAAGAATCACTACGAATGTACCCACCAGTTTT 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1019 ATAAAAAGGAAGGGAAGAAATCAGTTGGAAGGATTTGAAATCTATGAAA 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434 lySerArgMetCysValGlyLysGluPheAlaLysValLeuLeuLysIle 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 AlaAspValPheProAsnLysGluGluPheGlnProGluArgPheMetSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     928 GTTGCACCAATGGCCTTGATATTTAAGCTTCTATACTCCAATCCTGAATA 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 laMetLysGluAlaAlaThrGluLeuLeuPheGlyGlyHisGluThrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        828 GGTGTTGCTCACCTTCAGAGATGAAAAAGGGAACTCACTGACAGACCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             451 PheLeu 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 lvalGlnLysvalArgGluGluValGlnGluLysValGlu...MetGlyM 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        878 GGATTCTGGACAACTTTTCTGCTATGTTTCATGCTTCATATGACACCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oGlyGlyPheArgValAlaLeuLysThrPheGluLeuAsnGlyTyrGlnI 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  etTyrThrProGlyLysGlyLeuSerMetGluLeuLeuAspGlnLeuLys 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vigna radiata cytochrome P450 (CipCYP) mRNA, complete cds; nuclear gene for chloroplast product.
AF279252
                                                                                                                                                                                                                                                                                                                   Vigna radiata
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Vigna.
                                                                     Submitted (16-JUN-2000) Botany, National Taiwan University, No. Sec. 4 Roosevelt Road, Taipei, Taiwan
                                                                                                                        Yang, M.T. and Chen, Y.M. Direct Submission
                                                                                                                                                                                                                              P450
                                                                                                                                                                                                                                                   Cloning and sequencing of a Vigna radiata cDNA encoding cytochrome
                                                                                                                                                                                                                                                                           1 (bases 1 to 1649)
Yang, M.T. and Chen, Y.M.
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/organism="Vigna radiata"
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1. .1649
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                      441 TCTGTTGATGAAAGGCGCTCTGCACAAG...AGAATGCACTCGCTCACCA 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391 GATTGCAGTTACCCCGGTTCCATATCGAACCTGCTCGGAAAACACTCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341 CGGACCCGGAGCTGAACCGGTTCATTCTGCAGAACGAAGGGAAGCTGTTG 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 CGGCTCGATCTTCATGACGCACGTATTCGGCGAGCCGACGGTGTTCTCGG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 TATAAGAGTTCCAATCCGGAGCCGTTCATGGACGAGCGCGTGAGGCGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 GGAGCTATGGCCTTCATTGGCGAGACGCTGCAGCTGATATCTGCG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 etGlyAlaAspAsnValArgGlnIleLeuLeuGlyGluHisLysLeuVal 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 ArgArgLys......PheLeuArgMetLysArgGlnLysTy 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 GTTTCTCTGCCAACACTCCTTATTGTTCGCCGCCTCCGCC...GCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 rGlyCysIleTyrLysThrHisLeuPheGlyAsnProThrValArgValM 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 tLeuMetIleArgArgValAspProAsnCysArgSerProLeuProProG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 IleValLeuProValLeuLeuPheLeuAlaAlaValLysLeuTrpGluMe 30
                                                                                    GlnGlnGluValLysSerAlaIleGlnGluTrpLeuGlnLysAspSerCy 173
                                                                                                                                                                                   TGAGCTTCGCCAACTCCTCCATCATCAAGGATCACCTTCTCCACCACATC 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                           uSerAsnValHisGlyValGlnHisLysAsnLysLysLysAlaIleMetA 142
GACCGCCTCATCGGCCTCAACCTCGATACCTGGTCCGATCGT.....
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/product="cytochrome P450"
/prod
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91. .1515
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/db_xref="taxon:3916"
1. .1649
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Gaps: 15
Percent Identity: 29.375
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	ProThrMetLysThrGlyProThrIleTyrProVal 479	468
1445		1396
467	euThrGlnHisCysAsnTrpIleLeuSerA	455
454 1395	ysValGlyLysGluPheAlaLysValLeuLeuLysIlePheLeuValGlu	438 1346
ັພ ພ	pGlySerArgPheAsnTyrIleProPheGlyGlyGlyGlySerArgMetC ::::::	422 1296
422 1295	AsnLysGluGluPheGlnProGluArgPheMetSerLysGlyLeuGluAs ::: ::: ::::: :::: GATGCACGCACCTTCAACCCCTGGAGATGGCAGAGTAACTCATCGGAAGC	406 1246
405 1245	snVallleTyrSerIleCysAspThrHisAspValAlaAspValPhePro :: ::: ::: ::: AGGTCTTTGCATCATTTCGTGCTGTACATCTGAATCCTGAATATTACAAA	389 1196
389 1195	lalaLeuLysThrPheGluLeuAsnGlyTyrGlnIleProLysGlyTrpA :::::::::: agcaacgacagcaTcgacaTaaaagGTTaCaCTATTCCTAaGGGATGGA	372 1146
372 1145	IleLysGluThrLeuArgIleAsnProProValProGlyGlyPheArgVa:::::	356 1096
355 1095	ysGlyLeuSerMetGluLeuLeuAspGlnLeuLysTyrThrGlyCysVal ::: ::: :: : 	339 1046
339 1045	lArgGluGluValGlnGluLysValGluMetGlyMetTyrThrProGlyL::: ::::::::::::::::::::::::::::	322 1002
322 1001	ThrSerLeuValMetPheLeuGlyLeuAsnThrGluValValGlnLysVa	306 952
305 951	laAlaThrGluLeuLeuPheGlyGlyHisGluThrThrAlaSerThrAla	289 902
289 901	Prop CACT	272 862
272 861	AspAsnGluAsnGluGlnLysTyrLysAspAlaLeuGlnLeuLeuIleGl :::::::::: :::	256 814
255 813	heIleHisSerLysIleGluGluAsnIleArgLysLysIleGlnAspAsp:::::::::::::::::::::::::::::::::	239 767
239 766	eAspValProPheSerGlyLeuTyrArgGlyLeuArgAlaArgAsnP;::	223 720
223 719	0	207 670
206 669	rgIleLeuLeuGlyPheGluProGluGlnIleLysThrAspGluGlnGlu:	190 629
190 628	SValleuValTyrProGluMetLysLysLeuMetPheArgIleAlaMetA ::: :::: :::: ::::::	173 580

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JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by transcan-ser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
On Dec 17, 1999 this sequence version replaced gi:4512656.
The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
I (bases 1 to 16205)
Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D.,
Fujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E.,
Feldblyum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Ronning,C.M.,
Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., Vanaken,S.E., Umayam,L.,
Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H.,
Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D.,
Nierman,M.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and
Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC006931 116205 bp DNA PLN 05-APR-2000 Arabidopsis thaliana chromosome II section 231 of 255 of the complete sequence. Sequence from clones F14N22, F7D19. AC006931 AE002093
AC006931.5 GI:6598641
We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6523, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heeney, Lily Fu. Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prediction programs including GRAIL (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GRNSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the
                                                                                                                                                                                                                                                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are numbered from the top to bottom of the chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes were identified by a combination of three methods: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lin,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thale cress.
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This work was supported by the National Science Foundation.

Department of Energy and the US Department of Agriculture.

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="(GA)n"
complement(join(<7700. .78
8844. .8989,9294. .>9396))
/gene="At2g42670"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="(TA)n"
5756. .5806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="F7D19.34; predicted by genscan" complement(join(2761. .2943,3035. .316 3450. .3489,3570. .3646,3732. .3954)) /gene="At2q42660" /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(2132. .>116205)
/note="Sequence from clone F7D19"
/note="Sequence from .2943,3035. .31
complement(join(c2761. .2943,3035. .31)
3450. .3489,3570. .3646,3732. .>3954))
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LKHMNWKEQIEKACGAAMFFMRTGSCSAIKVAKLSMESDDIVENVTATLNGVVDVLPS
RWKYIRSLHLKLSESLSLPLYQTVPYLQLKIDPLGVEFVKNGEGLAKSDYDDSSSKSV
LEEFQPPDDFVIRRIPYRGPVIRT"
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complement(join(7700. .7818,7906. .811)
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YIRSNMPRLRWTPDLHLSFVRAVQRLGGPDRATPKLVLEMMNLKGLSIAHVKSHLQMY
RSKKLEPSSRPGFGAFMSGGRSYLMDMIDSRCIPHSDLRHAYNSKTVPSRVLNQDAVV
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KKIPQRNFTNAYRIPLPHPLINTTEDSPELCLIIDDRPESGLTEEDAKKNIKSENIPI
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/note="F14N22.8; predicted by genscan"
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/cultivar="Columbia"
                                                                                                                                                                                                       /note="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          .7818,7906. .8112,8195. .8348,
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4 TyrThrLeuMetValThrPheLeuCys.....ThrIleValLeuProVa 18 ::::::!!! ::: :: ::
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15513. .15664,15832. .17364,17446. .17514,17602. .17786)
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1.552
55.166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPEQDGSGGVVEGTTFDSDSEDEEGCKVMLGWLTIYTSNHPESKFTKLSLRSQLLAKI
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96 7664	AsnValArgGlnIleLeuLeuGlyGluHisLysLeuValSerValGlnTr ::: :::	112 67713
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129 7764	isGlyValGlnHisLysAsnLysLysLysAlaIleMetArgAlaPheSer:: ::: :::: ::: aaggCGAGAAGCATCGGGTCCTCAGAGGGATTGTAGCTAATAGTCTTAGC	145 67813
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195 7961	PheGluProGluGinIleLysThrAspGluGinGluLeuVaiGluAiaPh :::	211 67992
211 7993	.IleLysAsnLeuPheSerLeuProIleAspValProPheS ::::::::::::: :: TTAGAAGGTGTTTCCCTTTGCCGGTTGAGTTTCCTTGTT	228 68042
228 3043	erGlyLeuTyrArgGlyLeuArgAlaArgAsnPheIleHisSerLysIle 	244 68092
245 3093	GluGluAsnIleArgLysLysIleGlnAspAspAspAsnGluAsnGluGl :::::: ::: :::::: :::: GTTGGGAAGGTCAGGGAGAAAAGGGGAAGAAATGGAAAAAAGAGGGAGCTGA	261 68142
261 8143	nLysTyrLysAspAlaLeuGlnLeuLeuIleGluAsnSerArgArgS:: ::::::::::::::::::::::::::::::::	277 68179
277 3180	erAspGluProPheSerLeuGlnAlaMetLysGluAlaAlaThrGlu	292 68209
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68939 TAGCATGGATCCTCTCCCATTTCCGTCCCTTGGAATGCCAATCAAAATT 68988 487 hrsertyrval 490 :	437 etCysValGlyLysGluPheAlaLysValLeuLeuLysIlePheLeuVal 453 :: ::: ::: ::: ::: ::: ::: :::	404 PheProAsnLysGluGluPheGlnProGluArgPheMetSerLysGlyLe 420	68601 GGAAGGTTAACACATCCATCTCTTAAGATTCTTCAAGCTTCTAATCAAAA 68650 391	355 ValileLysGluThrLeuArgIleAsnProProValProGlyGlyPheAr 371	.ValargGluGluValGlnGluLysValGluMetGlyMetTyrThrProg ::: ::::: ::::: CATATCAGAACATGCTCAAATAAAGCAAACAAGGG	301 rAlaSerThrAlaThrSerLeuValMetPheLeuGly
AAACTTGCCCCCTGGTACTATGGCTACCACACATACTGGCCAC heIleGlyGluThrLeuGlnLeuIleLeuGlnArgArgLysPheLeuArg :::: ::::::::::::::::::::::::	alignment_block: US-09-668-482-2 x SLU54770 Align seg 1/1 to: SLU54770 from: 1 to: 1395 20 LeuPheLeuAlaAlaValLySLeuTrpGluMetLeuMetIleArgArgVa 36	ASE COUNT 4/0 a 242 C 268 g 415 C ORIGIN alignment_scores: Quality: 481.00	/translation="Martleflssfe" /translation="Martleflssfe" GETTEFIKLGPSFWKNQRARYGSFFW POSMIDILGKCNIAAVNGSAHKYMKG KVIDIQBKTNKMAFLSIKQIAGIES GFQARKIIVNLLRTLIEERRASKEIQ GYETVSTTSMMAVKYLHDHPKVLEBEINGY WADKSLBIQNSFLVFGGGTRQCPGKK VEAPNGLRIRVSAH"	/organism="Lycopersicon esculentum" /strain="GCR758" /db_xref=""taxon:4081" 1. 1395 cds /gene="dwarf" /codon_start=1 /product="cytochrome P450 homolog" /protein_id="ABH7070.1" /db xref="G1:1421741"	MEDLINE 96266705 REFERENCE 2 (bases 1 to 1395) AUTHORS Bishop,G. TITLE Direct Submission JOURNAL Submitted (11-APR-1996) Gerard Bishop, Sainsbury Laboratory, John Innes Centre, Colney Lane, Norwich, Norfolk, NR4 7UH, UK FEATURES Location/Qualifiers source 1, 1395	KEYWORDS SOURCE tomato. SOURCE tomato. ORGANISM Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon. Iycopersicon. Iycopersicon. I (bases I to 1395) AUTHORS Bishop,G.J., Harrison,K. and Jones,J.D. TITLE The tomato Dwarf gene isolated by heterologous transposon tagging encodes the first member of a new cytochrome P450 family JOURNAL Plant Cell 8 (6), 959-969 (1996)

386 1090	369 yPheArgValAlaLeuLysThrPheGluLeuAsnGlyTyrGlnIleProL ::: ::: :: :::	
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336 942	ValGlnGluLysValGluMetc ::::: :GGCTATTAGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA	
322 905	.yLeuAsnThrGluValVa ::: :: :: xTGATCATCCAAAAGTTCT	
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289 805	rgArgSerAspGluProPheSerLeuGlnAlaMetLy ::: TAACAGATGATGAGATGAT	
272 780	LeuI	
255 753	;LysIleGlnAspAsp :::{ ;GAAATTCAACATGATATGCTTGGTTACC	
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182 512	166 GluTrpLeuGlnLysAspSerCysValLeuValTyrProGluMetLysLy	
165 468	nGlnGluValLysSerAlaIleGln ::: :::: ::: TGAGTTTATGAGATCCCACTTAACC	
149 427	ArgAspAlaL TCAGAGACCAAC	
136 377	valGlnHisLySASnLy TCAGCTCACAAGTACAT	
119 327	rpProAlaSerValArgThrIle ::	

469 rMetLys 471 	453 ValGluLe:: :: 1285 CATTACTT	436 rgMetCys ::: 1235 GACAATGT	419 yLeuGluA: : 1191 CCTGGAAC	403 ValPhePro :::::: 1141 CTTTATCC	386 ysglyTrpAsnVal 1091 AAGGATGGAGAATA
471	453 ValGluLeuThrGlnHisCysAsnTrpIleLeuSerAsnGlyProProTh 469 :::::: ::: :::: 1285 CATTACTTCGTAACAAAATACAGATGGGAAGAAATAGGTGGAGATAAACT 1334	436 rgMetCysValGlyLysGluPheAlaLysValLeuLeuLysIlePheLeu	419 yLeuGluAspGlySerArgPheAsnTyrIleProPheGlyGlyGlySerA 436	ValPheProAsnLysGluGluPheGlnProGluArgPheMetSerLysGl 419 :::::: ::: ::: :: ::: ::: ::: ::: ::: ::: ::: :: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	386 ysGlyTrpAsnValIleTyrSerIleCysAspThrHisAspValAlaAsp 402
	469 1334	452 1284	436 1234	1190 1190	\$02 1140

||||||| | 1335 GATGAAA 1341

1884 1884 1512 1512 1512

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Strd Orig
Sequence
Sidequence
Sid
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Database length: 313950809
Search time (sec): 240.270000
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-Q-/cgn2_1/USP70_spool/US99668482_frunat_05112001_13354_10917/app_query.fasta_1.1680
-Q-/cgn2_1/USP70_spool/US99668482_vunat_05112001_13354_10917/app_query.fasta_1.1680
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-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPEXT=0.000 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
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-NORM-ext -MINLEN=0 -MAXLEN=2000000000
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Percent Identity:

100.000

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seq_documentation_block:
ID AAV09251 standard; cDNA; 1850 BP.
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Cytochrome zP450RAI cDNA sequence.
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Retinoid regulated gene; cytochrome KW cytochrome zP450RAI; reti
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Cytochrome zP450RAI cDNA sequence.
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KW Retinoid regulated gene; cytochrome xx
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/SIDS1/gcgdata/geneseq/geneseqn/NA1995.DAT:AAQ87171
/SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT28383
/SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT17399
                                                                                                    This nucleotide sequence encodes the cytochrome zP450RAI of the zebra fish. Its expression is dependent on the presence of retinoic acid (RA). The retinoid-regulated genes such as the inducible cytochrome P450RAI gene specifically metabolises a derivative of the RA. The cytochrome P450 gene in general produces enzymes involved in the oxidative metabolism of endogenous and exogenous compounds. The cytochrome P450 nucleotide sequence can be used to induce or suppress the expression of its protein. P450RAI is highly induced by RA in cell lines and tissues. This allows for development of a drug screen using promoters and nucleotide sequences to identify
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                                                                           drug screen using promoters and nucl drugs which are useful for reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Pages 59B-59D; 113pp; English.
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/product= "Cytochrome zP450RAI"
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sm; P450RAI; retinoic acid; '
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                                                         TCAGCTGTTGATCGAGAACAGCAGAAGAAGTGACGAACCTTTTAGTTTGC
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seq_documentation_block:

ID AAV12203 standard; cDNA; 1850 BP.

XX
AC AAV12203;

XX
DT 22-JUN-1998 (first entry)

XX
Exebrafish retinoid metabolising protein; P4501

XX

KW Retinoid metabolising protein; P4501

KW retinoic acid; zebrafish; inhibitor;

KW actinic keratosis; oral leukoplakia

KW actinic cell lung carcinoma; basa;

KW acute promyelocytic leukaemia; skin

KW acute promyelocytic leukaemia; skin

KW ichthyosis; therapy; diagnosis; scr

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Location/Qualifiers 88..1566 /*tag= a

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alignment_block:
US-09-668-482-2 x AAV12203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This cDNA clone codes for a novel zebrafish retinoid metabolising composed (see AAW44159) designated zp450RAI. The encoded protein is a cretinoid oxidase that has the ability to hydroxylate retinoic acid cat the 4 position of the beta-ionone ring and is inducible in composed to retinoic acid. To isolate the clone, composed to retinoic acid were compared using a differential display proceed to the composed composed (see AAV12213) was used to screen composed (see AAV12205) pa50RAI clones have also been identified. The composed (see AAV12205) pa50RAI clones have also been identified. The collated clones can be used in the recombinant production of pa50RAI proteins. Antisense nucleic acids can be used in a claimed composed for inhibiting retinoic acid hydroxylation for the treatment composed for inhibiting retinoic acid hydroxylation for the treatment composed to the head and/or neck, non-small cell lung carcinomas, basal cell carcinomas, acute promyelocytic leukaemia, skin cancer, and collation of collation collations. Promoter sequences (see AAV12206-08) are also collations.
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Ratio: 5.209
Percent Similarity: 100.000
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21-JUN-1996;
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96US-0667546.
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                           TyrThrGlyCysValIleLysGluThrLeuArgIleAsnProProValPr
                                                              etTyrThrProGlyLysGlyLeuSerMetGluLeuLeuAspGlnLeuLys
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oGlyGlyPheArgValAlaLeuLysThrPheGluLeuAsnGlyTyrGlnI 384
                 TACACTGGATGTGTGATTAAAGAGACTCTTAGAATCAACCCTCCTGTTCC
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ID AAV09247 standard; cD
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FF 23-JUN-1997; 97W0-C
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PD 31-DEC-1997.
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PD 31-DCT-1996; 96US-0
PR 21-JUN-1996; 96US-0
PR 1-PSDB; AAW37734.
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PI Identifying DNA encod
PT Lyserial in cancer chem
PT psoriasis
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Identifying DNA encod
PT Lyserial in cancer chem
PT psoriasis
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Example 4; Pages 56-5
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                                                      Identifying DNA encoding inducible or suppressible cytochrome P450 by screening for drugs which reduce the catabolism of retinoic acid useful in cancer chemotherapy and the treatment of acne and psoriasis
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                  Example 4; Pages 56-58; 113pp; English
                                                                                                                                                                                                                             (TOOH ) UNIV QUEENS KINGSTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cytochrome P450RAI cDNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                             96US-0724466.
96US-0667546.
                                                                                                                                                                                                                                                                                                                  97WO-CA00488
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1..1494
                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Cytochrome P450RAI"
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alignment_block:
US-09-668-482-2 x AAV09247
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Quality: 1738.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This nucleotide sequence encodes the human cytochrome P450RAI. Its expression is dependent on the presence of retinoic acid (RA). The retinoid-regulated genes such as the inducible cytochrome P450RAI gene specifically metabolises a derivative of the RA. The cytochrome P450 gene in general produces enzymes involved in the oxidative metabolism of endogenous and exogenous compounds. The cytochrome
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HisTyrIleProValIleGlnGlnGluValLysSerAlaIleGlnGluTr 167
                                                                                                                                                                                                                                                                                                                                                                           LeuLeuGlyGluHisLysLeuValSerValGlnTrpProAlaSerValAr 117
                                                                        pLeuGlnLysAspSerCys......ValLeuValTyrProGluM 180
                                                                                                                                                                                                    CACCATTCTGGGATCTGGCTGCCTCTCTAACCTGCACGACTCCTCGCACA
                                                                                                                                                                                                                                                                                                 gThrIleLeuGlySerAspThrLeuSerAsnValHisGlyValGlnHisL 134
                                                                                                                           TGCTACGTGCCGGTGATCACCGAGGAAGTGGGCAGCAGCCTGGAGCAGTG
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TGAAGCGCCTCATGTTCCGAATCGCCATGCGCATCCTACTGGGCTGCGAA

591

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV12204 alignment_scores:
Quality: 1738.00 alignment_block: Align seg 1/1 US-09-668-482-2 x AAV12204 Percent Similarity: Ratio: ţ. AAV12204 4.080 85.714 from: Percent

 \vdash

to: 1494

Identity:

Gaps:

5 68.008

414

c;

430

G;

318 T; 0 other;

seq_documentation_block:
ID AAV12204 standard; cDNA; 14
AC AAV12204;
XX AAV12204;
XY 22-JUN-1998 (first entry)
XX Retinoid metabolising proty
KW Retinoid metabolising proty
KW retinoic acid; human; inhil
KW actinic keratosis; oral lew
KW non-small cell lung carcino
KW acute promyelocytic lewkaew
KW ichthyosis; therapy; diagno
XX Homo sapiens.
XX W09749815-A1.
XX W09749815-A1.
XX J1-DEC-1997.
XX Homo sapiens.
XX W09749815-A1.
XX Homo sapiens.
XX W09749815-A1.
XX PP 31-DEC-1997; 97WO-CA0044
XX O1-OCT-1996; 96US-066754
XX O1-OCT-1996; 96US-066754
XX (TOOH) UNIV QUEENS KINGST
XX PP 23-JUN-1996; 96US-066754
XX (TOOH) UNIV QUEENS KINGST
XX Retinoid metabolising proty
Pr E.g. cancer, actinic keraty
Pr e.g. cancer, actinic seroeded
CC protein (see AAW44160) des
CC retinoid oxidase that has be
CC giaim 15; Page 55-57; 110p
XX Claim 15; Pa database, and an isolated clone was used to screen a cDNA library generated from an NT2 cell line treated with retinoic acid. The hp450RAI gene has been localised to 1023-24. Zebrafish, human and mouse p450RAI cDNA clones (see AAV12203-05) are claimed. They can be used in the recombinant production of P450RAI. Antisense nucleic acid by the used in a claimed method for inhibiting retinoic acid hydroxylation for the treatment of cancer, actinic karatosis, oral leukoplakia, secondary tumours of the head and/or neck, non-small cell lung carcinomas, basal cell carcinomas, acute This cDNA clone codes for a novel human retinoid metabolising protein (see AAW44160) designated hp450RAI. The encoded protein is retinoid oxidase that has the ability to hydroxylate retinoic acid at the 4 position of the beta-ionone ring and is inducible in epithelial cells exposed to retinoic acid. To isolate the clone, actinic keratosis; oral leukoplakia; head tumour; neck tumour; non-small cell lung carcinoma; basal cell carcinoma; acute promyelocytic leukaemia; skin cancer; acne; psoriasis; ichthyosis; therapy; diagnosis; screening; cytochrome P450; ss Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid; human; inhibitor; antisense; cancer; actinic keratosis; oral leukoplakia; head tunour; neck tunour; n Human retinoid metabolising protein hP450RAI cDNA promyelocytic leukaemia, skin cancer, and premalignancy associated with actinic keratosis, acne, psoriasis and/or ichthyosis. Promoter sequences (see AAV12206-08) for the P450RAI genes are als zebrafish P450RAI was used to search an expressed sequence tag Retinoid metabolising protein - useful to develop products to treat, e.g. cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or Page 55-57; 110pp; English (first entry) QUEENS KINGSTON 96US-0724466. 96US-0667546. 97WO-CA00440. Petkovich 1494 BP PM, White are also SS is

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                                                                 GGGCCAGGGCTGCAAAGACGCGCTGCAGCTGTTGATCGAGCACTCGTGGG
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AGAGGGGAGAGCGGCTGGACATGCAGGCACTAAAGCAATCTTCAACCGAA
                              rgSerAspGluProPheSerLeuGlnAlaMetLysGluAlaAlaThrGlu
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seq_documentation_block:

ID AAV09252 standard; cDNA; 1725 BF
XX
AC AAV09252;
XX
DT 07-JUL-1998 (first entry)
XX
DE Cytochrome P450RAI isoform cDNA
XX
Retinoid regulated gene; cytochr
KW cytochrom.
XX
OS Synthetic.
XX
Synthetic.
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EH Key Location/Qualifi
FT CDS /*tag-a
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XX
PD 31-DEC-1997.
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                                                                                                                                                                                                           Retinoid regulated gene; cytochrome P450 gene; enzyme; oxidative metabolism; P450RAI; retinoic acid; RA; promoter;
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                                                                                                                                                                                                                                                              Cytochrome P450RAI isoform cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heAsnTyrIleProPheGlyGlyGlySerArgMetCysValGlyLysGlu 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTATCTGTGATACTCATGATGTGGCAGAGATCTTCACCAACAAGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hrPheGluLeuAsnGlyTyrGlnIleProLysGlyTrpAsnValIleTyr 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alGlnGluLysValGluMetGlyMetTyrThrProGlyLysGlyLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTATCCTGTGGACAATCTCCCTGCAAGATTCACCCATTTC 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leTyrProValAspAsnLeuProThrLysPheThrSerTyr 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGACTGGCAGCTTCTAAATGGACCTCCTACAATGAAAACCAGTCCCACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sasnTrpIleLeuSerAsnGlyProProThrMetLysThrGlyProThrI 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAGCTTCATTCCATTTGGAGGAGGCCTTAGGAGCTGTGTAGGCAAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTTTGAATTAAATGGATACCAGATTCCCAAGGGCTGGAATGTTATCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTTCGACTGAATCCCCCAGTTCCAGGAGGGTTTCGGGTTGCTCTGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rLeuArgIleAsnProProValProGlyGlyPheArgValAlaLeuLysT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MetGluLeuLeuAspGlnLeuLysTyrThrGlyCysValIleLysGluTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PheAlaLysValLeuLeuLysIlePheLeuValGluLeuThrGlnHisCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerIleCysAspThrHisAspValAlaAspValPheProAsnLysGluGl
                                                                         /product= "Cytochrome P450RAI isoform"
                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                 ВP
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-668-482-2 x AAV09252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This nucleotide sequence encoding an isoform of cytochrome P450RAI. Its expression is dependent on the presence of retinoic acid (RA). The retinoid regulated genes such as the inducible cytochrome P450RAI gene specifically metabolises a derivative of the RA. The cytochrome P450 gene in general produces enzymes involved in the oxidative metabolism of endogenous and exogenous compounds. The cytochrome P450 nucleotide sequence can be used to induce or suppress the expression of its protein. P450RAI is highly induced by RA in cell lines and tissues. This allows for development of a drug screen using promoters and nucleotide sequences to identify drugs which are useful for reducing the catabolism of RA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-077193/07.
P-PSDB; AAW37735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996;
21-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying DNA encoding inducible or suppressible cytochrome P450 -
by screening for drugs which reduce the catabolism of retinoic acid,
useful in cancer chemotherapy and the treatment of acne and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Pages 59D-59F; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Petkovich PM;
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                                                                                                                                                                                                     Sequence 1725 BP; 408 A; 425 C; 475 G; 417 T; 0 other;
   325
                                  101
                                                                    275
                                                                                                                                     225 TCTGCAGATGAAGCGCAGGAAATACGGCTTCATCTACAAGACGCATCTGT 274
                                                                                                                                                                                                                                                                          125 GCAGCCGCGATCGCAGCTGCGCCCTTGCCCCCGGTACCATGGGC
                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                           84
                                                                                                                                                                                                                                                                                                          34 rgArgValAspProAsnCysArgSerProLeuProProGlyThrMetGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                 25 ATGGGGCTCCCGGCGCTGCTGCCAGTGCGCTCTGCACCTTCGTGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                   MetGlyLeuTyrThrLeuMetValIhrPheLeuCysThrIleValLeuPr
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heGlyAsnProThrValArgValMetGlyAlaAspAsnValArgGlnIle 100
                                                                                                                                                       eLeuArgMetLysArgGlnLysTyrGlyCysIleTyrLysThrHisLeuP 84
                                                                    TTGGGCGGCCCACGGTGCGGGTGATGGGCGCGGATAATGTGCGGCGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 1734.00
Ratio: 4.070
milarity: 85.887
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96US-0667546.
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Gaps: 4
Percent Identity: 67.742
                                                                                                                                                                                                                                                                               174
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410 1265 427	IleCysAspThrHisAspValAlaAspValPheProAsnLysGluGluPh	394 1216 410
	heGluLeuAsnGlyTyrGlnIleProLysGlyTrpAsnValIleTyrSer 	377 1166
377 1165	UARGIleAsnProProValProGlyGlyPheArgValAlaLeuLysThrP :::	360 1116
360 1115	GluLeuLeuAspGlnLeuLysTyrThrGlyCysVall1eLysGluThrLe	344 1066
343 1065	InGluLysValGluMetGlyMetTyrThrProGlyLysGlyLeuSerMet::::: :::: aGAGCAAGGGCTTACTTTGCAAGAGCAATCAAGACAACTTAGACATG	327 1016
327 1015	tPheLeuGlyLeuAsnThrGluValValGlnLysValArgGluGluValG ::: ::: :::	310 966
310 965	LeuPheGlyGlyHisGluThrThrAlaSerThrAlaThrSerLeuValMe 	294 916
293 915	eraspGluProPheSerLeuGlnAlaMetLysGluAlaAlaThrGluLeu ::::::: ::: :::: 	· 277 866
277 865	uGlnLysTyrLysAspAlaLeuGlnLeuLeuIleGluAsnSerArgArgS : :	260 816
260 815	GluGluAsnIleArgLysLysIleGlnAspAspAspAsnGluAsnGl 	245 766
244 765	erGlyLeuTyrArgGlyLeuArgAlaArgAsnPheIleHisSerLysIle	228 716
228 715	eGluGluMetI1eLysAsnLeuPheSerLeuProI1eAspValProPheS :::	211 666
211 665	ProGluGlnIleLysThrAspGluGlnGluLeuValGluAlaPh : 	197 616
196 615	etLysLysLeuMetPheArgIleAlaMetArgIleLeuLeuGlyPheGlu::: :::	180 566
180 565	PLEUGlnLysAspSerCysValLeuValTyrProGluM:	167 525
167 524	HisTyrIleProVallleGlnGluValLysSerAlaIleGlnGluTr 1	151 475
150 474	ysAsnLysLysLysAlaIleMetArgAlaPheSerArgAspAlaLeuGlu 1 :::::: ::: ::: ::: aGCAGCGAAAGAAGTGATTATGCAGGCCTTCAGCCGCGAGGCACTCCAG	134 425
L34 424	ThrileLeuGlySerAspThrLeuSerAsnValHisGlyValGlnHisL	117 g 1 375 C

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seq_documentation_block:
ID AAV12205 standard; cDNA; 1725 BP.
XX
AC AAV12205;
XX
DT 22-JUN-1998 (first entry)
XX
DE Mouse retinoid metabolising protein; P450
KW Retinoid metabolising protein; P450
KW retinoic acid; mouse; inhibitor; an actinic keratosis; oral leukoplakia in mouse promyelocytic leukaemia; skin ichthyosis; therapy; diagnosis; scr OS
Mus musculus.
XX
FH Key Location/Qualifiers FT CDS

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This cDNA clone codes for a novel mouse retinoid metabolising protein (see AAW44160) designated mp450RAI. The encoded protein is retinoid oxidase that has the ability to hydroxylate retinoic acid at the 4 position of the beta-lonone ring and is inducible in epithelial cells exposed to retinoic acid. The clone was isolated from a retinoic acid-treated P19 teratocarcinoma cDNA library using human P450RAI cDNA (see AAV12204) as probe. Zebrafish, human and mouse P450RAI cDNA clones (see AAV12203-05) are claimed. They
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1416
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                                                                                                                                                                                                                                                                                                                          Claim 15; Page 62-64; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid; mouse; inhibitor; antisense; cancer; actinic keratosis; oral leukoplakia; head tumour; neck tumour; non-small cell lung carcinoma; basal cell carcinoma; acute promyelocytic leukaemia; skin cancer; acne; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse retinoid metabolising protein mP450RAI cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ichthyosis; therapy; diagnosis; screening; cytochrome P450; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Petkovich PM,
                                                                                                                                                                                                                                                                                                                                                                                                                           useful to develop products to treat, oral leukoplakia, acne, psoriasis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             White JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             460
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alignment_block:
US-09-668-482-2 x AAV12205
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                       197
                                                                                                                                                           167
                                                                                                                                                                                           475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               can be used in the recombinant production of P450RAI proteins. Antisense nucleic acids can be used in a claimed method for inhibiting retinoic acid hydroxylation for the treatment of cancer, actinic keratosis, oral leukoplakia, secondary tumours of the head and/or neck, non-small cell lung carcinomas, basal cell carcinomas, acute promyelocytic leukaemia, skin cancer, and premalignancy associated with actinic keratosis, acne, psoriasis and/or ichthyosis. Promoter sequences (see AAV12206-08) for the P450RAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1725 BP; 408 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes are also claimed.
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ProGluGlnIle.....LysThrAspGluGlnGluLeuValGluAlaPh
                                                  TGAAGCGCCTCATGTTCCGCATCGCCATGCGCATCCTGCTGGGCTGCGAG
                                                                                    etLysLysLeuMetPheArgIleAlaMetArgIleLeuLeuGlyPheGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pLeuGlnLysAspSerCys......ValLeuValTyrProGlum
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                                                                                                                                                                                        TGCTACGTGCTCGTGATCGCTGAGGAAGTCAGCAGTTGTCTGGAGCAGTG
                                                                                                                                                                                                                        HisTyrIleProVallleGlnGlnGluValLysSerAlaIleGlnGluTr
                                                                                                                                                                                                                                                          AGCAGCGAAAGGATGATTATGCAGGCCTTCAGCCGCGAGGCACTCCAG
                                                                                                                                                                                                                                                                                                                              CACCATCCTGGGCGCTGGCTGCCTCCCAACCTGCACGATTCCTCGCACA
                                                                                                                                                                                                                                                                                                                                                     gThrIleLeuGlySerAspThrLeuSerAsnValHisGlyValGlnHisL
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                                                                                                                                                                                                                                                                                                                                                                                                                              LeuLeuGlyGluHisLysLeuValSerValGlnTrpProAlaSerValAr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heGlyAsnProThrValArgValMetGlyAlaAspAsnValArgGlnIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eLeuArgMetLysArgGlnLysTyrGlyCysIleTyrLysThrHisLeup 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTGCAGATGAAGCGCAGGAAATACGGCTTCATCTACAAGACGCATCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rgArgValAspProAsnCysArgSerProLeuProProGlyThrMetGly
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Ratio: 4.070
milarity: 85.887
                                                                                                                      AGCTGCGGCGAGCGCCCTCCTGGTCTACCCCGAGG
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alignment_scores:
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Ratio: 4.040
Percent Similarity: 85.915
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                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a human protein, designated PSEC64, which is related to neuron growth. The PSEC64 protein and its gene can be us for the development of a preventive agent for use in the treatment of diseases in which nerves are involved.
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                                                            LeuProPheIleGlyGluThrLeuGlnLeuIleLeuGlnArgArgLysPh
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                                                                                                               rgArgValAspProAsnCysArgSerProLeuProProGlyThrMetGly
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                                                                                                                                                                                                                                       CACTTACCTGGGGCTCTACCCACATGTTCTCCAGAAAGTGCGAGAAGAGC
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seq_documentation_block:
ID AAV12216 standard; DM
XX
AC AAV12216;
XC AAV12216;
XX
DT 22-JUN-1998 (first &
XX
Mouse retinoid metabolising
KW retinoid keratosis; oncuse;
KW retinoic keratosis; therapy;
XW actinic keratosis; therapy;
XW ichthyosis; therapy;
XX
MO9749815-Al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid; mouse; inhibitor; antisense; cancer; actinic keratosis; oral leukoplakia; head tumour; neck tumour; non-small cell lung carcinoma; basal cell carcinoma; acute promyelocytic leukaemia; skin cancer; acne; psoriasis; ichthyosis; therapy; diagnosis; screening; cytochrome P450; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443
       This sequence comprises a genomic clone of a novel mouse retinoid metabolising protein designated mp450RAI. A cDNA clone (see AAVI2205) that includes a coding sequence for the full-length mp450RAI protein (see AAWI4161) is also provided. The encoded
                                                                                                                                                                                    Disclosure; Page 69-70; 110pp;
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                                                                                                                                                                                                                                                                                             Retinoid metabolising protein - useful to develop products to treat, e.g. cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse retinoid metabolising protein mP450RAI genomic DNA.
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CC keratosis, oral leukoplakia, secondary tumours of the head and/or CC neck, non-small cell lung carcinomas, basal cell carcinomas, acute	96 nvalArgGlnIleLeuLeuGlyGluHisLysLeuValSerValGlnTrpP 113 ::: :::	SS1 GAAAGMAGAATTGAAACACTCTTGCTGGGGGGTGCTCAGGTGAT 500
	igi S-i	igi
	lignment_scores: Quality: 1169.00 Gaps: 16 Percent Similarity: 36.872 Percent Identity: 29.858 lignment_block: US-09-668-482-2 x AAV12216 Align seg 1/1 to: AAV12216 from: 1 to: 4164 41	lignment_scores: Quality: 1169.00 Gaps: 16 Ratio: 3.005 Gaps: 16 Gaps: 16 Gaps: 16 Gaps: 16 Gaps: 16 Gaps: 17 Gaps: 16 Gaps: 17 Gaps: 18 Gaps: 18 Gaps: 18 Gaps: 19 Gaps: 18 Gaps: 18 Gaps: 19 Gaps: 18 Gaps: 18 Gaps: 10 Gaps: 18 Gaps: 18 Gaps: 18 Gaps: 18 Gaps: 18
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149	2 AGGGTGGCATTGGTCTAGAGAGCTGTGGAAGGGGGTGGCTGAGCAATGGG	144:
284		284
144	2 AAAGATAATTTTATCGTTGGGGGTCACCACAACACGAGGAACCGTATTAA	1392
284		284
139	2 TTACATCAAGAAACATAACAGTAGCAAAATTACCGTTATGAAGTAGCAAC	1342
284		284
134	2 CAAACAACCCTTTCAGAAGGGTCGCCTAAGAGCATCTGCATATCCGATAT	1292
284		284
129	2 TGCTAGGTCTAGAGCTTTTCAACCTGTGGGTCGTGACCCCTTCACGGAGC	1242
284		284
124	2 GGGTCTCCAAAGCCCTGTCAAGGCCCCAGCTACTTCCAAGTGGGCGGCGA	1192
284		284
119:	AAGGTGCCAAGGGCCGGGGAGTGCCTCTGACTTTCCAGACACACTTTCTG	1142
284		284
1141	TCGTGGGAGAGGGGAGAGAGCTGGATATGCAGGTGAGAAGCAATTTCAA	1092
284	SerArgArgSerAspGluProPheSerLeuG	274
273 1091	snGluAsnGluGlnLysTyrLysAspAlaLeuGlnLeuLeuIleGluAsn :: CAGAGCCGGATGGGGGTTGCAAGGACGCGCTGCAGCTCCTGATTGAGCAC	257 1042
1041	CGCGCGCATCGAGGAGAACATTCGCGCCCAAGATCCGCCGGCTTCAGGCTA	992
257	sSerLysIleGluGluAsnIleArgLysLysIleGlnAspAspAspA	241
9	CCGCCACGCTCTCCGCGCTCAGGGGGTGAAGGCGCGGAACCTTATACA	,Ā (
241	Glv.LeuArqAlaArqAsnPheIleHi	u
941	GCGGTTTGCGGAGTCGGAGTAGGGGAACGCAAGCTCGGGCATCCGCTCA	892
232		232
891	CTCTTCCCATTGACGTGCCCTTTAGCGGCCTGTACCGGGTAAG	842
232	euPheSerLeuProIleAspValProPheSerGlyLeuTyrArg	218
841	GGAGGAGCAGCAGCTCGTGGAGGCTTTCGAGGAGATGACCCGCAAT	9
217	sThrAspGluGlnGluLeuValGluAlaPheGluGluMetIleLysAsn	
791		742
201	<pre>flealametArgIleLeuLeuGlyPheGluProGluGlnIleL</pre>	186
741	GCGAGCGCGCCTCCTGGTCTACCCCGAGGTGAAGCGCCTCATGTTCCG	692
186	ValLeuValTyrProGluMetLysLysLeuMetPheAr	
691	InGlnGluValLysSerAlaILeGLnGLuTrpLeuGLnLysAspSerCys ::: :: :: :: ::: CTGAGGAAGTCAGCAGTTGTCTGGAGCAGTGGCTAAGCTGC	157 651
ı (GCAGGCCTTCAGCCGCGAGGCACTCCAGIGCIACCIACCGIGCCCGIGAICO	_
157	targalapheSerargAspalaLeuGluHisTyrIleProValIleG	-4-

339		339
2391	AGGTTTAGTTAACAGGTGAGTCCTGCTGGGCTGACTTTTTTTT	2342
339		339
2341	ATCAGGCCATCAGCTCTTTCCCTTTTATCCTCTCCCATCCAGACGCCTTC :	2292
339		339
2291	ACATTGTCTGGATAATGGGTTTAGGCTGAGGAAGTGTGGAAAGGAAGG	2242
339		339
N	TGTTGGTGAGGGCTCAGGGTATGACCCTTTATATACCTGATAAGCA	2192
39	${\tt uMetGlyMetTyrThrProGlyLys}$	331
₽4	GTGATTAGAGCCAATAGCTGATCAGGGTC	2142
330		330
2141	AAGGTTCTCCTTTCC	2092
330		330
2091	GGCAGAATTTGACCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCC	2042
330		330
2041	TCCACCTCGTGAATTTAAAAAAGGCAGTTGTTTGTACTGGGCTCTCTCT	1992
330		330
1991	TACTATGACAGTGAAGATCTGAGAGCTAGGTGGGAACTGTGGGGGGAGAGAC	1942
330		330
1941	TAACCACCACCACCCCCCACTGTATATAAGTTTTGCTCGATACACCCAG	1892
330		330
1891	GGATGATTCTAGAGGTTCCCCCATTTGCCTAGGACATTCCTCTAT	1842
۵	1	329
328 1841	euglyLeuAsnThrGluValValGlnLysValArgGluGluValGlnGlu 	312 1792
312 1791	eGlyGlyHisGluThrThrAlaSerThrAlaThrSerLeuValMetPheL 	295 1742
295 1741	TTCCGTTTTTATCCTTAGGCACTAAAACAATCGTCAACAGAGCTCC	1692
6	GGTCAGGTCTTTGTAACAGTGCTATAAACTGCACTCAGATCTGTATAAA	4 0
		- 00
1641	CTATGAACAAAACGGATTTTACCCTTGAAGTCTTCCGTGCAATATTCTCA	1592
284		284
1591	AAGAGCAGGATTAAGGGAGTTTTGCGTTTTTGTTGTGGTCTTTGACTTT	1542
284		284
1541	GAAGATCCCAAAGTTCAAAGGGCAAGGCTCATCTACAAAGGTTAAAGCGG	1492
284		284

н->	: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV12214	seq_name
	ThrserTyr 489 ::: ACCCACTTC 3150	487 3142
486 3141	etLysThrGlyProThrIleTyrProValAspAsnLeuProThrLysPhe	470 3092
470 3091	lGluLeuThrGlnHisCysAsnTrpIleLeuSerAsnGlyProProThrM	453 3042
453 3041	MetCysValG1yLysG1uPheAlaLysValLeuLeuLysIlePheLeuVa 	437 2992
436 2991	euGluAspGlySerArgPheAsnTyrIleProPheGlyGlyGlySerArg ::: ::::::	420 2942
420 2941	lPheProAsnLysGluGluPheGlnProGluArgPheMetSerLysGlyL:	403 2892
403 2891	GlyTrpAsnValIleTyrSerIleCysAspThrHisAspValAlaAspVa 	387 2842
386 2841	AATTCTTAGGATTTTTTTTTTTTTAAACAGGGATACCAGATCCCCAAG	379 2792
2791	CCATGCTAGTAATGACTTTTTGTTGCTTGCAAGCTCAGGGCCGGGATTGTC	2742
7	CTGCCTCCTATGGTACTGGGAACCAATTTGCTCTCCTCTCTTAATGCCA	2692 378
378		378
3/8 2691	TGTTGAGCATCAGCTGCCCAGAGCAGTGGCTCACTGCCCTTGACAGTGTC	2642
1 0	CACCTCCTGTCCCCCACCCCCAGCCCT	2592
378		378
378 2591	5 lProGlyGlyPheArgValAlaLeuLysThrPheGlu	366 2542
366 2541	LysTyrThrGlyCysVallleLysGluThrLeuArgIleAsnProProVa ::: AAATACACTGGGTGTCATTAAGGAGACCCTGCGATTGAATCCTCCGGT	350 2492
349 2491	CCAAGAGCAATCAAGACAACAAGATTAGGAAACTTTGGCACAGCTT	340 2442
2441	CCCAGGGATCCATCACTCACTTTTTATCTGTTTCCATAGGGCTTACTTT	2392

seq_documentation_block:
ID AAV12214 standard; DNA; 2677 BP.
XX
AC AAV12214;
XX
DT 22-JUN-1998 (first entry)
XX
DE Human retinoid metabolising protein

Human retinoid metabolising protein hP450RAI genomic DNA.

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alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence comprises a genomic clone of a novel human retinoid cometabolising protein designated hP450RAI. Another genomic clone (see AAV12215) is also provided, as well as a cDNA clone (see AAV12204) that includes a coding sequence for the full-length hP450RAI exidase composed in (see AAW44160). The encoded protein is a retinoid oxidase contains the ability to hydroxylate retinoic acid at the 4 position of the beta-lonone ring and is inducible in epithelial cells composed to retinoic acid. The hP450RAI gene has been localised to composed to retinoic acid. The hP450RAI gene has been localised to composed to retinoic acid. The hP450RAI gene has been localised to composed to retinoic acid. The hP450RAI gene has been localised to compose the combinant of anylogation of P450RAI. Antisense nucleic acid scan be used in a composed to a cancer, actinic keratosis, oral leukoplakia, secondary tumours of the head and/or neck, non-small cell lung carcinomas, composed to cancer, actinic keratosis, oral leukoplakia, secondary composed compose
                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
                                                                                                                                                                                                                                                                                                                                                   US-09-668-482-2 x AAV12214
                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AAV12214
                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid; human; inhibitor; antisense; cancer; actinic keratosis; oral leukoplakia; head tumour; neck tumour; non-small cell lung carcinoma; basal cell carcinoma; acute promyelocytic leukaemia; skin cancer; acne; psoriasis; ichthyosis; therapy; diagnosis; screening; cytochrome P450; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996;
21-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 68; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Retinoid metabolising protein - useful to develop products to treat, e.g. cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-077178/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2677 BP; 489 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ichthyosis
                                                                                                                                                                                      676 ATGGGGCTCCCGGCCGCTGCTGCCAGTGCGCTCTGCACCTTCGTGCTGCC 725
                                                                                    726 GCTGCTGCTTCCTGGCTGCGATCAAGCTCTGGGACCTGTACTGCGTGA 775
34 rgArgValAspProAsnCysArgSerProLeuProProGlyThrMetGly 50
                                                                                                                              oValLeuLeuPheLeuAlaAlaValLysLeuTrpGluMetLeuMetIleA 34
                                                                                                                                                                                                                     MetGlyLeuTyrThrLeuMetValThrPheLeuCysThrIleValLeuPr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
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96US-0667546.
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2.891
40.713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              775 C; 868 G; 511 T;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 673
Gaps: 13
Percent Identity: 31.947
                                                                                                                                                                                                                                                                                                   to: 2677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 other;
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203	187 IleAlaMetArgIleLeuLeuGlyPheGluProGluGlnIleLySThrAs 	, 1
186 1666	174ValLeuValTyrProGluMetLysLysLeuMetPheArg :::: ::: :::	16
173 1616	157 nGlnGluValLysSerAlaIleGlnGluTrpLeuGlnLysAspSerCys. ::: ::::::::::: 576 CGAGGAAGTGGGCAGCAGCCTGGAGCAGTGGCTGAGCTGCG	15 1
157 1575	141 MetArgAlaPheSerArgAspAlaLeuGluHisTyrIleProValIleG1	15
1525	139A.Halle :::	14
- 4	GACTGGGGGTGTCTGGAAGGGGACGGCGGTAGACGAG	14
138	138	_
1425	376 AGGACCCTCTGCCAGCTCCAGGTTAGCTTTCCCAGCTCG	13
138	138	1
1375	GCTGATGGATGCTAGGCGCGGGCTAGCA	13
138	138	_
1325		12
138	138	_
138 1275	123 AspThrLeuSerAsnValHisGlyValGlnHisLysAsnLysLysLys	12
122 1225	106 ysleuvalservalGlnTrpProAlaSerValArgThrIleLeuGlySer::	11.
106 1175	89 largValMetGlyAlaAspAsnValArgGlnIleLeuLeuGlyGluHiSL 	11:
89 1125	73 GlnLysTyrGlyCysIleTyrLysThrHisLeuPheGlyAsnProThrVa :::	10.
	 TYMCTCCCAMAGCGGARSAARNKCYKGMRGATGAAGCGC	10;
	70 CAUDUCTIONCOURAGE OF THE CONTROL	
	03	٥
69	26 GCTGAAGTCGGGGTAGGCGCCCCCGGGAGGCAIGCTAITIGCGGCTAGGAG	. 9
1 0		σ.
925	76 TGGGGGGACAGGCTGCTTCCCCGGAGCCCGGCGCGCGCTCTGGGCTTCT	87
69		σ
67 875	51 LeuProPheIleGlyGluThrLeuGlnLeuIleLeuGlnArgArg.LysP:::: ::: :::	8 5
825	776 GCGGCCGCGACCGCAGTTGTGCCCTCCCATTGCCCCCCGGGACTATSGGS (77

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AAT85306 standard; CDNA to mRNA; 1608 BP
XX
AC AAT85306;
XC AAT85306;
XC AAT85306;
XC Id-APR-1998 (first entry)
XX
DT 14-APR-1998 (first entry)
XX
DT 14-APR-1998 (first entry)
XX
DT 14-APR-1998 (first entry)
XX
CS Arabidopsis thaliana cytochrome P450-type
XX
CYtochrome P450-type hydroxylase; identification of modified plant
XX
CYTOCHROME P450-TYPE
XX
CS Arabidopsis thaliana.
XX
XX
CS 27-MAR-1997: 97WO-EP01586.
XX
XX
CS 27-MAR-1997: 97WO-EP01586.
XX
XX
XX
ALTANAR-1996; 96US-0622166.
XX
XX
ALTANAR-1996; 96US-0622166.
XX
XX
ALTANAR-1996; 96US-0622166.
XX
XX
ALTANAR-1996; 96US-0622166.
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ALTANAR-1997: 97WO-EP01586.
XX
XX
ALTANAR-1996; 96US-0622166.
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ALTANAR-1997: 97WO-EP01586.
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ALTAN
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                                                                                                                                                                                                                                            The present sequence encodes Arabidopsis thaliana cytochrome P450-type hydroxylase. The hydroxylase can be used to identify brassinosteroids or brassinosteroid inhibitors, useful to produce plants with modified physiological and/or phenotypic characteristics. The modified plants may show, e.g. stimulation of growth, increased cell elongation, increased wood production, accelerated seed germination at low temperatures, an increase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2614
                                                                                                                                          dry weight, repressed anthocyanin production during growth in ligh and/or inhibited de-etiolation which is induced, e.g. by cytokinin in the dark or an increase in stress tolerance. The hydroxylase or
                                                                                                         in the dark or an increase in stress tole its coding sequence can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated plant cytochrome P450-type hydroxylase gene - used to identify substances acting as brassino-steroid(s) or brassinosteroid inhibitors for the production of modified plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2664 CACATGTTCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytochrome P450-type hydroxylase; identification; brassinosteroid inhibitor; modified plant; recomb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana cytochrome P450-type hydroxylase cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hrGluValValGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= cytochrome_P450-type_hydroxylase
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              374 G; 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Szekeres MA;
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                                                                                                         the recombinant production
              T; 0 other
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                                                                                                                                                                                  by cytokinin,
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alignment_block:

Percent Similarity:

Ratio:

552.50 1.811 62.887

Percent Identity:

Length:

485 14 29.897

alignment_scores

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Align seg 1/1 to: AAT85306 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 TACACGTTACCGT...CGGATGGGTCTGCCTCCGGGAAGCCTTGGTCTCC 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 oGluMetLysLysLeuMetPheArgIleAlaMetArgIleLeuLeuGlyP 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 gValAspProAsnCysArgSerProLeuProProGlyThrMetGlyLeuP 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 CTCCTCCTCTCTCCATCGCCGGCGGCTTCCTCCTACTCCGCCG
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                                            819 .....GCGGCGGATGATGGATTTTCCGATGAAGAGATTGTTGACTTCT
290 laThrGluLeuLeuPheGlyGlyHisGluThrThrAlaSerThrAlaThr 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spAlaLeu.....GluHisTyrIleProValIleGlnGlnGluValLys 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yValGlnHisLysAsnLysLysLysAlaIleMetArgAlaPheSerArgA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaSerValArgThrIleLeuGlySerAspThrLeuSerAsnValHisGl 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alArgGlnIleLeuLeuGlyGluHisLysLeuValSerValGlnTrpPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCGGTTTGTTCTTCAGAACGAAGGGAAGCTTTTTGAGTGTTCTTATCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTCAATCATTAAAGACCATCTCATGCTTGATATTGACCGGTTAGTCCGG
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                                                                                                                                                              AsnGluAsnGluGlnLysTyrLysAspAlaLeuGlnLeuLeuIleGluAs
                                                                                                                                                                                                                                                                                                           TCTC...TTCTCCACCACTTACCGCAAAGCCATCCAAGCGCGGAGGAAGG
                                                                                                                                                                                                                                                                                                                                                 pValProPheSerGlyLeuTyrArg...GlyLeuArgAlaArgAsnPheI
                                                                                                                                                                                                                                                                                                                                                                                             ATCGAAGGCTTC......TTCTCTCTCTCCTCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                           ValGluAlaPheGluGluMetIleLysAsnLeuPheSerLeuProIleAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heGluPro.....GluGlnIleLysThrAspGluGlnGluLeu 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTAATCTTGATTCTTGG.....TCTTCTCGTGTTCTCCTCATGGA 550
                                                                                                                                                                                                                                                               leHisSerLysIleGluGluAsnIleArgLysLysIleGlnAspAspAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGATCCAGGGGAATGGAGTGAGAGTTTAAGGAAAGAGTATCTTCTTGTC
                                                                                        nSerArgArgSerAspGluProPheSerLeuGlnAlaMetLysGluAlaA
                                                                                                                                    GAAGAAGGAGCGGAGAAAAAAAGATATGCTTGCGGCGTTGCTT....
                                                                                                                                                                                                                          TGGCGGAGGCGTTGACGGTGGTGGTGATGAAAAGG...AGGGAGGAGGAG
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seq_documentation_block:
ID AAC48157 standard; DNA; 1646 BP.
XX
AC AAC48157;
XX
T 18-OCT-2000 (first entry)
XX
DT 18-OCT-2000 (first entry)
XX
Whybridisation assay; genetic mappi
KW Hybridisation assay; genetic mappi
KW protein identification; signal tra
KW pr
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                                    GACGTGAAGTCAATGAAGTTCACTCGAGCTGTGATTTATGAGACATCAAG
                                                                   LeuLeuAspGlnLeuLysTyrThrGlyCysValIleLysGluThrLeuAr
                                                                                                                                     luLysValGluMetGlyMetTyrThrProGlyLysGlyLeuSerMetGlu 344
                                                                                                                                                                          TCACCCAAAAGCTCTTCAAGAACTAAGAGCTGAGCATTTGGCATTCAGGG
                                                                                                                                                                                                  uAsnThrGluValValGinLysValArgGluGlu......ValGinG
                                                                                                                                                                                                                                                TACGAAACTGTCTCTACGACCTCAATGATGGCTCTTAAGTACCTTCATGA
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                                                                                                        AAAGAAAACGACAG......GACGAACCACTCGGTCTTGAG
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                                                                                                                       508 GACCATCTCTTGCCTAAGATTGATGATTTCATGAGAAACTATCTTTGCGG
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   605 TGGCATTT.....
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                                                                                       uTrpLeuGlnLysAspSerCysValLeuValTyrProGluMetLysLysL 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                          138
                                                                                                                                                                                                                                               ZIP: M5L 1A9
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuProPheIleGlyGluThrLeuGlnLeuIleLeuGlnArgArgLysPh
                                                                                                                                              rgArgValAspProAsnCysArgSerProLeuProProGlyThrMetGly
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                                                                                                                GACGAGTCGATCCGAACTGCAGAAGTCCTCTACCGCCAGGTACCATGGGC
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-238-821B-14 + 270.50
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US95-05744-14 + 270
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-750-703-1 + 270.00
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-948-564-11 + 269.50
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-948-564-13 + 268.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-724-466B-3
                                                                   US-09-668-482-2 x US-08-724-466B-3
                                                                                                                        Quality: 2563.00
Ratio: 5.209
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/667,
FILING DATE: June 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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APPLICANT: Beckett,
                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1850 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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RMATION FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/724,466B
                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                         nucleic acid
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SYSTEM: MS-DOS
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                                US-08-724-466B-3
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Gaps: 0
Percent Identity: 100.000
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           TyrThrGlyCysVallleLysGluThrLeuArgIleAsnProProValPr 367
                                                                             AGTGGTGCAGAAGGTCAGAAGGAGGAGGAGAAGGTTGAAATGGGCA 1087
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APPLICATION NUMBER: US/08/882,164D
FILING DATE: June 25, 1997
PRIOR APPLICATION NUMBER: 08/667,546
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-2653
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1850 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
; Sequence 3, Application US/08882164D
; Patent No. 6306624
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APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Diskette, 3 1/2 inch,
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
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STREET: Box 25, Cor
CITY: Toronto
STATE: Ontario
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ZIP: M5L 1A9
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alignment_scores:
Quality: 2563.00
Patio: 5.209
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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-882-164D-3
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US-09-668-482-2 x US-08-882-164D-3
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                     LysThrAspGluGlnGluLeuValGluAlaPheGluGluMetIleLysAs
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euArgAlaArgAsnPheIleHisSerLysIleGluGluAsnIleArgLys
                                                              AAGACGGACGAGCAAGAACTGGTGGAAGCTTTTGAGGAAATGATCAAAAA
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                                                                                                                                                           TCAGCTGTTGATCGAGAACAGCAGAAGAAGTGACGAACCTTTTAGTTTGC
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                CCAAATTCACTAGTTATGTCAGAAAT
                 1563
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seq_documentation_block: Sequence 5, Application Patent No. 6063606 GENERAL INFORMATION:

US/08724466B

APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein NUMBER OF SEQUENCES: 30

Protein

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alignment_scores:
Quality: 1738.00
Ratio: 4.080
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MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IEM PC compatible
COMPUTER: MORD PERFECT
CURENT APPLICATION NOTA:
APPLICATION NOMBER: US/08/724,466B
FILING DATE: October 1, 1996
PRIOR APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 50767/00004
FELEMANE: Hunt, John C.
REGISTRATION NUMBER: 50767/00004
FELEMANE: (416) 863-434
FELEPAX: (416) 863-434
FELEPAX: (416) 863-434
FELEPAX: (416) 863-263
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1494 base pairs
STRANDENNESS: Single
TOPOLOGY: Linear
FORDION FOR SERVINGER: STRANDENNESS: SINGLE
TOPOLOGY: Linear
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US-09-668-482-2 x US-08-724-466B-5
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ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Toronto
ZIP: M5L 1A9
COUNTRY: Canada
                                                                                                                  9ThrIleLeuGlySerAspThrLeuSerAsnValHisGlyValGlnHisL 134
                                                 Percent Identity: 68.008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1494
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126	409 uPheGlnProGluArgPheMetSerLysGlyLeuGluAspGlySerArgP 4	
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276 838	59 nGluGlnLysTyrLysAspAlaLeuGlnLeuLeuIleGluAsnSerArgA 	
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seq_documentation_block:
Sequence 5, Application US/08882164D
Patent No. 6306624
GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
ADDRESSEE: Blake, Cassels & Graydon
                                                                                                                alignment_scores:
Quality: 1738.00
Ratio: 4.080
Percent Similarity: 85.714
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STRANDEDNESS: single
TOPOLOGY: linear
US-08-882-164D-5
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US-09-668-482-2 x US-08-882-164D-5
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FILING DATE: June 25, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
APPLICATION NUMBER: 08/724,466
APPLICATION NUMBER: 05/724,466
APPLICATION NUMBER: 05/724,466
APPLICATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
FELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEPAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
IFENERY: 1404 hesc pairs
Align seg 1/1 to: US-08-882-164D-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1389 TGACTGGCAGCTTCTAAATGGACCTCCTACAATGAAAACCAGTCCCACCG 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: Canada
ZIP: M5L 1A9
ZIP: M5L 1A9
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: M5-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
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CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1494 base pairs
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                                                                                                                Length: 497
Gaps: 5
Percent Identity: 68.008
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27 83) nGluGlnLysTyrLysAspAlaLeuGlnLeuLeuIleGluAsnSerArgA 	259 789
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                                                                                                                                                                                                         Patent No. 6306624

GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 31, Application US/08882164D
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MEDIUM TYPE: Diskette, 3 1/2 inch, COMPUTER: COMPAQ, IBM PC compatible OPERATING SYSTEM: MS-DOS 5.1
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CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 MetGluLeuLeuAspGlnLeuLysTyrThrGlyCysValIleLysGluTh 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   989 TGAAGAGTAAGGGTTTACTTTGCAAGAGCAATCAAGACAACAAGTTGGAC
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           APPLICATION NUMBER: US/08/
FILING DATE: June 25, 1997
                                                                                                                                                            ZIP: M5L 1A9
                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGACTGGCAGCTTCTAAATGGACCTCCTACAATGAAAACCAGTCCCACCG 1438
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APPLICATION DATA:
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                                                                                                                                                                          Canada
                               US/08/882,164D
                                                                                                                     1.4
                                                                                                                     ₹
                                                                                                                     storage
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alignment_scores:
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Ratio: 4.070
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FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: OCCOBET 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-2653
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 1725 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-882-164D-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 GCAGCCGCGATCGCAGCTGCGCCCTCCCCTTGCCCCCGGTACCATGGGC 174
                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 rgArgValAspProAsnCysArgSerProLeuProProGlyThrMetGly
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                                                                               HisTyrIleProValIleGlnGlnGluValLysSerAlaIleGlnGluTr
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                                                                                                                                                                                                                                                                                                                                                            heGlyAsnProThrValArgValMetGlyAlaAspAsnValArgGlnIle 100
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Gaps: 4
Percent Identity: 67.742
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565
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616 CCGGGTCCAGCGGGCGGCGGGGAGGACGAGCAACAGCTCGTGGAGGCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGGGGTTGCAAGGACGCGCTGCAGCTCCTGATTGAGCACTCGTGGGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lnGluLysValGluMetGlyMetTyrThrProGlyLysGlyLeuSerMet 343
                 nTrpIleLeuSerAsnGlyProProThrMetLysThrGlyProThrIleT 477
                                                                                                                                                                                     eGlnProGluArgPheMetSerLysGlyLeuGluAspGlySerArgPheA 427
                                                                                                                                                                                                                                                                                                                                 ATCTGTGACACCCACGATGTGGCAGATATCTTCACTAACAAGGAGGAATT
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TTGGCAGCTTCTAAATGGACCTCCTACAATGAAGACAAGCCCCACTGTGT
                                                                               GCAAAAATTCTTCTTAAGATATTTACAGTGGAGCTGGCTAGGCACTGTGA
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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-882-164D-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
TOPOLOGY:
US-08-882-164D-38
                                                                                                                                                                                                                                                                                                                                      alignment_block:
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                                                                                                                                                                                                                                                                                                               US-09-668-482-2 x US-08-882-164D-38
                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 38, Application US/08882164D
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MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,164D
FILING DATE: June 25, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION UNMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR EGO ID NO: 388
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      477 yrProValAspAsnLeuProThrLysPheThrSerTyr 489
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                                                                                                                                                                                                                     ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Box 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: Canada ZIP: M5L 1A9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Blake, Cassels & Graydon STREET: Box 25, Commerce Court West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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                                    LysThrHisLeuPheGlyAsnProThrValArgValMetGlyAlaAspAs
                                                                                                                AGAGGGGTAGACGAGACCAGATGCTCCCCGGCGCCCCCTCATGCGGGTTG
                                                                                                                                                       .GlyThrMetGlyLeuProPheIleGlyGluThrLeuGlnLeuIleLeuG
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Ratio: 3.005
milarity: 36.872
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273	257 snGluAsnGluGlnLysTyrLysAspAlaLeuGlnLeuLeuIleGluAsn::: :::
	2 CGCGCGCATCGAGGAGAACATTCGCGCCAAGATCCGCCGGCTTCAGG
257	ysLysIleGlnAspAspAsp
991	CGTGAAGGCGCGGAACC
241	.LeuArgAlaArgAsnPheIleH
941	aacgcaagctcgggcatc
232	
891	42 CTCTCTCTCTCCCATTGACGTGCCCTTTAGCGGCCTGTZ
w	8 LeuPheSerLeuProIleAspValProPheSerGlyLeuTyrArg
841	
	.spGluGlnGluLeuValGluAlaPheGluGluMetIleLysAs
201 791	18 911eAlaMetArgiieLeuteudlyPheGluProGluGlnIleL
741	92
186	7.4
691	651 CTGAGGAAGTCAGCAGTTGTCTGGAGCAGTGGCTAAGCTGC
173	157 lnGlnGluValLysSerAlaIleGlnGluTrpLeuGlnLysAspSerCys
157 650	140 eMetArgAlaPheSerArgAspAlaLeuGluHisTyrIleProValIleG :::
600	
140	ω
550	501 CTGAAATTCTTGAAAGGGTACTCGGAAAGGCGAAGGGGGGGG
138	138
500	451 GAGATCCACTTTAGCTTTTCTGCTAGCACGTGGGTTAGTCCTGGGGGGGA
138	138
450	401 GCGGGGCGAGGGCTAGTCCTATGTGGTGGGGACCAGGACCCTCTCTATCT
138	138
400	351 TGGCTGGCAGGGAGACCTCATCCTATGGCTTGGTTCAGGCAAAATAGAAT
138	138
350	301 GATTCCTCGCACAAGCAGCGAAAGAAGGTGAGGGTGAGCTGGCAACTCCT
138	130 GlyValGlnHisLysAsnLysLysLys
300	TOTAL SELVE A LALE JULIE LE
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113 250	96 nValArgGlnIleLeuLeuGlyGluHisLysLeuValSerValGlnTrpp 11
200	

1991	TACTATGACAGTGAAGATCTGAGAGCTAGGTGGGACTGTGGGGGGAGAGAC	1942	
330		ũ	
1941	TAACCACCACCACCCCCACTGTATATAAGTTTGCTCGATACACCCAG	ف	
330		330	
1891	AAGGTAGGATGATTCTAGAGGTTCCCCATTTGCCTAGGACATTCCTCTAT	1842	
328 1841		1792	
312 1791		295 1742	
295 1741	TTCCGTTTTATCCTTAGGCACTAAAACAATCGTCAACAGAGCTCCTCTT	285 1692	
1691	GGTCAGGTCTTTGTAACAGTGCTATAAACTGCACTCAGATCTGTATAAAC	1642	
284		284	
1641	CTATGAACAAAACGGATTTTACCCTTGAAGTCTTCCGTGCAATATTCTCA	1592	
284		284	
1591	${\tt AAGAGCAGGATTAAGGGAGTTTTGCGTTTTTGTTGTGGTCTTTGACTTT}$	1542	
284		284	
1541	GAAGATCCCAAAGTTCAAAGGGCAAGGCTCATCTACAAAGGTTAAAGCGG	1492	
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1491	AGGGTGGCATTGGTCTAGAGAGCTGTGGAAGGGGGGTGGCTGAGCAATGGG	1442	
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1441	AAAGATAATTTTATCGTTGGGGGTCACCACAACACGAGGAACCGTATTAA	1392	
284		. 284	
1391	TTACATCAAGAAACATAACAGTAGCAAAATTACCGTTATGAAGTAGCAAC	1342	
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1341	CAAACAACCCTTTCAGAAGGGTCGCCTAAGAGCATCTGCATATCCGATAT	1292	
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284		284	
284	TCGTGGGAGAGGGGAGAGAGGCTGGATATGCAGGTGAGAAGCAATTTCAA	1092	
<u>ب</u> د	CAGAGCCGGATGGGGGTTGCAAGGACGCGCTGCAGCTCCTGATTGAG	1042	
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403 2891	387 GlyTrpAsnVall1eTyrSerI1eCysAspThrHisAspValAlaAspVa
2841	379LeuAsnG_Y\\yrG_Inite\rou\ys
7	42 CCATGCTAGTAATGACTTTTTGTTGCTTGCAAGCTCAGGGCCGGGATTG
378	378
2741	2692 CTGCCTCCTATGGTACTGGGAACCAATTTGCTCTCCTCTCTTAATGCCAT
378	378
2691	2642 TGTTGAGCATCAGCTGCCCAGAGCAGTGGCTCACTGCCCTTGACAGTGTC
378	378
2641	2592 CACCTCCTGTCCCCCACCCCCAGCCCTCGTCCACGTCCACTCTGCTATGC
378	378
378 2591	366 lproglyglypheargValAlaLeuLysThrPheGlu
366 2541	350 LysTyrThrGlyCysVallleLysGluThrLeuArgIleAsnProProVa
4	42 GCAAGAGCAATCAAGACAAGTTAGACATGGAAACTTTGGCACAGCTT
2441 349	CCAGGGATCCATCACTTTTTTTTATCTGTTTCCATAGGGCTTACTTT
	339
2391	2342 AGGTTTAGTTÁACAGGTGAGTCCTGCTGGGCTGACTTTTTTTTTGGAGTG
339	339
2341	2292 ATCAGGCCATCAGCTCTTTCCCTTTTATCCTCTCCCATCCAGACGCCTTC
339	339
2291	2242 ACATTGTCTGGATAATGGGTTTAGGCTGAGGAAGTGTGGGAAAGGAAGG
339	339
2	92 GCAGTGTTGGTGAGGGCTCAGGGTATGACCCTTTATATACCTGATAAGCA
ů Q	231 Gly WetGlyWetTyrThrDroGlyTys
2191	AATAATGTGATTAGAGCCAATAGCTGATCAGGGTC
330	330 3
2141	2092 TCCACCACCACCATCACCACCTTTTATAGAGCAAGGTTCTCCTTTCC 2
330	330 3
2091	2042 GGCAGAATTTGACCCTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCC 2
330	330 3
2041	1992 TCCACCTCGTGAATTTAAAAAGGCAGTTGTTTGTACTGGGCTCTCTTTG 2
330	330 3

alignment_scores: Quality: 792.00 Length: 673 Ratio: 2.891 Gaps: 13	REGISTRATION NUMBER: 36,424 REFERENCE_DOCKET NUMBER: 50767/00010 FELECOMMUNICATION INFORMATION: TELEPHONE: (416) 863-4344 TELEPAX: (416) 863-4263 INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS: LENGTH: 2677 Dasee pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear US-08-882-164D-36	LICATION DATA ON NUMBER: U. TE: June 25, CATION DATA: ON NUMBER: OTE: OCTOBER ENT INFORMATION, NUMBER:	STATE: ODTOILO STATE: ONTATIO COUNTRY: Canada ZIP: M5L 1A9 COMPUTER READABLE FORM: COMPUTER: Diskette, 3 1/2 inch, 1.4 Mb storage COMPUTER: COMPAQ, IBM PC compatible COMPUTER: COMPAQ, IBM PC compatible OPERATING SYSTEM: MS-DOS 5.1 SOFTWARE: WORD PERFECT	seq_documentation_block: Sequence 36, Application US/08882164D Patent No. 6306624 GENERAL INFORMATION: APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein NUMBER OF SEQUENCES: 43 CORRESPONDENCE ADDRESS: ADDRESSEE: Blake, Cassels & Graydon STREET: Box 25, Commerce Court West	487 ThrSerTyr 489	453 IGluLeuThrGlnHisCysAsnTrpIleLeuSerAsnGlyProProThrM 4 [:::: :::	1PheProAsnLysGluGluPheGlnProGluArgPheMetSerLysGlyL
			Ф			DAA 3091 DAA 3091 Phe 486 	4 4 4 4 4

Percent	Similarity: 40.713 Percent Identity: 31.947
lignmen US-09-6	t_block: 68-482-2 x US-08-882-164D-36
Align s	eg 1/1 to: US-08-882-164D-36 from: 1 to: 2677
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17 726	LeuTrpGluMetLeu ::::: CTCTGGGACCTGTAC
34 776	rgArgValAspProAsnCysArgSerProLeuProProGlyThrMetGly 50
51 826	LeuPropheIleGlyGluThrLeuGlnLeuIleLeuGlnArgArg.Lysp 67 ::: :::
67	Arg
	TGGGGCGGGACAGCCTGCTTCCCCGGAGCCCGGCGCGCGC
926	GCTGAAGTCGGGGTAGGCGCCCCCGGGAGGCATGCTATTTCGCGCTAAGAC 07s
69	
976	CGCTCCCCGGMKYMCSCTCAWGC
70 1026	TMWCCTCCGCCTYMCTCCCAMAGCGGARSAARWKCYKGMRGATGAAGCGC 1075
73 1076	GlnLysTyrGlyCysIleTyrLysThrHisLeuPheGlyAsnProThrVa 89 :::
89 1126	largValMetGlyAlaAspAsnValArgGlnIleLeuLeuGlyGluHisL 106
106 1176	ysLeuValSerValGlnTrpProAlaSerValArgThrIleLeuGlySer 122 :: :sGCTGGTGTCGGTCCACTGGCCACCGTCGGTCGCGCACCATTCTGGGATCT 1225
123 1226	AspThrLeuSerAsnValHisGlyValGlnHisLysAsnLysLysLys 138 ::::
138	
138	GGGGGCAGGAGGGCTGGACAGGGAGGGGGGACCCCATTTATGAGCG 1325
1326	CGGGCTAGCAGCTTGAGGTGGGC
138	
1376	AGGACCCTCTGCCAGCTCCAGGTTAGCTTTCCCAGCTCGGAGAGTGCCAT 1425
138	
Ñ	GTGTCTGGCAGGACTGGGGGTGTCTGGAAGGGGACGGCGGTAGACGAGAG 1475
139	

2413	ACTAAAGGGACGTT 2	2364
280	2	280
2363	GAACCTTGCGATTTTAATAAAACTAAGACTTTAACTCAGGAGTTTCCGGT 2	2314
280	2	280
2313	CTTTAMCAGGTTTCAAAGGGAAAGTTGGAATTTGCAAAAATGTTAATAAA 2	2264
280	2	280
2263	CAGGAGAGCT	2214
280	2	280
2213	CGGCTCAGACTACAGCTATGGAATCCCGAAGGAAGGCTGAGACACC	2164
280	ArgArgSerAspGluPro	275
2163	TGGGGCCCCCAAAGCGCGCGCCTGGGGCCCAGCTTTCTGGAGTGGGCGGC	2114
274		274
2113	AGACCAGGCACTGCGGAGTTTGGTCCCCTGGCTTTCCCAAGGCGCTGTTCC	2064
274		274
2063	ACTCGTGGGAGAGGGGAGAGCGGCTGGACATGCAGGTGAGTAGCAGCTTC	2014
274	snSer	273
2013	FILE CONTROL OF THE PROPERTY O	σ (
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256 1963	HISSETTYSIIEGLUGLUASNILEATGLYSLYSIJEGLNASPASPAS	1914
ø	CACCGCGCGCTCTCTGCGCTCAGGGCATGAAGGCGCGGAACCTCATT	- σ
240	Gly.LeuArgAlaArgAsnPheIle	23
1863	AGGGCGGCAAACGGGCTGCGGACTAGGGGCGCGGGACCTGGGCGTCTGCT	1814
232		232
232 1813	snLeuPheSerLeuProIleAspValProPheSerGlyLeuTyrArg	217 1764
1763	CGGGGACTCCGAGCAGCAGCTTGTGGAGGCCTTCGAGGAAATGACCCGCA	1714
217	pGluGlnGluLeuValGluAlaPheGluGluMetIleLysA	203
1713	ATCGCCATGCGCATCCTACTGGGCTGCGAACCCCAACTGGCGGCGA	166
2 :	T]eA]aMetArgT]eLeuLeuG]vDheG]uDroG]uG]nT]eLvsThras	187
186 1666	ValLeuValTyrProGluMetLysLysLeuMetPheArg	174 1617
1616		157
173	ysSerAlaIleGlnGluTrpLeuGlnLysAspSerCys.	15
1575	ATGCGGGCCTTCAGCCGCGAGGCACTCGAATGCTACGTGCCGGTGATCAC	1526
i G	GGGCGGATGGAGGCTTTTAACGCTGTCCCCTCCTCGGGACTCAGGTGATT	147

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seq_documentation_block:
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                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTMARRE: PAtentin Release #1.0, Versi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/622,166A
FILING DATE: 27-MAR-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SYENSSON, LEONARD R.
REGISTRATION NUMBER: 30,330
REGISTRATION NUMBER: 30,330
REGISTRATION NUMBER: 0147-0153P
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8050
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDITICANT: KONCZ, CSABA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2514 CCTTCTGTCAAACCGCAGGCAGACTTGTGAGAATGTGGGTCTCACTCTAT 2563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2464 TTAGCCCTTCTAGTCTTCCCTCCAGAACTCTCAGTTCGATTCTGAGTAAT 2513
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APPLICANT: SZEKERES, MIKLOS
APPLICANT: ALTMANN, THOMAS
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING CYTOCHROME
TITLE OF INVENTION: P450-TYPE PROTEINS INVOLVED IN THE BRASSINOSTEROID SYNTHESIS
NUMBER OF SEQUENCES: 4
                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1608 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                     ORIGINAL SOURCE:
                                                               MOLECULE TYPE:
                                           ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP STREET: P.O. Box 747 CITY: Falls Church Common. With the common common.
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ORGANISM: A. thaliana
                                                                                                                                 STRANDEDNESS:
                                                                                                                                                           TYPE: nucleic acid
                                                                                                             TOPOLOGY:
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                                                                                          cDNA to mRNA
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NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
LIBRARY: lambd
                                                                                                                                                                                                                                                                                                                                                                                                                                               460
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alignment_scores:
    Quality:
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US-09-668-482-2 x US-08-622-166A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 AlaSerValArgThrIleLeuGlySerAspThrLeuSerAsnValHisGl 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      313 ACCGGTTTGTTCTTCAGAACGAAGGGAAGCTTTTTGAGTGTTCTTATCCT 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 GACGCATCTTTTTGGTGAACCGACGATTTTCTCAGCTGACCCGGAAACGA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 CCTGAGCCTTTCATCGACGAGAGAGTAGCCCGGTACGGTTCGGTTTTCAT 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 CTCTGATAGGAGACTTTTCAGCTGATCGGAGCTTACAAAACAGAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 sThrHisLeuPheGlyAsnProThrValArgValMetGlyAlaAspAsnV 97
97 alArgGlnIleLeuLeuGlyGluHisLysLeuValSerValGlnTrpPro 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 ArgArgLysPheLeuArgMetLysArgGlnLysTyrGlyCysIleTyrLy 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 gValAspProAsnCysArgSerProLeuProProGlyThrMetGlyLeuP 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 CTCCTCCTCTCTTCCATCGCCGCCGGCTTCCTCCTACTCCGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLONE: C204
                                                           ATCGAAGGCTTC.....:.....TTCTCTCTTCCTCTCCC
                                                                                                                                                                                   heGluPro.....GluGlnIleLysThrAspGluGlnGluLeu
                                                                                                                                                                                                                               AGAAGCCAAAAAGATAACGTTTGAGCTAACGGTGAAGCAGTTGATGAGCT
                                                                                                                                                                                                                                                         oGluMetLysLysLeuMetPheArgIleAlaMetArgIleLeuLeuGlyP 195
                                                                                                                                                                                                                                                                                                                 TTTAATCTTGATTCTTGG......TCTTCTCGTGTTCTCCTCATGGA 550
                                                                                                                                                                                                                                                                                                                                           SerAlaIleGlnGluTrpLeuGlnLysAspSerCysValLeuValTyrPr 178
                                                                                                                                                                                                                                                                                                                                                                                                  CTTCAATCATTAAAGACCATCTCATGCTTGATATTGACCGGTTAGTCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                        spAlaLeu.....GluHisTyrIleProValIleGlnGlnGluValLys 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCTTTGCATAAA...CGTATGCACTCTCTCACCATGAGCTTTGCTAATT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yValGlnHisLysAsnLysLysAlaIleMetArgAlaPheSerArgA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValGluAlaPheGluGluMetIleLysAsnLeuPheSerLeuProIleAs
                                                                                                                                                 TTGATCCAGGGGAATGGAGTGAGAGTTTAAGGAAAGAGTATCTTCTTGTC
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48..1466
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1.811
62.887
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Gaps: 14
Percent Identity: 29.897
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seq_documentation_block:
    Sequence 11, Application US/08724466B
    Patent No. 6063606
    GENERAL INFORMATION:
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    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                             GTTACGAGCTGGCTAGGGTTGCACTCTCTGTTTTCCTTCACCGCCTAGTG
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Petkovich, P. Martin, White,
                                                                                                                                                                                                                                                                                                                                         .CCTGCAGAGCAAGACAA 1390
Jay A.,
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (416) 863-2653
INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 base pairs
TYPE: nucleic acid
   301
                                                                251
                                                                                                 375
                                                                                                                               201
                                                                                                                                                                                               151
                                                                                                                                                                                                                               342
                                                                                                                                                                                                                                                                                                325
                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
                 392 TyrSerIleCysAspThrHisAspValAlaAspValPheProAsnLysG1 408
                                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                                                                                        308 uValMetPheLeuGlyLeuAsnThrGluValValGlnLysValArgGluG
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APPLICATION NUMBER: 0
FILING DATE: June 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: COMPAQ, IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,466B
FILING DATE: October 1, 1996
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MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Beckett, Barbara R., TITLE OF INVENTION: Retinoid Me NUMBER OF SEQUENCE: 30
CORRESPONDENCE ADDRESS:
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TOPOLOGY: li
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|ACCCTTCGACTGAATCCCCCAGTTCCAGGAGGGTTTCGGGTTGCTCTGA
                                                                                                                                                                                           GACATGGAAATTTTGGAACAACTTAAATACATCGGGTGTGTTATTAAGGA
                                                                                                                                                                                                                                                                                                                             TACAGTATCTGTGATACTCATGATGTGGCAGAGATCTTCACCAACAAGGA
                                                             AGACTTTTGAATTAAATGGATACCAGATTCCCCAAGGGCTGGAATGTTATC
                                                                                ysThrPheGluLeuAsnGlyTyrGlnIleProLysGlyTrpAsnValIle
                                                                                                                                                                                                                            SerMetGluLeuLeuAspGlnLeuLysTyrThrGlyCysValIleLysGl
                                                                                                                                                                                                                                                            AGCTGAAGAGTAAGGGTTTACTTTGCAAGAGCAATCAAGACAACTTG
                                                                                                                                                                                                                                                                                           luValGlnGluLysValGluMetGlyMetTyrThrProGlyLysGlyLeu
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seq_documentation_block:
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US-09-668-482-2 x US-08-882-164D-11
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                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                            Align seg 1/1 to: US-08-882-164D-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/667,546

FILING DATE: June 21, 1996

APPLICATION NUMBER: 08/724,466

FILING DATE: October 1, 1996

ATTORNEY/AGENT INFORMATION:

NAME: HUNT, JOHN C.

REGISTRATION NUMBER: 36,424

REGISTRATION NUMBER: 36,424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (416) 863-2653 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
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REFERENCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Petkovich, APPLICANT: Beckett, Ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
101
                                  325 luValGlnGluLysValGluMetGlyMetTyrThrProGlyLysGlyLeu 341
                                                                                             308 uValMetPheLeuGlyLeuAsnThrGluValValGlnLysValArgGluG 325
                                                                                                                                                                                          292 GluLeuLeuPheGlyGlyHisGluThrThrAlaSerThrAlaThrSerLe 308
                                                                        APPLICATION NUMBER: US/US/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleion STRANDEDNESS:
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: nucleic acid
NDEDNESS: single
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Percent Identity: 74.359
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; NAME/KEY: CDS
; LOCATION: (74)..(1606)
US-08-991-677-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
; Sequence 3, Application US/08991677A
; Patent No. 6252135
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                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-991-677-3 from: 1 to:
                                                                                                                                                                                                                                                                                                         US-09-668-482-2 x US-08-991-677-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/08/991,677A CURRENT FILING DATE: 1997-12-16 EARLIER APPLICATION NUMBER: US 60/033,381 EARLIER FILING DATE: 1996-12-16 NUMBER OF SEQ ID NOS: 11 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chiang, Vincent L
APPLICANT: Carraway, Daniel T
APPLICANT: Smeltzer, Richard H
TITLE OF INVENTION: Production of Syringyl Lignin in
FILE REFERENCE: 50617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Liquidambar styraciflua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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248 CACCGAGGACTCGCCAAACTCGCCAAACAATACGGCGGTCTATTCCACCT 297
                           65 ArgLysPheLeuArgMetLysArgGlnLysTyrGlyCysIleTyrLysTh 81
                                                                                                                                                                  31 uMetIleArgArgValAspProAsnCysArgSerProLeuProProGlyT 48
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                                                                  CGGCTTCGCCAG.....AGACTACCATACCACCAGGCC 197
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YCysValIleLysGluThrLeuArgIleAsnProProValProGlyGlyP 370
                                              GAAGAGAAAGAC..
                                                                           ProGlyLysGlyLeuSerMetGluLeuLeuAspGlnLeuLysTyrThrGl 353
                                                                                                                                                          lnLysValArgGluGluValGlnGluLysValGluMetGlyMetTyrThr 336
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                                                                                                                                                                                                                                                                                  ...GluAlaAlaThrGluLeuLeuPheGlyGlyHisGluThrThrAlaSe 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACGTCAGGCTCAACAAGGCACGAGGGGCGCTTGATGGGTTTATTGACAAG
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                                                                                                                     AGAAGGTCCAACAAGAACTCGCCGTGGTGGTGGGTCTTGACCGGCGAGTC 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                             TACTGATATGGTAGATGATTTACTTGCTTTTTACGGTGAGGAAGCCAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCGACTCGGCAGTACGAGTGGTCGCGTCCAATATTGGGTCGACGGTGAA 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAGATGGGATTCTTACACATGGTGGCCGTTTCCACACCCGACATGGCTC
                                       .TTCGAGAAGCTCACCTACTTGAA 1155
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seq_documentation_block:
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                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PACEDOS/MS-DOS
SOFTMARE: PACEDOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,981E
FILING DATE: February 10, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Selby
REGISTRATION NUMBER: 38,298
REFERENCE/DOCKET NUMBER: 22000.0022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3
Patent No.
                                                                                                                           TELEFAX: (404) 688-9880 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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MOLECULE TYPE: DO HYPOTHETICAL: NO
                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SANDHU, Punam
APPLICANT: GILLAM, Elizabeth M.
TITLE OF INVENTION: EXPRESSION /
TITLE OF INVENTION: HUMAN
TITLE OF INVENTION: CYTOCHROME I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1406 CGTCGGTCTTGCCCCGGTATGCAACTCGGACTCTACGCGCTAGAGACGAC 1455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 heArgValAlaLeuLysThrPheGluLeuAsnGlyTyrGlnIleProLys 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          387 GlyTrpAsnValIleTyrSerIleCysAspThrHisAspValAlaAspVa
                                          TOPOLOGY:
                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 30303-1811
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CITY: Atlanta
                                                                                                         LENGTH:
                                                                                                                                                                                               TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTGGCTCACCTCCTT...CACTGTTTCACGTGGGAGTTGCCGGACGGG 1501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCCCGATTTCAAAGGGAACAACTTCGAGTTCATCCCATTCGGGTCAGGT 1405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lPheProAsnLysGluGluPheGlnProGluArgPheMetSerLysGlyL 420
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5. 5886157
                                                                                     nucleic acid
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                                                                                                       1591 base pairs
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                                            linear
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                      DNA (genomic)
                                                              single
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US-08-194-981E-3

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alignment_block:
US-09-668-482-2 x US-08-194-981E-3
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-08-194-981E-3 from: 1 to: 1591
                                                                                                                                                                                                                                                                                                                                                                                                                                              118
                                                                                                                                                                                                                     482 CCTCACCCTGTGATCCCACTTTCATCCTGGGCTGTGCTCCCTGCAATGTG
                                                                                                                                                                                                                                                                                                  432 TGTTCAAGAGGAAGCCCGCTGCCTTGTGGAGGAGTTGAGAAAAAACCAAGG 481
                                                                                                                                                                                                                                                                                                                                 167 pLeuGlnLysAspSerCysValLeuValTyrProGluMetLysLysLeuM 184
                                                                                                                                                                                                                                                                                                                                                                  397 AATTTT......GGGATGGGGAAGAGGAGCATTGAGGACCG 431
                                                                                                                                                                                                                                                                                                                                                                                               151 HisTyrIleProValIleGlnGlnGluValLysSerAlaIleGlnGluTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318 TAACAGAGGA.....TTTGGAATTGTTTTCAGCA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 rIleLeuGlySerAspThrLeuSerAsnValHisGlyValGlnHisLysA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 LeuGlyGluHisLysLeuValSerValGlnTrpProAlaSerValArgTh 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 TCTCTCAAAGGTCTATGGCCCTGTGTTCACTCTGTATTTTGGCCTGAAAC 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206
                                                                                                                                                 532 ATCTGCTCCATTATTTTCCATAAACGTTTTGATTATAAAGATCAGCAATT 581
                                                                                                                                                                                                                                                           184 etPheArgIleAlaMetArgIleLeuLeuGlyPheGluProGluGlnIle 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 tLysArgGlnLysTyrGlyCysIleTyrLysThrHisLeuPheGlyAsnP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 CCTTTCA.....CTCTGGAGA.....CAGA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             632 CCTGGATCCAGATCTGCAATAATTTTTCTCCTATCATTGATTAC...TTC 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AGCCTAGTGGTCCTTGTGCTCTGT.....CTCTCATGTTTGCTTCT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        roThrValArgValMetGlyAlaAspAsnValArgGlnIleLeu..... 101
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                                                                                                      TCTTAACTTAATGGAAAAGTTGAATGAAAACATCAAGATTTTGAGCAGCC
                               339.50
1.183
55.513
                                                                                                                                                                                    .....LysThrAspGluGln.. 205
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Gaps: 22
Percent Identity: 26.886
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	483 0 483	
483 1439	467 ProprothrMetLysthrGlyProthrIleTyrProValAspAsnLeuPr	1
466 1389	450 lePheLeuValGluLeuThrGlnHisCysAsnTrpIleLeuSerAsnGly :: ::::::: ::: 1340 TATTCCTGACCTCCATTTACAGAACTTTAACCTGAAATCTCTGGTTGAC	
450 1339	433 yGlySerArgMetCysValGlyLysGluPheAlaLysValLeuLeuLysI 	
433 1289	421 GluaspGlySerArgPheAsnTyrIleProPheGlyGl	
420 1239	404 heProAsnLysGluGluPheGlnProGluArgPheMetSerLysGlyLeu	
404 1201	388 pAsnvallleTyrSerIleCysAspThrHisAspValAlaAspValP :::::::	
388 1154		
372 1104	356 leLysGluThrLeuArgIleAsnProProValProGlyGlyPheArgVal :: ::: ::::: 1055 TGCACGAGGTCCAGAGATGCATTGACCTTCTCCCCACCAGCCTGCCCAT	
356 1054	341 uSerMetGluLeuLeuAspGlnLeuLysTyrThrGlyCysValI 	
341 1004	GlyMetTyrThrProGlyLysGlyLe ::::: GGCAGAAACCG	
324 975	308 euValMetPheLeuGlyLeuAsnThrGluValValGlnLysValArgGlu :::::::: ::: ::: 926 CTCTCCTTCTCGTGCTGAAGCACCCAGAGGTCACAGCTAAAGTCCAGGAA	
308 925	TG TL	
291 875	276 ArgSerAspGluProPheSerLeuGlnAlaMetLysGluAlaAlaTh: :::::::::::::::::::::::::::::::::::	
275 825	259 snGluGlnLysTyrLysAspAlaLeuGlnLeuLeuIleGluAsnSerArg :	
259 775	242 rLysileGluGluAsnīleArgLysLysIleGlnAspAspAspAsnGluA:	
242 725	228 SerGlyLeuTyrArgGlyLeuArgAlaArgAsnPheIleHisSe 2	

seq_documentation_block:
; Sequence 10, Application US/08201118
; Patent No. 5786191

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alignment_scores:
    Quality:
    Ratio:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/201,118
FILING DATE: 22-FEB-1994
CLASSIFICATION DATA:
APPLICATION UNMBER: US 07/864,962
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APR-1992
ARTORNEY/AGENT INFORMATION:
MAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 15280-192-1
FELECOMMUNICATION: HTORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2400
TELEPAX: (415) 326-2420
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1852 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: nucleic acid STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: cDNA US-08-201-118-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-668-482-2 x US-08-201-118-10
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APPLICANT: GOLDSTEIN, Joyce A.

APPLICANT: ROMKES-SPARKS, Marjorie

APPLICANT: ROMKES-SPARKS, Marjorie

TITLE OF INVENTION: CLONING AND EXPRESSION OF COMPLEMENTARY

TITLE OF INVENTION: DNAS FOR MULTIPLE MEMBERS OF THE HUMAN CYTOCHROME P450 2C

TITLE OF INVENTION: SUBFAMILY

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:
178 TCTCTCAAAGGTCTATGGCCCTGTGTTCACTCTGTATTTTGGCCTGAAAC 227
                                                                                     128 GGAAATATCCTACAGATAGGTATTAAGGACATCAGCAAATCCTTAACCAA 177
                                                                                                                                                                              70 tLysArgGlnLysTyrGlyCysIleTyrLysThrHisLeuPheGlyAsnP 87
                                                                                                                21 eLeuAlaAlaValLysLeuTrpGluMetLeuMetIleArgArgValAspP 38
                                                                                                                                                                                                                                                                                                                                                                 17 TCTCTTGTGGTCCTTGTGCTCTGT......CTCTCATGTTTGCTTCT 57
                                                                                                                                                                                                                                                                                                                                                                                         5 ThrLeuMetValThrPheLeuCysThrIleValLeuProValLeuLeuPh 21 :::|||:::|| |||||||::
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CITY: Palo Alto
STATE: California
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1.183
55.513
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Gaps: 22
Percent Identity: 26.886
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32 4 985	uAsnThrGluValValGlnLysValArgGlu ::: ::: GCACCCAGAGGTCACAGCTAAAGTCCAGGAA	308 936
308 935	rGluLeuLeuPheGlyGlyHisGluThrThrAlaSerThrAlaThrSerL:::: ::: :::: ::::: TGACTTGTTTGGAGCTGGGACAGGAGAGCACAAGCACAACCCTGAGATATG	291 886
291 885	ArgSerAspGluProPheSerLeuGlnAlaMetLysGluAlaAlaTh : :::::::::::::::::::::::::::::::::::	276 836
275 835	TLYSASPALALEUGINLEULEUIIEGIUASNSETATG : :::::::::::::::::::::::::::::::::	259 786
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216 641	GluLeuValGluAlaPheGluGluMetIleLys 	206 592
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200 541	.PheArgIleAlaMetArgIleLeuLeuGlyPheGluPro 	184 492
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167 441	ProVal	151 407
150 406	SILYSLYSLYSAlaIleMetArgAlaPheSerArgAll SISTEM SI	135 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 433 yGlySerArgMetCysValGlyLysGluPheAlaLysValLeuLeuLysI 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   483 o 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
COMMISSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: GOLDSTEIN, Joyce A.

APPLICANT: ROMKES-SPARKS, Marjorie
APPLICANT: DE MORAIS, Sonia M.F.

TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT OF
TITLE OF INVENTION: MEPHENYTOIN METABOLISM
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,821B
               CLASSIFICATION: 435
PATOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                       FILING DATE: 06-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lePheLeuValGluLeuThrGlnHisCysAsnTrpIleLeuSerAsnGly 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProProThrMetLysThrGlyProThrIleTyrProValAspAsnLeuPr 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluAspGlySerArgPheAsn.....TyrIleProPheGlyGl 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATTCCTGACCTCCATTTTACAGAACTTTAACCTGAAATCTCTGGTTGAC 1399
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Liebeschuetz, Joe
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US-08-238-821B-10
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US-09-668-482-2 x US-08-238-821B-10
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REFERENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION:
TELEPHONE: (650) 326-2400
TELEPAC: (650) 326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1852 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-238-8218-10
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                                                                          407
                                                                                                           151 HisTyrIleProValIleGlnGlnGluValLysSerAlaIleGlnGluTr 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                              LeuGlyGluHisLysLeuValSerValGlnTrpProAlaSerValArgTh 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tLysArgGlnLysTyrGlyCysIleTyrLysThrHisLeuPheGlyAsnP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAAATATCCTACAGATAGGTATTAAGGACATCAGCAAATCCTTAACCAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roAsnCysArgSerProLeuProProGlyThrMetGlyLeuProPheIle 54
                                                                                                                                                                             snLysLysLys...AlaIleMetArgAlaPheSerArgAspAlaLeuGlu
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                                                                                                                                                                                                                                   TAACAGAGGA...
                                                                                                                                                                                                                                                                      rIleLeuGlySerAspThrLeuSerAsnValHisGlyValGlnHisLysA 135
                                                                                                                                                                                                                                                                                                               CTTGGAGAGGAGTTTTCTGGAAGAGGCATTTTCCCCACTGGCTGAAAGAGC
                                                                                                                                                                                                                                                                                                                                                                                            roThrValArgValMetGlyAlaAspAsnValArgGlnIleLeu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTCTCAAAGGTCTATGGCCCTGTGTTCACTCTGTATTTTGGCCTGAAAC 227
TGTTCAAGAGGAAGCCCGCTGCCTTGTGGAGGAGTTGAGAAAAACCAAGG 491
                                 {\tt pLeuGlnLysAspSerCysValLeuValTyrProGluMetLysLysLeuM}
                                                                        AATTTT.....GGGATGGGGAAGAGGAGCATTGAGGACCG
                                                                                                                                                    ATGGAAAGAAATGGAAGGAGATCCGGCGTTTCTCCCCTCATGACGCTGCGG
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1.183
55.513
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Gaps: 22
Percent Identity: 26.886
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1165 AACCATATTAATTTCCCTGACTTCTGTGCTACATGACAACAAGAA...T 1211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1015 GAGCCCCTGCATGCAAGACAGGAGCCACATGCCCTACACAGATGCTGTGG
                                                                                                                                                                                                                                                                                                                               1212 TTCCCAACCCAGAGATGTTTGACCCTCATCACTTT...
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1300 AGGAAAACGGATTTGTGTGGGAGAAGCCCTGGCCGGCATGGAGCTGTTTT 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388 pAsnValIleTyrSerIleCysAspThr...HisAspValAlaAspValP 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373 AlaLeuLys...ThrPheGluLeuAsnGlyTyrGlnIleProLysGlyTr 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 uSer.....MetGluLeuLeuAspGlnLeuLysTyrThrGlyCysValI 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               736 TTATATTTTGGAAAAAGTAAAAGAACACCAAGAATCAATGGACATGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       592 TCTTAACTTAATGGAAAAGTTGAATGAAAACATCAAGATTTTGAGCAGCC 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206
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                                                                                                                                                                                                                                  421 GluaspGlySerargPheasn.....TyrIleProPheGlyG1 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325 GluValGlnGluLysValGluMetGlyMetTyrThrProGlyLysGlyLe 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 euValMetPheLeuGlyLeuAsnThrGluValValGlnLysValArgGlu 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 rGluLeuLeuPheGlyGlyHisGluThrThrAlaSerThrAlaThrSerL 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 rLysIleGluGluAsnIleArgLysLysIleGlnAspAspAspAsnGluA 259
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                                                                                                                                                                                                                                                                                                                                                                                                 heProAsnLysGluGluPheGlnProGluArgPheMetSerLysGlyLeu 420
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                                                                  yGlySerArgMetCysValGlyLysGluPheAlaLysValLeuLeuLysI 450
                                                                                                                                                           GATGAAGGTGGCAATTTTAAGAAAAGTAAATACTTCATGCCTTTCTCAGC 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....LysThrAspGluGln., 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ......AsnLeuPheSerLeuProIleAspValProPhe
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                                                                                                                                                                                                                                                                                                                      ....CTG 1249
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alignment_block:
                                                                                                                                                                                             ; TOPOLOGY: 1:
; MOLECULE TYPE:
PCT-US95-05744-10
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                                                                                                                               alignment_scores:
US-09-668-482-2 x PCT-US95-05744-10
                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application PC/TUS9505744 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1450 G 1450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ROMKES-SPARKS, Marjorie
APPLICANT: DE MORAIS, Sonia M.F.
TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT
TITLE OF INVENTION: OF S-MEPHYNYTOIN METABOLISM
NUMBER OF SEQUENCES: 61
                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 22-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 09-APR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               467 ProProThrMetLysThrGlyProThrIleTyrProValAspAsnLeuPr 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US OF TILING DATE: 06-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/864,962 FILING DATE: 09-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                       TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US95/05744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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Percent Identity: 26.886
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450 1349	3 yGlySerArgMetCysValGlyLysGluPheAlaLysValLeuLeuLysI 	433 1300
433 1299	1 GluaspGlySerArgPheAsnTyrIleProPheGlyGl :::::: :::: ::: GATGAAGGTGGCAATTTTAAGAAAAGTAAATACTTCATGCCTTTCTCAGC	421 1250
420 1249	4 heproAsnLysGluGluPheGlnProGluArgPheMetSerLysGlyLeu	40 4 1212
404 1211	8 pAsnVallleTyrSerIleCysAspThrHisAspValAlaAspValP::::::::: :::: :::	388 1165
388 1164	3 AlaLeuLysThrPheGluLeuAsnGlyTyrGlnIleProLysGlyTr	373 1115
372 1114	leLysGluThrLeuArgIleAsnProProValProGlyGlyPheArgVal::	356 1065
356 1064	uSerMetGluLeuLeuAspGlnLeuLysTyrThrGlyCysValI ::: ::: :: gAGCCCCTGCATGCAAGACAGGAGCCACATGCCCTACACACAGATGCTGTGG	341 1015
341 1014	GluvalGlnGluLysValGluMetGlyMetTyrThrProGlyLysGlyLe ::::::: ::::::: :::::::	325 986
324 985	euValMetPheLeuGlyLeuAsnThrGluValValGlnLysValArgGlu:::::::: :::::::: ::::::: ::::::	308 936
308 935	rGluLeuLeuPheGlyGlyHisGluThrThrAlaSerThrAlaThrSerL:::: :::	291 886
291 885	ArgSerAspGluProPheSerLeuGlnAlaMetLysGluAlaAlaTh ::::::::: ::::::::::::::::::::::::	276 836
835	ACCCTCAGGACTTTATTGATTGCTTCCTGATGAAAATGGAGAAGGAAAAG	786

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gb_est29.AL539668
gb_est71:BE189825
gb_est29.AL532445
gb_est29.AL532445
gb_est23:AJ584636
gb_est43:AW171465
gb_est43:AW513600
gb_est48:AW513600
gb_est51:AW765767
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9b_est83:RM1283136
9b_est83:BF055367
9b_est82:BF055367
9b_est82:BF055367
9b_est82:BF04665907
9b_est40:AV668503
9b_est40:AV668503
9b_est23:AF236872
9b_est43:AW191734
9b_est47:AW4605507
9b_est47:AW4605507
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9b_est47:AW4605434
9b_est47:AW4605434
9b_est47:AW46054
                     gb_gss5: CNS05PUU
gb_est49: AW640733
gb_est51: AW767659
gb_est14: AI004222
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Query length: 492
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gb_est102:BG578446
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-DB-EST -QFMT-fastap -SUEFIX-rst -GAPOD-12.000 -GAPEXT-4.000
-MINADTCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000 -QGAPOD-4.500
-QGAPEXT-0.050 -XGAPOD-10.000 -XGAPEXT-0.500 -FGAPOD-6.000
-FGAPEXT-7.000 -YGAPOD-10.000 -YGAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -YGAPOD-10.000 -YGAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -START-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MXS-100 -THR_MIN-0
-ALIGN-15 -MODE-LOCAL -CUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN-200000000 -USER-US09668482_@CGN1_1_5307 -NCPU-6
-ICPU-3 -LONGLOG -NO_XLPXY -WAIT -THREADS-1
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1313.37
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1.9e-62
6.6e-62
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4.1e-83
4.6e-82
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7.9e-76
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7.6e-116 72
7.0e-106 64
9.0e-102 66
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3.1e-54
1.7e-53
1.7e-53
5.6e-49
2.8e-48
2.8e-49
2.8e-49
3.7e-43
3.7e-43
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7.9e-61
3.7e-61
3.8e-60
1.9e-59
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.9e-64
.5e-63
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version
                                                                                                                                                                                                                                                      BG515142 dad60f10.y1 Wellcome C AA239785 mx80a03.rl Soares mous BE236243 143959 MARC IPIG SUS BG578446 de99c02.y1 Wellcome CF AI545454 fb81e05.xl Zebrafish W BG364937 dc99f02.yl NICHD XGC BF385034 602045632Fl NCI_CGAP_I BF33769 602073982Fl NCI_CGAP_I BF533769 f02073982Fl NCI_CGAP_I BF533769 f02073982Fl NCI_CGAP_I BF533769 f02073982Fl NCI_CGAP_I BF533769 f02073982Fl NCI_CGAP_I BF05367 7]79812.xl Soares_NSC BF047649 dc80h02.yl NICHD XGC BF426259 df59e06.yl Xenopus lae AW595907 da29g11.yz Xenla Jaka AI626269 fc12e02.yl Zebrafish W BF236072 602027980Fl NCI_CGAP_I BF047648 f02027980Fl NCI_CGAP_I BF0468650 da29g11.xl Xenla 13Lic R51129 y971h05.rl Soares infant
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| BE189825 db61c05.yl Wellcome CR |
| AL532445 AL532445 LTT_KPL001_WR |
| AL532445 AL532445 LTT_KPL001_WR |
| AN194636 fb81e05.yl Zebrafish W |
| AN171465 f142a06.xl Ncjano Kawa |
| ANN513600 xo47b06.xl Ncj_CAP_Ut |
| ANN765767 da77a02.yl Harland sta |
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A11667038 fc24h03.yl zebrafish
AW128823 fe37yll.yl zebrafish
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  alignment_block:
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gb_est100:BG408452
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E 1 (bases 1 to 720)

S Sugano, S., Kawakani, K., Johnson, S., Li, F., Marra, M., Eddy, S., Hillier, L., Clifton, S., Allen, M., Gibbons, M., Jost, S., Kucaba, Martin, J., Pape, D., Steptoe, M., Underwood, K., Theising, B., Rit, E., Bowers, Y., Wylie, T., Waterston, R. and Wilson, R. Washu Zebratish EST Project 1999

L Unpublished (1999)

Other ESTs: fi42a06.x1

Contact: S.L. Johnson

Washington University School of Medicine
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2640274 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
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314 286 1810
                                                                                                                                      /lab_host="DHIOB (phage resistant)"
/lab_host="DHIOB (phage resistant)"
/note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
/note="Vector: pME18S-FL3; Site_1: Ist strand cDNA was primed site_2: DraIII (CACCATGTG); Ist strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG, xhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science) and kindly donated by Dr. Koichi Rawakami. Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCACCTCAACACA."

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="mixed (one male and one unfertilized eggs)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="AB"
/db_xref="taxon:7955"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Sugano Kawakami zebrafish DRA"
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Sequencing Center
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACTACATTCCCGTGATCCATCAGGAGGTGAAGAGCGCCATACAGGAATG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi Cypriniformes; Cyprinidae; Rasborinae; Danio.
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Danio rerio cDNA 5' similar to 26;, mRNA sequence.
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Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 640)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., S.L., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Und, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritteer, Charles, G., Stan, M., Carles, C., Carles, M., Carles, C., Carle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Matthew Clark. DNA Sequencing Genome Systems, St. Louis,
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Possible reversed clone: similarity on wrong strand Seq primer: T3 ET from Amersham High quality sequence stop: 474.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  www.rzpd.de)
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                                               156
                                                                                                                                                                                                        control.
a 162
                                                                                                                                     were sequenced additional times
                                                                                                                                                                           sequenced to assess clustering parameters or single clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Danio rerio"
/db_xref="taxon:7955"
/clone_lib="Zebrafish WashU MPIMG
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="26 somite embryos, adult livers,
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alignment_scores:

Quality: Ratio: 5.166 100.000 997.00 Gaps: Percent Identity:

100.000

alignment_block:

US-09-668-482-2 x AI667038

Align seg 1/1 . 6 AI667038 from: 6

- 62 1 MetGlyLeuTyrThrLeuMetValThrPheLeuCysThrIleValLeuPr ATGGGGCTGTACACCCTTATGGTCACCTTCTCTGCACCATCGTGCTACC
- 17 oValLeuLeuPheLeuAlaAlaValLysLeuTrpGluMetLeuMetIleA 34

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COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
ORGANISM
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LOCUS ลพาวคลวว
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_est43:AW128823
                                                                                                                                                                                                                                                                                                                        REFERENCE
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                                                                                                                                                                                                                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pLeuGlnLysAspSerCysValLeuValTyrProGluMetLysLysLeuM 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HisTyrIleProVallleGlnGlnGluValLysSerAlaIleGlnGluTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAACAAGAAAAAGGCCATTATGAGGGCGTTCTCTCGAGATGCTCTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGCAAAAAGACTCCTGCGTGCTGGTTTATCCAGAAATGAAGAAACTCA
                                                                           Unpublished (1998)
Other ESTs: fe37g11.x1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW128823 662 bp mRNA EST 25-OCT-1999 fe37g11.yl Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar SW:CP26_BRARE P79739 CYTOCHROME P450 26 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasborinae; Danio.

1 (bases 1 to 662)
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                                                                                                                                                                                                       and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                        Danio rerio
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cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed
                                       Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                Zebrafish EST Project 1998
                zbrafish@watson.wustl.edu
                                                                               St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150
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156

174 g

155 t

3 others

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source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 446.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer: T3 ET from Amersham
                                                            double-stranded CDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I stranded the Not I and Sal I adaptors of the psportly vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). cDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                control."
174 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stage embryos"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Danio rerio"
/db_xref="taxon:7955"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="XL1-blue MRF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="26 somite embryos, adult livers, shield
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alignment_block: alignment_scores: US-09-668-482-2 x AW128823 Percent Similarity: Quality: Ratio: 5.090 97.927 962.00 Percent Identity: Length: Gaps: 193 0 97.409

Align seg 1/1 to: AW128823 from: 1 to: 662

ATGGGGCTGTACACCCTTATGGTCACCTTTCTCTGCACCATCGTGCTGCC

134

84

34 rgArgValAspProAsnCysArgSerProLeuProProGlyThrMetGly 50

51 LeuProPheIleGlyGluThrLeuGlnLeuIleLeuGlnArgArgLySPh 283

eLeuArgMetLysArgGlnLysTyrGlyCysIleTyrLysThrHisLeuP TCTGCGCATGAAACGGCAGAAATACGGGTACATCTACAAGACGCACCTCT 333 84

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KEYWORDS
SOURCE
ORGANISM
                                                          alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_est29:AL532444
  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTNTCGGATAGCTATGAGAATCCTGCTT 662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 1028)
11.W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVWX cedex - France
Email: segref@genoscope.cns.fr, Web: www.ge
                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL532444
                  Ratio:
                                                                                                                                      265
                                                                                                                      /note-Worgan: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
                                                                                                                                      ω
867.00
3.905
82.222
                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODM014YL13"
                                                                                                                                                                                                                                                                                                                                                 /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="LTI_NFL001_NBC4"
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  Percent
Identity:
                Length:
Gaps:
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                              GAAAWCYAGTCCCACCGTGTATCCTGTGGACAATCTCCCTGCAAGATTCA
                                               tLysThrGlyProThrIleTyrProValAspAsnLeuProThrLysPheT
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                                                                                         GAGCTGSCCAGGCATTGTSACTGGCMGCTTCTAAATGGACYTCCTACAAT
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AL539668
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1 (bases 1 to 974)
Li,W.B., Gruber,C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL539668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Onote-*Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           week, 24 week and 26 week)"

/lab_host="DH10B"

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ccrccrgGrcraccccGAGGrGAAGCGCCTCATGTTCCGAATCGCCATGC
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Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
                                                 Amphibia; Batrachia; Anura;
Xenopodinae; Xenopus
1 (bases 1 to 696)
                                                                                                                         African clawed frog.
Xenopus laevis
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                MetArgAlaPheSerArgAspAlaLeuGluHisTyrIleProValIleGl 157
                                                                                                          hrLeuSerAsnValHisGlyValGlnHisLysAsnLysLysLysAlaIle 140
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GCACAAGCCTTCTCCCGAGATGCCCTCGACAATTACGTGCCGCAGATGGA
                                                                             GTCTGTCCAACCTGCACGACTCTGAGCACAAGTACACCAAGAAAGTGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashIJ Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
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washU Xenopus EST project, 1999
Unpublished (1999)
On Jun 22, 2000 this sequence version replaced
Other ESTs: db61c05.x1
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Fax: 314 286 1810
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/note="Vector: pBluescript SK; Site_1: NotI; Site_2:
ECORI; cDNAs were oligo-dT primed and directionally
cloned. Library was constructed by N. Garrett, P. LeMair
A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute).
Note: This is a Xenopus Gene Collection (XGC) library."
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/lab_host="DH10B (
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/clone="IMAGE:3377480"
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/db_xref="taxon:8355"
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1 (bases 1 to 893)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                                                                                                                                                                        91006 EVRY cedex - France segref@genoscope.cns.fr, V
note-"Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:
                                                                                                                                                                                                         /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
                                                                                                                                                                                                                                                    /sex="male"
                                                                                                                                                                                                                                                                   /clone_lib="LTI_NFL001_NBC4"
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/db_xref="taxon:9606"
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fb81e05.y1 Zebrafish WashU MPIMG
TR:P79739 P79739 CYTOCHROME P450
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1 (bases 1 to 530)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems. St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WashU Zebrafish EST Project 1998
Unpublished (1998)
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                             Possible reversed clone: similarity on wrong strand
Seq primer: T3 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     www.rzpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 493.
stage embryos"
                                                                                                                                                                                                                                                                                                           /organism="Danio rerio"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                    /tissue_type="26 somite embryos, adult livers,
                                                                                                                                                                                                                                                           /sex="mixed"
                                                                                                                                                                                                                                                                                 /clone_lib="Zebrafish WashU MPIMG
                                                                                                                                                                                 /lab_host="XL1-blue MRF"
                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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DEFINITION
                                                                                  seq_documentation_block:
LOCUS AW171465
                                                                                                                                           seq_name: gb_est43:AW171465
ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTGCGCATGAAACGGCAGAAATACGGGTGCATCTACAAGACGCACCTCT 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGTTTTACTCTTCTCGCCGCGGTGAAGTTGTGGGAGATGTTAATGATCC
                                AW171465 765 bp mRNA
fi42a06.x1 Sugano Kawakami zebrafish
2640274 3' similar to SW:CP26_BRARE E
                 mRNA sequence.
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alignment_block:
US-09-668-482-2 x AW171465/rev
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                                                                                                    338 yLysGlyLeuSerMetGluLeuLeuAspGlnLeuLysTyrThrGlyCysV
                                                                         718 CATAGGTTTGAGCATGGAGCTGTTGCACCAGCTGAAGTACACTGGATGTG
                                                                                                                                                                                                                        322 ValArgGluGluValGlnGluLysValGluMetGlyMetTyrThrProGl
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alIleLysGluThrLeuArgIleAsnProProValProGlyGlyPheArg
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Ratio:
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Contact: S.L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sugano,S., Kawakami,K., Johnson,S., Li,F., Marra,M., Eddy,S., Hiller,L., Clifton,S., Allen,M., Gibbons,M., Jost,S., Kucaba,T., Martin,J., Pape,D., Steptoe,M., Underwood,K., Theising,B., Ritter, E., Bowers,Y., Wylie,T., Waterston,R. and Wilson,R. WashU Zebrafish EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA Sequencing by: Washington University Genome Sequencing Center Seq primer: T7 ET from Amersham High quality sequence stop: 514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                      to reverse of: AW171465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab.host="DHIOB (phage resistant)"
/lab.host="DHIOB (phage resistant)"
/note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
with an oligo(dT) primer (ATGTGGCCTTTTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TGTTGGCCTACTGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science) and
kindly donated by Dr. Koichi Kawakami. Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer CGACCTGCAGCTCGAGCACA.
174 c 154 g 212 t
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4.845
92.398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Sugano Kawakami zebrafish DRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="2640274"
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TGAGTAAGAACCT.CTCAGAATCAACCCTCCTGTTCCTGGAGAATTCAGA

/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall Site_2: NotI; Cloned unidirectionally. Primer: Oligo c Average insert size 1.75 kb. Life Technologies catalog 11538-014"

Salī; igo dī.

adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"

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JOURNAL
COMMENT
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AUTHORS
TITLE
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SOURCE
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VERSION
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                                                                                                                                                                                                                CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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AW513600.1 GI:7151678
                                                                                                                                            Possible reversed clone: similarity on wrong strand Seq primer: -400P from Gibco
                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
                                                                                                          quality sequence stop: 440.
Location/Qualifiers
/clone="IMAGE: 2707091"
/clone_lib="NCI_CGAP_Utl"
/tissue_type="well-differentiated
                                                      /db_xref="taxon:9606"
                                                                      /organism="Homo sapiens"
     endometrial
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IMAGE:2707091 3'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProThrValArgValMetGlyAlaAspAsnValArgGlnIleLeuLeuGl
                                      LeuTyrArgGlyLeuArgAla 236
                                                                        AAATGACCCGCAATCTCTTCTCGCTGCCCATCGACGTGCNCTTCAGCGGG
                                                                                     luMetIleLysAsnLeuPheSerLeuProIleAspValProPheSerGly
                                                                                                                                     LeuMetPheArgIleAlaMetArgIleLeuLeuGlyPheGluProGluGl 199
                                                                                                                                                                                                                     GCCGGTGATCACCGAGGAAGTGGGCAGCAGCAGCCTGGAGCAGTGGCTG.... 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                     yGluHisLysLeuValSerValGlnTrpProAlaSerValArgThrIleL 120
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                                                                                                                        ACTGGCGGGCGACGGGACTCCGAGCAGCAGCTTGTGGAGGCCTTCGAGG
                           CTGTACCGGGGCATGAAGGCN
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LOCUS AW765767
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1 MetGlyLeuTyrThrLeuMetValThrPheLeuCysThrIleValLeuPr
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Washu Xenopus EST project, 1999
Unpublished (1999)
Other_ESTs: da77a02.x1
Contact: Sandy Clifton, Ph.D.
Washu Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     da77a02.yl Harland stage 19-23 Xenopus laevis cDNA clone IMAGE: 3200906 5' similar to gb:gb|Ar057566.1|Ar057566 Xenopus laevis retinoic acid converting enzyme (XENOPUS);, mRNA sequence. AW765767
AW765767 GI:7697743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: Xenopus clones from t
through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
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Location/Qualifiers
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/lab_host="pH10B (phage-resistant)"
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/cDNA made by oligo-dT priming. Library constructed by
Dr. Francesca Mariani in the laboratory of R. Harland,
Ph.D. (University of California, Berkeley). References:
XBF-2 is a transcriptional repressor that converts
ectoderm into neural tissue. Mariani, FV. Harland, RM.,
Development. 1998 Dec;125(24):5019-31. PMID: 9811886; UI:
99030283; Use of large-scale expression cloning screens in
the xenopus laevis tadpole to identify gene function.
Grammer TC. Liu KJ. Mariani FV. Harland RM., Dev Biol.
2000 Dec 15;228(2):197-210. PMID: 11112324; UI: 20564075;
Note: This is a Xenopus Gene Collection (XGC) library."
37 a 206 c 187 g 139 t
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FEATURES
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LOCUS AL539667
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                      Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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AL539667 LTI_FL013_FBrn1
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                                                                                                                                                                                                                                                                                                                                            prime, mRNA sequence.
AL539667
                    Email: segref@genoscope.cns.fr,
                                                                                                                                                                              Mammalia; Eutheria;
1 (bases 1 to 847)
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Location/Qualifiers
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                    Web : www.genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              740 GACACGAAACCACGGCCAGTGCAGCCACATCTCTGATCACTTACCTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 oPheSerLeuGlnAlaMetLysGluAlaAlaThrGluLeuLeuPheGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264 LysAspAlaLeuGlnLeuLeuIleGluAsnSerArgArgSerAspGluPr 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACAACTCMAATMCCNCGGGTGTGTTATTAAGGAGACCCCTCGACTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lGluMetGlyMetTyrThrProGlyLysGlyLeuSerMetGluLeuLeuA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCCACCCACACGCTCCCCAGAAAGCGCGAGAAGAGCTGAAGAGTAAGGG
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oPheGlyGlySerArgMetCysValGlyLysGluPheAlaLysValL 447
                                                                                                ArgPheMetSerLysGlyLeuGluAspGlySerArgPheAsnTyrIlePr 430
                                                                                                                                                                                                 hrHisAspValAlaAspValPheProAsnLysGluGluPheGlnProGlu 413
                                                                                                                                                                                                                                                                                                nGlyTyrGlnIleProLysGlyTrpAsnValIleTyrSerIleCysAspT 397
                                                     CGATTCATGCTGCCTCACCCMGAGGACGCACCCMGGCTCAGCCCCATCCC
                                                                                                                                                      CCCATGATGTGGCAGAGATCTTCACCAACAAGGAAGAATTTAACCCTGAC
                                                                                                                                                                                                                                                       TGGATCCCMGANCCCCAAGGGCTGGAATGTTATCTACAGTATCTGTGATA
                                                                                                                                                                                                                                                                                                                                                     CCCCCMGNCCCAGGAGGGTTNCGGGNNGCTCCGAASMCTTCTGAATCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Onote-"Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="CSODF036YG04"
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week, 24 week and 26 week)"
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3.921
79.464
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190 c 204 g 229 t 2
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                                                                                                         BASE COUNT
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerAsnGlyProProThrMetLysThrGlyProThrIleTyrProValAs 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Other_ESTs: dad60f10.x1
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Silurana tropicalis
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BG515142.1 GI:13485799
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Seq primer: -40RP from Gibco
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Fax: 314 286 1810
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Library constructed by A. Zorn and J. Mason (Wellcome/CRC Institute ). DNA Sequencing by: Washington University Genome Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopodinae; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: Xenopus clones from this library are available hrough the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
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                                                                                                                                                   123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 503.
Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
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/note="Vector: pcS107; Site_1: Not1; Site_2: EcoRI; cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                            CRC pCS107 tropicalis egg"
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Percent Similarity:

Quality:

Ratio:

672.00 4.123 89.560

Percent Identity:

0 67.033

Length:

alignment_block: US-09-668-482-2 x BG515142

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seq_documentation_block:
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                    COMMENT
                                                                                                                                                            REFERENCE
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                                   TITLE
JOURNAL
                                                                                                                                                                                                                ORGANISM
                                                                                                                                              AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 GCCGCAAGGATGCCAGCTGCAGAAACCCTTTGCCCCCTGGCACTATGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 AGTACTACTCCTGCTCACAGCTGCCAAGCTATGGGAAGTGTACTGCCTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                        CACTATCCTGGGGGCCGGCTGTCTGTCCAACCTGCACGACTCCGAGCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eLeuArgMetLysArgGlnLysTyrGlyCysIleTyrLysThrHisLeup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATTACGTCCCGCTGATGGAAGAAGAACTCAGACGCTCCGTCAACCTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                          gb_est4:AA239785
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 474)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                  AA239785 474 bp mRNA mx80a03.rl Soares mouse NML Mus similar to TR:G1001252 G1001252
           Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                 mRNA sequence.
                                                 The WashU-HHMI Mouse EST Project
                                                                       Waterston, R.
                                                                                                                                                                                                                                                                AA239785.1 GI:1863825
 WashU-HHMI Mouse
                                                                                                                                                                                                                                 house mouse.
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    Quality:
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lyCysValIleLysGluThrLeuArgIleAsnProProValProGlyGly
                                                 CCAGAGGATGCTTCCCGGTTCAGCTTCATTCCATTTGGAGGAGGCCTTCG
                                                              LeuGluAspGlySerArgPheAsnTyrIleProPheGlyGlyGlySerAr 436
                                                                                                TCTTCACTAACAAGGAGGAATTTAATCCCGACCGCTTTATAGTGCCTCAT
                                                                                                                                                                                               TCAAGACAACTTAGACATGGAAACTTTGGAACAGCTTAAATACACTG
                                                                                                                                                                                                                                                 GGTGTGTCATTAAGGAGACCCTGCGATTGAATCCTCCGGTTCCAGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
TMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: -28m13 rev2 ET from High quality sequence stop: 461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
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/clone="TMAGE:692620"
/clone_lib="Soares mouse N
/tissue_type="Liver"
/lab_host="DH10B"
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REFERENCE
AUTHORS
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DOCUS

BE236243

DEFINITION 143959 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.

ACCESSION

BE236243
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US-09-668-482-2 x BE236243
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451 ATGAAGACAAGCCCCACTGTGTAC 474
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25 ValLysLeuTrpGluMetLeuMetIleArgArgValAspProAsnCysAr 41
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                                                                                        ATCAAACTCTGGGACCTGTACTGCGTGAGCAGCCGGGACCGCAGCTGCAC
                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
Email: smitheemail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmarch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 85 row: B column: 21
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST discovery in swine Unpublished (2000) Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Keele, {\tt J.W.} Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /Organism="Sus scrofa"
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/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pcMV SPORT6; Site_1: xbaI; Site_2: xhoI;
/ibrary made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
a 163 c 174 g 104 t
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4.141
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Percent Identity: 67.797
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L74 142 GAGCGC 187 eAlaMe	.41 targalaPi ::: 51 GCAGGCCTT 55 InGluVali ::	.08 alserv		58 euGlnL : 01 TGCAGA 75 TyrGly 51 TACGGT	
ValLeuValTyrProGluMetL ::: ::::: GAGCGCGGCCTCCTGGTTTACCCCCAGGTGA GALAMetArgIleLeuLeuGlyPheGluPro	targAlaPheSerargAspAlaLeuGluHisT ::: :: :: CAGGCCTTCAGCCGCGAGGCGCTCCAGTGCT InGluValLysSerAlaIleGlnGluTrpLeu :: :::::::	alGlnTrpProAlaSerVa	.yAlaAspAsnValArgGln ;:: rgcagacaacgTgCgGCGC	euileLeuGlnArgArgLy ::::: :TGGTGCTACAGCGAAGGAA CyslleTyrLysThrHisL	
	targalaPheSerargAspAlaLeuGluHisTyrIleProValIleGlnG ::: :: :: ::	alSerValGlnTrpProAlaSerValArgThrIleLeuGlySerAspThr :::	1MetGlyAlaAspAsnValArgGlnIleLeuLeuGlyGluHisLysLeuV 	euGlnLeuIleLeuGlnArgArgLysPheLeuArgMetLysArgGlnLys ::::: :::	
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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AAG20783
AAG46490
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AAW44160
AAW37735
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Human cytochrome P
Human retinoid met
Cytochrome P450RAI
Mouse retinoid met
Cytochrome zp450RA
Zebrafish retinoid
Human PSEC64 prote
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
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Arabidopsis thalia A P450-2 protein i A P450-2 protein i Sweetgum coniferyl Amino acid sequenc B. napus F5H polyp B. napus F5H polyp B. napus F5H polyp Human ORFX ORF321 Arabidopsis thalia			3873 3873 511 511 513 513 513 520 520 520 520 520 520 520 520 520 520	13.3 13.3 13.3 13.3 13.3 13.3 13.3 13.3	348.5 348.5 335.5 335.5 335.3 335.3 335.3 335.3 335.3 335.3 335.3 332.3 327.2 327.2 327.2 327.3 3.3 3 3.3 3 3.3 3 3.3 3 3.3 3 3.3 3 3.3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
Arabidopsis	AAG20784 AAB07921 AAG30049 AAG30048 AAW27153 AAG44571 AAG445022 AAG45021 AAG44570 AAG44572 AAG44572 AAG44572 AAG44572 AAG44573 AAG11836 AAG11834 AAG30050 AAB07776	21 21 21 21 21 21 21 21 21 21 21 21	430 513 489 472 491 4492 4461 4461 4333	17.1 16.8 16.6 16.6 16.6 16.6 16.6 16.6 15.8 15.8 15.8 15.8 15.8 15.8	445.5 439434.3 433.5 433.5 433.5 433.5 423	12 13 14 15 16 17 17 18 19 20 20 21 22 23 23

ALIGNMENTS

AAW37734 RESULT

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AAW37734 standard; Protein; 497

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AAW37734;

WPI; 1998-077193/07. N-PSDB; AAV09247. 01-OCT-1996; 21-JUN-1996; 23-JUN-1997; 31-DEC-1997. WO9749832-A2 Homo sapiens Petkovich (TOOH) UNIV QUEENS KINGSTON 96US-0724466. 96US-0667546. 97WO-CA00488

Retinoid regulated gene; cytochrome P450 gene; enzyme; oxidative metabolism; P450RAI; retinoic acid; RA; prom

RA; promoter.

Human cytochrome P450RAI protein. 07-JUL-1998 (first entry)

Identifying DNA encoding inducible or suppressible cytochrome P450 - by screening for drugs which reduce the catabolism of retinoic acid, useful in cancer chemotherapy and the treatment of acne and

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RESULT
AAW44160
ID AAW4
XX AAW4
XX AAW4
XC AAW4
XX 22-J
DT 22-J
XDT 22-J
XDE Huma
XX Reti
KW reti
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Best Local
 actinic
            Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid; human; inhibitor; antibody; cancer;
                                                 Human retinoid metabolising protein hP450RAI.
                                                                                                                               AAW44160 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression is dependent on the presence of retinoic acid (RA). The retinoid-regulated genes such as the inducible cytochrome P450RAI gene specifically metabolises a derivative of the RA. The cytochrome P450 gene in general produces enzymes involved in the oxidative metabolism of endogenous and exogenous compounds. The cytochrome P450 nucleotide sequence can be used to induce or suppress the expression of its protein. P450RAI is highly induced by RA in cell lines and tissues. This allows for development of a drug screen using promoters and nucleotide sequences to identify drugs which are useful for reducing the catabolism of RA.
                                                                               22-JUN-1998
                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Pages 58-59; 113pp; English.
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                                                                                                                                                                                                                                                                                                                                                   MGLPALLASALCTEVLPLLLELAAIKLWDLYCVSGRDRSCALPLPPGTMGFPFFGETLQM 60
                                                                                                                                                                                                                                                            APHPEDASRFSFIPFGGGLRSCYGKEFAKILLKIFTVELARHCDWOLLNGPPTMKTSPTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSGCLSNLHDSSHKQRKKVIMRAFSREALECYVPVITEEVGSSLEQWLSCGERGLLVYPE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is the amino acid sequence of the human cytochrome P450RAI. It
                                                                                                                                                                                                                                                aphpedasrfsfipfggglrscvgkefakillkiftvelarhcdwgllngpptmktsptv
                                                                                                                                                                                                                                                                                                   {\tt ketlrlnppvpggfrvalktfelngyqipkgwnviysicdthdvaeiftnkeefnpdrfs}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VKRLMFRIAMRILLGCEPQLAGDGDSEQQLVEAFEEMTRNLFSLPIDVPFSGLYRGMKAR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vlqrrkflqmkrrkygfiykthlfgrptvrvmgadnvrrillgddrlvsvhwpasvrtil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        497;
 keratosis;
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                                                                                                                                 Protein;
          inhibitor;
leukoplakia;
                                                                                                                                 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2611; DB 19;
Pred. No. 1.5e-253;
); Mismatches 0;
antibody;
kia; head
 tumour;
neck tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                      Matches 497;
                                                                                                                                                        • 121
                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Retinoid metabolising
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21-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUN-1997;
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                                                                                                                          MGLPALLASALCTFVLPLLLFLAAIKLWDLYCVSGRDRSCALPLPPGTMGFPFFGETLQM
                    VLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWPASVRTIL
                                                                                                                                                                                vlqrrkflqmkrrkygfiykthlfgrptvrvmgadnvrrillgddrlvsvhwpasvrtil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page
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                                                                                                                                                                                                                                                                                      Conservative
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96US-0667546.
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keratosis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                   Score 2611; DB 19;
Pred. No. 1.5e-253;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful to develop oral leukoplakia,
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     Query Match
Best Local Similarity
Matches 464; Conserv
                                                          This amino acid sequence is of an isoform of cytochrome zP450RAI. Its expression is dependent on the presence of retinoic acid (RA). The retinoid-regulated genes such as the inducible cytochrome P450RAI gene specifically metabolises a derivative of the RA. The cytochrome P450 gene in general produces enzymes involved in the oxidative metabolism of endogenous and exogenous compounds. The cytochrome P450 nucleotide sequence can be used to induce or suppress the expression of its protein. P450RAI is highly induced by RA in cell lines and tissues. This allows for development of a drug screen using promoters and nucleotide sequences to identify drugs which are useful for reducing the catabolism of RA.
                                                                                                                                                                                                                                                                                    01-OCT-1996;
21-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                             Retinoid regulated gene; cytochrome P450 gene; oxidative metabolism; P450RAI; retinoic acid; F
                                                                                                                                                                                       Identifying DNA encoding inducible or suppressible cytochrome P450 by screening for drugs which reduce the catabolism of retinoic actions and the treatment of acne and useful in cancer chemotherapy and the treatment of acne and
                                                                                                                                                                                                                                                                                                            23-JUN-1997;
                                                                                                                                                                                                                                                                                                                             31-DEC-1997.
                                                                                                                                                                                                                                                                                                                                                                                                      Cytochrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW37735 standard;
                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                    WPI; 1998-077193/07
                                                                                                                                                                                                                                                                                                                                             WO9749832-A2
                                              Sequence
                                                                                                                                                                Disclosure; Pages 59G-59H; 113pp; English.
                                                                                                                                                                                 psoriasis
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                                                                                                                                                                                                                           AAV09252
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      Conservative
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96US-0667546.
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              93.3%;
       14;
              Score 2437;
Pred. No. 4.
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       Mismatches
       DB 19;
1.6e-236;
nes 19;
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21-JUN-1996;
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                                                                                                                                    WO9749815-A1
                                                                                                                                                    Mus musculus.
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                                                                                                                                                                                                                                                                                                                              AAW44161 standard;
                  WPI; 1998-077178/07
N-PSDB; AAV12205.
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                                                                                                                                                                                                                                                                                        (first entry)
                                                Jones G,
                                                                 QUEENS KINGSTON
                                                                                                                                                                                                                                                                     metabolising protein mP450RAI.
                                                                                      96US-0724466.
96US-0667546.
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                                                                                                                                                                                                                                                                                                                               Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
  07-JUL-1998
                              AAW37733;
                                                      AAW37733
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                                                                                                                                                                       NLIHARIEQNIRAKICGLRASEAGOGCKDALQLLIEHSWERGERLDMQALKQSSTELLEG
                                                                                                                                                                                                                              ketlrlnppvpggfrvalktfelngyqipkgwnviysicdthdvadiftnkeefnpdrfi
                                                                                                                                                                                                                                           KETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVAEIFTNKEEFNDDRFS
                                                                                                                                                                                                                                                                                                                                                                                           GSGCLSNLHDSSHKQRKKVIMRAFSREALECYVPVITEEVGSSLEOWLSCGERGLLVYPE
                                                                                                                                                                                                                                                                                                                                                                                                           VKRLMFRIAMRILLGCEPQLAGDGDSEQQLVEAFEEMTRNLFSLPIDVPFSGLYRGMKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                  gagclsnlhdsshkqrkkvimqafsrealqcyvlviaeevsscleqwlscgergllvype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vlqrrkflqmkrrkygfiykthlfgrptvrvmgadnvrrillgehrlvsvhwpasvrtil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWDASVRTIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGLPALLASALCTFVLPLLLFLAAIKLWDLYCVSGRDRSCALPLPPGTMGFPFFGETLOM 60
                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         497 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           actinic keratosis, oral leukoplakia, acne, psoriasis
                                                     Protein; 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.4%; Score 2437; DB 19;
93.4%; Pred. No. 4.6e-236;
"1'. Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 497;
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                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the amino acid for cytochrome zP450RAI of the zebra fish. Its expression is dependent on the presence of retinoic acid (RA). The retinoid-regulated genes such as the inducible cytochrome P450RAI gene specifically metabolises a derivative of the RA. The cytochrome P450 gene in general produces enzymes involved in the oxidative metabolism of endogenous and exogenous compounds. The cytochrome P450 nucleotide sequence can be used to induce or suppress the expression of its protein. P450RAI is highly induced by RA in cell lines and tissues. This allows for development of a drug screen using promoters and nucleotide sequences to identify drugs which are useful for reducing the catabolism of RA.
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                   297
                                                               234
                                                                                         237
                                                                                                                                                   178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Pages 53-55; 113pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying DNA encoding inducible or suppressible cytochrome P450 -by screening for drugs which reduce the catabolism of retinoic acid, useful in cancer chemotherapy and the treatment of acne and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAV09251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996;
21-JUN-1996;
                                                                                                                                                                                121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TOOH ) UNIV QUEENS KINGSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oxidative metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Retinoid regulated gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytochrome zP450RAI protein
                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                               \vdash
                                                                                                                                                                                                                                                                                                       1 MGLPALLASALCTEVLPLLLFLAAIKLWDLYCVSGRDRSCALPLPPGTMGFPFFGGTLQM 60
MKARNLIHARIEQNIRAKICGLRASEAGOGCKDALQLLIEHSWERGERLDMQALKQSSTE
                                                                                                                               YPEVKRLMFRIAMRIILGCEP-QLAGDGDSEQQLVEAFEEMTRNLFSLPIDVPFSGLYRG
                                                                                                                                                                         ilqrrkflrmkrqkygciykthlfgnptvrvmgadnvrqillgehklvsvqwpasvrtil 120
                            LLFGGHETTASAATSLITYLGLYPHVLQKVREELKSKGLLCKSNQDNKLDMEILEQLKYI
                                                                                                                                                                                                                                                VLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWDASVRTIL 120
                                                                                                                ypemkklmfriamrillgfepeqiktd---eqelveafeemiknlfslpidvpfsglyrg
                                                                                                                                                                                                                                                                                         mglytlmvtflotivlpvllflaavklwemlmirrvdpncrsplppgtmglpfigetiq1 60
                                                         lrarnfihskieenirkkiqd-ddneneqkykdalqlliensrrsdepfslqamkeaate
                                                                                                                                                                                                                                                                                                                                                                                                                              492
                                                                                                                                                                                                                                                                                                                                                      Conservative
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96US-0667546.
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                                                                                                                                                                                                                                                                                                                                                                 66.6%; Score 1738; DB 19; 68.0%; Pred. No. 7.5e-166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ne; cytochrome P450 gene; enzyme;
P450RAI; retinoic acid; RA; prom
                                                                                                                                                                                                                                                                                                                                                        63;
                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                     84;
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                               Length 492;
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5

Query Match

Length 492;

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RESULT
AAW44159
ID AAW4
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B
                                    retinoic acid. Zebrafish, human and mouse P450RAIs (see AAW44159-6 are claimed. They can be expressed in host cells and used to metabolize retinoic acid in an organism or cell, in drug screening, and to raise antibodies useful for inhibiting retinoic acid hydroxylation for the treatment of cancer, actinic keratosis, oral leukoplakia, secondary tumours of the head and/or neck, non-small cell lung carcinomas, basal cell carcinomas, acute promyelocytic leukaemia, skin cancer, and premalignancy associated with actinic
                                                                                                                                             This protein comprises a novel zebrafish retinoid metabolising protein, designated zP45CRAI. Its amino acid sequence was deduced from a cDNA clone (see ANV12203) isolated from a 6-18 hr embryo library. It includes a haem-binding motif characteristic of cytochrome P450 proteins. zP45ORAI is a retinoid oxidase that has the ability to hydroxylate retinoic acid at the 4 position of the beta-tonome ring, and is inducible in epithelial cells exposed to retinoic acid. Zebrafish, human and mouse P45ORAIs (see ANAV4159-61)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996;
21-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid; zebrafish; inhibitor; antibody, cancer; actinic keratosis; oral leukoplakia; head tumour; neck tumour; non-small cell lung carcinoma; basal cell carcinoma; acute promyelocytic leukaemia; skin cancer; acne; psoriasis; acute promyelocytic leukaemia; skin cancer; acne; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW44159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW44159 standard; Protein; 492 AA.
                                                                                                                                                                                                                                                                                     Claim 1; Page 50-51; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                   Retinoid metabolising protein - e.g. cancer, actinic keratosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TOOH ) UNIV
                                                                                                                                                                                                                                                                                                                      ichthyosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ichthyosis; therapy; diagnosis; screening.
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                           acne, psoriasis
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96US-0667546.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Petkovich
                           and/or ichthyosis.
                                                                                                                                                                                                                                                                                                                                   useful to develop products to treat, oral leukoplakia, acne, psoriasis or
                                                                                                                                                                                                                                                                                                                                                                                                                              PM,
                                                                                                                                                                                                                                                                                                                                                                                                                              White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   476
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Sequence

492 AA;

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                   A protein related protein -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; PSEC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PSEC64 protein sequence SEQ ID NO: 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-2000
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                                                                                                   N-PSDB;
                                                                                                                                                                                                                               19-NOV-1998;
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                                                                                                                                                                             (HERI-) HERIKKUSU KENKYUSHO
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                                                                                                2000-468126/41.
DB; AAA60752.
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                                              neuron and
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7.5e-166;
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RESULT

AAG20783

ID AAG2

XX AAG2

XX AFAb

XX Prot

XW 105-8

PR 05-8

PR 05-8

PR 05-8

PR 25-9

PR 30-1

PR 30-1

PR 30-1

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05-MAR-1999

09-MAR-1999

23-MAR-1999

24-MAR-1999

25-MAR-1999

01-APR-1999

06-APR-1999

16-APR-1999

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30-APR-1999

05-MAY-1999

06-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a human protein, designated PSEC64, which is related to neuron growth. The PSEC64 protein and its gene can be used for the development of a preventive agent for use in the treatment of diseases in which nerves are involved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 23102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-OCT-2000 (first entry)
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   990S-0121825

990S-0123180

990S-0125788

990S-0126768

990S-0127662

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990S-0127662

990S-012871

990S-0130077

990S-0130077

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990S-013048

990S-0132486

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Pred. No. 1.4e-103;
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99US-0145224. 99US-0145276. 99US-0145913. 99US-0145918. 99US-0145919.

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3-0146386. 3-0146388. ;-0145919. ;-0145951. 99US-0145192. 99US-0145145. 99US-0145218.

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                        Arabidopsis thaliana
                                                            Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 58494.
                                                                                                                        18-OCT-2000
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                                                  termination
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                                                                                                                                                                                                                                                                                              -PHPEDASRESFIPEGGGLRSCVGKEFAKILLKIFTVELARHCDWOLLNGPPTMKTSPTV
                                                                                                                                                                                                                                                                                                                                ETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVAEIFTNKEEFNPDRFSA 421
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nilarity 27.6%;
Conservative 9
                                                  sequence
                                                                                                                        (first entry)
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990S-0160980.
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990S-0161404.
990S-0161406.
990S-0161359.
990S-0161359.
990S-0161361.
990S-0161393.
990S-01619920.
990S-0161993.
990S-0161993.
                                                                                                                                                                         Protein; 461
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; Pred. No. 2.7e-39;
96; Mismatches 211;
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990S-0146389 990S-0147038 990S-014704 990S-0147260 990S-0147260 990S-0147493 990S-0148119 990S-0148341 990S-0148341 990S-0149368 990S-0149368 990S-0149368 990S-0149368 990S-0149723 990S-0149723 990S-0149929 990S-0150866 990S-0150866 990S-0150866 990S-0151080 990S-0151080 990S-0151080 990S-0151303 990S-0151330 990S-015479 990S-0154658 990S-0158659 990S-0158659 990S-0158659 990S-0158659 990S-0159638 990S-0159294 990S-0159330 990S-0159331 990S-0159331 990S-0159331 990S-0159638 990S-0159638

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31-AUG-1999;
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hybridisation assay; genetic mapping; gene expression control; promoter
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Pred. No. 1.5e-36;
6; Mismatches 203;
                                        Indels
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hybridisation assay; genetic mapping; gene expression control;
termination sequence.
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   99US-0123180
99US-012548
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99US-0126264
99US-0126785
99US-0127462
99US-0128234
99US-0128714
99US-0138077
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promoter;
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Best Local
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                                         Arabidopsis thaliana protein fragment SEQ ID NO: 23103.
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            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                          17-OCT-2000
                                                                          AAG20784;
                                                                                      AAG20784 standard; Protein;
                                                                                                                             446
                                                                                                                                                            388
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                                                                                                                                            473 TMKTSPTVYP 482
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                                                                                                                                                                                                                  ifnpwrwmkksle--sqnscfvfgggtrlcpgkelgiveissflhyfvtryrweeiggde
                                                                                                                                                                 lm----vfp 450
                                                                                                                                                                                               QMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWPASVRT 118
                                                                                                                                                                                                                                                                                                                                                                       136;
                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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99US-0161405.
99US-0161405.
99US-0161359.
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99US-0161351.
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99US-0160814.
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99US-0160981.
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                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 450.5; DB 21; Length; Pred. No. 1.5e-36; 96; Mismatches 203; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                      465;
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Arabidopsis thaliana

99US-0145087
99US-0145087
99US-0145192
99US-0145218
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99US-0145218
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99US-0130449. 99US-0130891 99US-0132485. 99US-0132487. 99US-0132487. 99US-0132487. 99US-0134218. 99US-0134218. 99US-0134219. 99US-0134370. 99US-0135124. 99US-0135124. 99US-0135124. 99US-0135124. 99US-0135722. 99US-0135021. 99US-0135021. 99US-0135021. 99US-0135021. 99US-0135021. 99US-0135021. 99US-0135021. 99US-013502. 99US-0136021. 99US-0137528. 99US-0137528. 99US-0139453.	011222
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20-SEP-1999;
22-SEP-1999;
23-SEP-1999;
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28-OCT-1999
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05-OCT-1999
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lfrnihhnpkyfsnpevfdpsrfevnpkpn----tfmpfgsgvhacpgnelaklqilif
                   SICDTHDVAEIFTNKEEFNPDRFSA-PHPEDASRFSFIPFGGGLRSCVGKEFAKILLKIF
                                                           KSNQDNK-LDMEILEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIY 396
                                                                                                                        gynsfpmslpgtsyhkalmark----qlktivseiicerrekralq--tdflghllnfkn 219
                                                                                                                                             ---SLPIDVPFSGLYRGMKARNLIHARIEQNIRAKICGLRASEAGQGCKDALQLLIEHSW 279
                                                                                                                                                                                                                                                              MGFPFFGETLQMVLQR-RKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGDDRL 107
                                                                                ekgrvltqeqiadniigvlfaaqdttascltwilkyl----hddqklleavkaeqkaiye
                                                                                                    ERGERLDMQALKQSSTELLFGGHETTASAATSLITYLGLYPHVLQKVREELKS--KGLLC
                                                                                                                                                                  anmpi--vstyqemkkfafdvgilaifg------hlessykeilkhnynivdk 165
                                                                                                                                                                                     LSCGERGLLVYPEVKRLMFRIAMRILLGCEPQLAGDGDSEQQLVEAFEEMTRNLF-----
                                                                                                                                                                                                                             VSVHWPASVRTILGSGCLSNLHDSSHKQRKKVIMRAFSREALECYVPVITEEVGSSLEQW
                                                                                                                                                                                                                                                 \verb|mgwpylgetlqlysqnpnvfftskqkrygeifktrilgypcvmlaspeaarfvlvthahm|
                                       {\tt ensrekkpltwrqtrnmplthkviveslrmasiisftfreavvdveykgylipkgwkvmp}
                                                                                                                                                                                                         fkptyprskekligpsalffhqgdyhshirklvqssfypetirklipdiehialsslqsw 120
                                                                                                                                                                                                                                                                                               124;
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990S-0161406.
990S-0161359.
990S-0161360.
990S-0161361.
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99US-0161993.
99US-0162142.
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99US-0160815.
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99US-0158369.
99US-0159293.
99US-0159294.
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S-0160815.
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s-0159330.
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                                                                                                                                                                                                                                                                                                      17.18;
                                                                                                                                                                                                                                                                                             87;
                                                                                                                                                                                                                                                                                                       Score 445.5;
Pred. No. 4.4
                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                      4.4e-36;
                                                                                                                                                                                                                                                                                                               DB 21;
                                                                                                                                                                                                                                                                                            201;
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                                                                                                                                                                                                                                                                                                                Length 430;
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                     455
  390
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                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                        The present sequence represents a DWF4 polypeptide. The polypeptide is cytochrome P450 enzyme that mediates multiple steps in synthesis of brassinosteroids. Specifically, it mediates multiple 22alpha-hydroxylation steps in brassinosteroid biosynthesis. The DWF4 polynucleotide is used for altering the phenotype of a plant. DWF4 plants display a dramatic reduction in the length of different organs, and this size reduction is attributable to a defect in cell elongation. The DWF4 polynucleotides and polypeptides can be used in diagnostic assays and to generate antibodies, which can be used to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 50; Fig 11; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated \text{dwf4} polynucleotide useful for altering the phenotype of plants, for diagnostic assays and in the production of antibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-549142/50.
N-PSDB; AAA59599.
   174
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11-FEB-1999;
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                                                                                                                                                                                     3 LPALLASALCTFVLPLLLFLAAIKLWDLYCVSGRDRSCALPLPPGTMGFPFFGETL----
GLLVYPEVKRLMFRIAMRILLGCEPQLAGDGDSE-QQLVEAFEEMTRNLFSLPIDVPFSG 232
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                                                                                                                       -QMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWPASVR 117
                                                                                                                                                    lpllllpsl----lslllflillk-----rrnrktrfnlppgksgwpflgetigylk 57
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27.0%;
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Pred. No. 2.5e-35;
5; Mismatches 226;
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RESULT 14
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25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
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24-MAR-1999;
01-APR-1999;
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24-MAY-1999;
14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                             25-FEB-2000;
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99US-0130510

99US-0132048

99US-0132487

99US-0132486

99US-0132486
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99US-0125788.
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RESULT 15
AAG30048
ID AAG300
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XY
AG AAG300
DT 17-OCT
XX
DE Arabid
XW
Protei
KW Protei
KW hybrid
KW termin
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Best Local Similarity
                                                                                                                                                                                                                                                        Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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26-OCT-1999,
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28-OCT-1999,
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05-MAR-1999;
                                                                  25-FEB-2000; 2000EP-0301439
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28.0%;
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Pred. No. 7.4e-35;
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99US-015566 99US-0151066 99US-0151066 99US-0151080 99US-0151080 99US-0151303 99US-0151333 99US-0152363 99US-0152363 99US-0153778 99US-0154018 99US-0154018 99US-0154018 99US-0155139 99US-0155139 99US-0155659 99US-0156659 99US-0156659 99US-0156659 99US-0156659 99US-0156659

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99US-0160980.

S-0159638. S-0159584. S-0160741. S-0160767. S-0160767.

99US-0161404. 99US-0161405. 99US-0161406.

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990S-0134219 990S-0134219 990S-0134761 990S-0134768 990S-0135353 990S-0135629 990S-0136529 990S-0136529 990S-0137528 990S-0137528 990S-0139450 990S-0139450 990S-0139450 990S-0139450 990S-0139450 990S-0139450 990S-0139451 990S-0139451 990S-0139451 990S-0139451 990S-0139451 990S-0139451 990S-0139451 990S-0139451 990S-0139461 990S-0139461 990S-0139461 990S-0139463 990S-0139463 990S-0139463 990S-0140554 990S-0140534 990S-0140833 990S-014287 990S-014287 990S-014287 990S-014287	99US-0125788 99US-0125788 99US-0126785 99US-0127462 99US-0127462 99US-0129845 99US-0130077 99US-0130510 99US-0130610 99US-0131449 99US-0131449 99US-0133407 99US-0132484 99US-0132484 99US-0132486 99US-0132486 99US-0132486 99US-0132486 99US-0132486 99US-0132486 99US-0132486 99US-0132486 99US-0132486 99US-0132486
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990S-0145918 990S-0145918 990S-0145918 990S-0145918 990S-0146386 990S-0147308 990S-0147302 990S-0147302 990S-01477303 990S-01477416 990S-0147493 990S-0148341 990S-0148341 990S-0148341 990S-0149735 990S-014975 990S-0149722 990S-0149723 990S-0149733 990S-0149733 990S-0149733 990S-0149733 990S-0149733 990S-0151066 990S-0151066 990S-0151066 990S-0151303 990S-0151303 990S-0151303 990S-0151303 990S-0151303 990S-0155139	

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Best Local Similarity 28.0%;
Matches 140; Conservative 80
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                                                                                                                                                                                                                                                     413 EFNPDRFSAPHPEDASRFSFIPFGGGLRSCVGKEFAKILLKIFTVELARHCDWQLLN-GP 471
                                                                                                353 LKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVAEIFTNKE 412
                                                                                                                                                  292 lllmylnaghessghltmwatilmqehpmilqkakee--qerivkkrapgqkltlketre
                                                                                                                                                                                                      233 yhralkarkklvaaf-qsivtnrrngrkqnissnrkdmldnlidvkdengrvlddeeiid
                                                                                                                                                                                                                     233 LYRGMKARNLIHARIEQNIRAKICGLRASEAGQGCKDALQLLIEHSWERGERLDMQALKQ 292
                                                                                                                                                                                                                                                                             173 RGLLVYPEVKRLMFRIAMRILLGCEPQLAGDGDSEQQLVEAFEEMTRNLFSLPIDVPFSG 232
                                                                                                                                                                                                                                                                                                             120
467 pvm-flphnrpkdnclarit 485
                                                                                                                                                                            293 SSTELLFGGHETTASAATSLITYLGLYPHVLQKVREELKSKGLLCKSNQDNKLDMEILEQ
                                                                                                                                                                                                                                                                                                                                114 ASVRTILGSGCLSNLHDSSHKQRKKVIMRAFS-REALECYVPVITEEVGSSLEQWLSCGE 172
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                                              ks {\tt tmkligrksfvgisfee} hkrlrrlt sapvngpeals vyiq fieet vnt dlekwsk mge
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                         PTMKTSPTVYPVDNLPARFT 491
                                                                                                                                                                                                                                                                                                                                                                       V-----LQRRKFLQMKRRKYG--FIYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWP 113
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99US-0158232.
99US-0158369.
99US-0159293.
99US-0159294.
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; Pred. No. 7.5e-35;
80; Mismatches 248; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                    409
                                                                                                                                                     349
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Search completed: November 6, 2001, 13:25:25
Job time: 12653 sec

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Run
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Maximum DB
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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      pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
      2611
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2611
1 MGLPALLASALCTE
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Match
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1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/DTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*
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US-08-622-166A-4
US-08-991-677-4
US-08-991-432-2
US-08-948-564-4
US-08-948-564-4
US-08-948-564-8
US-08-948-564-8
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US-09-292-768-68
US-09-292-768-68
US-09-292-768-68
US-09-292-768-69
US-09-292-768-69
US-08-457-274A-25
PCT-US95-05758-2
US-08-457-274A-28
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                                                                                                                                      APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: HINT, John C
REGISTERMENT, John C
                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/88
ETILING DATE: June 25, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667, 5
ETILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724, 4
                                                  TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 4:
                                                                                               NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                            ZIP: M5L 1A9
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
                SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
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CORRESPONDENCE ADDRESS:
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APPLICANT: Beckett, Barbara R., Jones, Glenville
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CITY: Toronto
STATE: Ontario
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                                                                                    (416) 863-4344
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4
COMPUTER: COMPAQ, IBM PC compatible
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,164D
FILING DATE: June 25, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
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APPLICANT: Peckovich, P. Martin, White, Jay A.,

APPLICANT: Beckett, Barbara R., Jones, Glenville

TITLE OF INVENTION: Retinoid Metabolizing Protein

NUMBER OF SEQUENCES: 43
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Best Local
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CITY: Toronto
STATE: Ontario
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Pred. No. 2.3e-279;
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US-08-724-466B-2
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
                                                                                                                                         Sequence 2, Application US/08724466B Patent No. 6063606 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                             NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
                                                                                         APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein
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STRANDEDNESS: sir
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REGISTRATION NUMBER: 36,424
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M5L 1A9
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er 1, 1996
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RESULT 5
US-08-882-164D-2
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Best Local Similarity
Matches 338; Conserval
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TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 2:
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FILING DATE: June 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 5076
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diskette, 3 1/2 inch, 1
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
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LENGTH: 492 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Sequence 2, Application US/08882164D Patent No. 6306624

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Best Local Similarity
Matches 338; Conser
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MEDIUM TYPE: Diskette, 3
COMPUTER: COMPAQ, IBM PC
COMPRATTING SYSTEM: MS-DOS
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NAME: Hunt, John C.
REGISTRATION NUMBER: 50,424
REFERENCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
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LENGTH: 492 amino acids
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APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/:
FILING DATE: June 25, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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CITY: Toronto
STATE: Ontario
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OPERATING SYSTEM:
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GCVIKETLRINPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADVFPNKEEFQP 412
                  GCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVAEIFTNKEEFNP 416
                                                                                                LLFGGHETTASAATSLITYLGLYPHYLQKVREELKSKGLLCKSNQDNKLDMEILEQLKYI 356
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663-2653
NO: 2:
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Patent No.
                                                                                                                                                                                                                                                                                                           Best Local Sir
Matches 129;
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TELEX: 248345
INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
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NAME: SVENSSON, LEONARD R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TITLE OF INVENTION: P450-TYPE PROTEINS INVOLVED IN THE BRASSINOSTEROID SYNTHESI
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    182
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473 GPTIYPVDNLPTKFTSY 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/622,166A FILING DATE: 27-MAR-1996 CLASSIFICATION: 800
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STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
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                                                                                                                                                     RYGSVFMTHLFGEPTIFSADPETNRFVLQNEGKLFECSYPASICNLLGKHSLLLMKGSLH 125
                                                                          KRMHSLTMSFANSSIIKDHLMLDIDRLVRFNLDSWSS----RVLLMEEAKKITFELTVKQ 181
                                    LLGCEPQLAGDGDSEQQLVEAFEEMTRNLFSLPIDVPFSGLYR-GMKARNLIHARIEQNI 251
                                                                                                                                                                                                                                LLLLSSIAAGFLLLLR-RTRYRRMGLPPGSLGLPLIGETFQLIGAYKTENPEPFIDERVA 65
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                                                                                                               KQRKKVIMRAFSREALECYVPV-ITEEVGSSLEQWLSCGERGLLVYPEVKRLMFRIAMRI 192
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3. 5952545
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
-GEWSESLRKEYLLVIEGFFSLPLPL-FSTTYRKAIQARR---
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Pred. No. 5e-39;
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KVAEAL 231
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RESULT 7
US-08-622-166A-4
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                                                    Best Local Similarity Matches 129; Conserv
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                                                                                                                                                                                                                                                   TELEFAX: (703) 205-80: TELEX: 248345 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 27-MAR-199
CLASSIFICATION: 800
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING CYTOCHROME
TITLE OF INVENTION: P450-TYPE PROTEINS INVOLVED IN THE BRASSINOSTEROID SYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 30,330
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                                                                                                                                                                                             amino acid
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ALTMANN, THOMAS
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                                                      Conservative
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                                                                       16.6%;
26.5%;
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                                                      90; Mismatches
                                                                       Score 433.5; DE Pred. No. 5e-39;
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                                                                                        DB 2;
                                                      228;
                                                      Indels
                                                                                        Length
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Patent No. 6252135
GENERAL INFORMATION:
APPLICANT: Chiang, Vincent L
APPLICANT: Carraway, Daniel T
APPLICANT: Smeltzer, Richard H
                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 511
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/08/991,677A CURRENT FILING DATE: 1997-12-16
                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: US 60/033,381
EARLIER FILING DATE: 1996-12-16
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Production of Syringyl Lignin FILE REFERENCE: 50617
                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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                                                                                                                                                18 FIIPLLLLLGLVSRL-----RQR---LPYPPGPKGLPVIGNMLMMDQLTHRGLAKLAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRFSFIPFGGGLRSCVGKEFAKILLKIFTVELARHCDWQLLNGPPTMKTSPTVYPVDNLP 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVVVMKRREEEEEGAERKKDMLAALLAADDGFSDEEIVDF-----LVALLVAGYETTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAKICGLR--ASEAGQGCKDALQLLI--EHSWERGERLDMQALKQSSTELLFGGHETTAS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLGCEPQLAGDGDSEQQLVEAFEEMTRNLFSLPIDVPFSGLYR-GMKARNLIHARIEQNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KYGFIYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWPASVRTILGSGCLSNLHDSSH
                                                                       KRYPIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSNVFTPFGGGPRLCPGYELARVALSVFLHRLVTGFSW-----VPAEQDKLVFFPTTRTQ 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIIGGVFRRAMTDVEIKGYKIPKGWKVFSSFRAVHLDPNHFKDARTFNPWRWQSNSVTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVAEIFTNKEEFNPDRFSAPHPEDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMTLAVKFLTETPLALAQLKEE--HEKIRAMKSDSYSLEWSDYKSMPFTQCVVNETLRVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATSLITYLGLYPHYLOKVREELKSKGLLCKSNODNKLDMEILEOLKYIGCVIKETLRLN 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LMSFDP-----GEWSESLRKEYLLVIEGFFSLPLPL-FSTTYRKAIQARR----KVAEAL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRMHSLIMSFANSSIIKDHLMLDIDRLVRFNLDSWSS----RVLLMEEAKKITFELTVKQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RYGSVFMTHLFGEPTIFSADPETNRFVLQNEGKLFECSYPASICNLLGKHSLLLMKGSLH
     DMAFAHYGPFWRQMRKLCVMKLFSRKRAESWESVRDEVDSAVRVVASNIGST----VNIG
                                                                                                                                                                                                                     136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464
                                                                                                                                                                                                                       Conservative
                                     -HKORKKVIMRAFSREALECY------VPVITEEVGSSLEQWLSCG 171
                                                                                                                                                                                                                                      13.3%;
                                                                                                                                                                                                                       80;
                                                                                                                                                                                                                     Score 348.5; DB 4;
Pred. No. 1.4e-29;
0; Mismatches 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in Gymnosperms
                                                                                                                                                                                                                                                         Length 511;
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                         87;
                                                                                                                                                                                                                       Gaps
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TITLE OF INVENTION: A Method For Regulation Of
FILE REFERENCE: 7024-325
CURRENT APPLICATION NUMBER: US/09/091,432
CURRENT FILING DATE: 1998-06-18
EARLIER FILING DATE: 1996-12-19
EARLIER APPLICATION NUMBER: US 60/009,119
EARLIER APPLICATION NUMBER: US 60/009,119
EARLIER APPLICATION NUMBER: US 60/013,388
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: US 60/013,388
EARLIER FILING DATE: 1996-03-14
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Microsoft Word 2.0C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-09-091-432-2
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 2
LENGTH: 520
                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09091432
Patent No. 5981837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chapple, Clint
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial
FEATURE:
                               177 VYPEVKRLMFRIAMRILLGCEPQLAGDGDSEQQLVEAFEEMTR--NLFSLPIDVPFSGLY 234
   180 IFALTRNITYRAAFG--SACE
                                                                       123 MAFAHYGPFWRQMRKVCVMKVFSRKRAESWASVRDEVDKMVRSVSCNVGKPINVGEQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398
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                                                                                                                                                                                                                                                                                                         Local Similarity
nes 129; Conserv
                                                                                                                                                                                            75
                                                                                                                                                                                                                          VVSLFIFISFI-----TRRRPPYPPGPRGWPIIGNMLMMDQLTHRGLANLAKK 70
                                                                                                                                                                                                                                                              VLPLLLFLAAIKLWDLYCVSGRDRSCALPLPPGTMGFPFFGETLQMVLQRRKFLQMKRRK 74
                                                                                                                                                  YGGLCHLRMGFLHMYAVSSPEVARQVLQVQDSVFS-NRPATI-----AISYLTYDRAD
                                                                                                                                                                                    YGFIYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWPASVRTILGSGCLSNL-HDSS- 132
                                                                                                         -----HKQRKKVIMRAFSREALECYVPV-----ITEEVGSSLEQWLSCGERGLL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SESDDLQNSIKLTKDNIKAIMDVMFGGTETVASAIEWAMTELMKSPEDLKKVQQELAVVV 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERGLLVYPEVKRLMFRIAMRILLGCEPQLAGDGDSEQQLVEAFEEMTR--NLFSLPIDVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIYSICDTHDVAEIFTNKEEFNPDRFSAPHPED--ASRFSFIPFGGGLRSCVGKEFAKIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GL-----DRRVEEKDFEKLTYLKCVLKEVLRLHPPIPLLLHETAEDAEVGGYYIPAKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLLCKSNQDNKLDMEILEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GERLDMQ-ALK-----QSSTELLFGGHETTASAATSLITYLGLYPHVLQKVREELK-SK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WLKWVPQGINVRLNKARGALDGFIDKIIDDHIQKGSKNSEEVDTDMVDDLLAFYGEEAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F-----SGL-YRGMKARNLIHARIEQNIRAKI--CGLRASEAGQGCKDALQLLIEHSWER 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E----LVFALTKNITYRAAFGTI------SHEDQDEFVAILQEFSQLFGAFNIADFIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LET-TVAHLLHCFTWEL---PDGMKPS 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VMINACAIGRDKNSWADPDTFRPSRFLKDGVPDFKGNNFEFIPFGSGRRSCPGMQLGLYA 457
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                       12.3%;
25.0%;
                                                                                                                                                                                                                                                                                                       90;
                                                                                                                                                                                                                                                                                                     Score 322; DB 2;
Pred. No. 1.2e-26;
0; Mismatches 198
-KGQDEFIRILQEFSKLFGAFNVADFIPYFGWI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             477
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                                                                                                                                                                                                                                                                                                       198;
                                                                                                                                                                                                                                                                                                                                         Length 520;
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                     98;
                                                                                                                                                                                                                                                                                                   Gaps
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QΥ

ALPLPPGT----MGFPFFGETLQMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADN 96

Indels

138;

Gaps

22;

-HGAVYKL-AFGPKAFVVVSDPI 125

Matches

Conservative

밁

78 41

SMPIAEGAVSDLLGRPLFFSLYDWFLE---

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: prot
US-08-948-564-16
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                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6121512
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/08948564 Patent No. 6121512
                                                                                                                                                                                                                TELEFAX: 919-854-1401
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-854-1400
                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 800
CLASSIFICATION: 800
ATTORNEY_AGENT INFORMATION:
NAME: Bennett, Virginia C.
NAME: Bennett, Virginia C.
NAME: 37,992
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 576 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Corbin, Frederick T.
TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and
TITLE OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    448 AKILLKIFTVELA----RHC-DWQLLNGPPTMKTS
| :: ::|| || |:| | || ||
                                                                                                                                                                                                                  TELEPHONE: 919-854-1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                463 ----LGLYALDLAVAHILHCFTWKL---PDGMKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331 -KSKGLLCKSNQDNKLDMEILEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIP : || | | ::: :|: ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        404 KKSRVMINAFAIGRDPTSWTDPDTFRPSRFLEPGVPDFKGSNFEFIPFGSGRRSCPGMQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            390 KGWNVIYSICDTHDVAEIFTNKEEFNPDRFSAPHPED--ASRFSFIPFGGGLRSCVGKEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290 KLYSETADLQNSIKLTRDNIKAIIMDVMFGGTETVASAIEWALTELLRSPEDLKRVQQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UZIP: 27627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: PO Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 DPQGINKRLVKARNDLDGFIDDIIDEHMKKKE-NQNAVDDGDVVDTDMVDDLLAFYSEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WERGERLDMQ------ALKQSSTELLFGGHETTASAATSLITYLGLYPHVLQKVREEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No.
                                                                                                                                                                        576 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PO Box 37428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dewey, Ralph E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Siminszky, Balazs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virginia C. Bennett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6121512th Carolina
                                                                                                                    protein
11.1%; Score 289; DB 3; 23.7%; Pred. No. 6.3e-23; tive 86; Mismatches 187;
                                                                                                                                                                                                                  16:
                                                                                                                                                                                                                                                                                            5051-409
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                                      Length 576;
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US-08-948-564-4

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                                                                                                                            ATTORNEY/AGENT INFORMATION:

NAME: Bennett, Virginia C.

REGISTRATION NUMBER: 37,092

REFERENCE/DOCKET NUMBER: 5051

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-854-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                          TELEFAX: 919-854-1401 INFORMATION FOR SEQ ID NO: 4:
                 SEQUENCE CHARACTERISTICS:
LENGTH: 510 amino acid
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Siminszky, Balazs
APPLICANT: Dewey, Ralp.
APPLICANT: Corbin, Frederick T.
APPLICANT: Corbin, Frederick T.
TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and
TITLE OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic Plants
NUMBER OF ESQUENCES: 23
CORRESPONDENCE ADDRESS:
 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               510 LPFGGGPRKCVGDQFALMESTVALTMLLQNFDVELKGTPESVELVTGATIHTKNGMWCR
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CITY: Raleigh
CITY: No. 6121512th Carolina
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                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -LGCEPQLAGDGDSEQQLVEA----FEEMTRNLFSLP--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NKLDMEILEQLKYIGCVIKETLRLNPPVPGGFRVALKT------FELNGYQIPKGWNV 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VINTCLDGLIRNAK----ESRQETDVEK----LQQRDY-LNLKDASLLRFLVD---MRG
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PO Box 37428
                                                   510 amino acids
                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
protein
                                                                                                                                                                                                                                                                                                                     Release #1.0, Version
                                                                                                                                                                                                                                                                                  US/08/948,564
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RESULT 12
US-08-948-564-2
; Sequence 2, Application US/08948564
; Patent No. 6121512
; GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        APPLICANT: Corbin, Frederick T.
TITLE OF INVENTION: No. 6121512
TITLE OF INVENTION: Methods of
                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                     STREET: PO Box 37428
CITY: Raleigh
STATE: No. 6121512th Carolina
COUNTRY: USA
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                                                APPLICATION NUMBER: FILING DATE:
                                  CLASSIFICATION:
                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DWKLPN 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DWQLLN 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKARNLIHA--RIEQNIRAKICG-----LRASEAGQGCKDALQLLIEHSWERGERLDMQA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSIYSMTFGIAARAAFGKKSRY-----QQVFISNMHKQLMLLGGFSVADLYPSSRVFQM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPLMHLKLGEVSNIIVTSPEMAQEIMKTHDLNFSDRPDFVLSRIVSYN------GSG
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                                                                                                                                                                              27627
Bennett,
                                                                                                                                                                                                                                          PO Box 37428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                          Siminszky, Bala
Dewey, Ralph E.
 Virginia
                                    800
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                                                                                                                                                                                                                                                                                                            No. 6121512el Cytochrome P-450 Constructs and Methods of Producing Herbicide-Resistant Transgenic
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                                                                  US/08/948,564
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   G
                                                                                                 Version #1.30
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RESULT 13
US-08-313-075A-50
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                                                                                                                                                                                                                                                                    Sequence 50, Application US/08313075A Patent No. 5639870
                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                         APPLICANT: Holton, Timothy A.
APPLICANT: Cornish, Edwina C.
APPLICANT: Tanaka, Yoshikazu
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-854-1400
                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 513 amino acids
                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                436 NGQDFQLIPFGIGRRGCPAMSFGLASTEYVLANLLYWFNWNM 477
                                                                                                                                                                                                                                                                                                                                                                                                                     426 DASRFSFIPFGGGLRSCVGKEFAKILLKIFTVELARHCDWQL 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               370 VPGGFRVALKT---FELNGYQIPKGWNVIYSICDTHDVAEIFTNKEEFNPDRFSAPHPE- 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 EWTFAEFLRNPNTMKKAQEEVRR---VVGINSKAVLDENCVNQMNYLKCVVKETLRLHPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 EHESSNKKND-----DFLGILLQLQ-ECGRLDFQLDRDNLKAILVDMIIGGSDTTSTTL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 AKICGLRASEAGQGCKDALQLLIEHSWERGE---RLDMQALKQSSTELLFGGHETTASAA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107
              STATE: New York COUNTRY: U.S.A.
                                                                      STREET:
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nes 132; Conserv
                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           LP--LLIARETSSSYKLRGYDIPAKTMYFINAWAIQRDPELWDDPEEFIPERFETSQYDL 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQQLVEAFEEMTRNL-----FSLPIDVP-----FSGLYRGMKARNL-IHARIEQNIR 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIRQEVVTELVEAIGEACGSERPCVNLTEM--LMAASNDIVSRCVLGRKCDDACGGSGSS 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -ITEEVGSSLEQWL--SCG-ERGLLVYPEVKRLMFR---IAMRILLG--CEPQLAGDGDS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVSVHWPASVRTILGSGCLSNLHDSSHKQRKKVIMRAFSREALE-CYVPV------ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TMGFPFFGETLQM-VLQRRKFLQMKRRKYGF1YKTHLFGRPTVRVMGADNVRRILLGDDR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALLASAL------CTFVLPLLLFLAAIKLWDLYCVSGRDRSCALPLPPG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSLITYLGLYPHVLQKVREELKSKGLLCKSNQDNKLDMEILEQLKYIGCVIKETLRLNPP 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----SFAALGRKIMRLLSAFSYGDFFPSLGWVDYLTGLIPEMKTTFLAVDAFLDEVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALLSSVLKQLPHELSSTHYLTVFFCIFLILLQLI-------RRNKYNLPPS
                                                  Garden City
11530
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                                                                E: Scully, Scott, Murphy & Presser
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Best Local
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
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TOPOLOGY: line=-
WOLECHTE -
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LENGTH: 496 amino acid:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: AU PCT/AU93/00127
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9433
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 07-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P
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APPLICATION NUMBER:
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    435
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                                                                                                                                                                                                                                                                                                                                                                     163
                                                                                                                                                                                                                                             257
                                                                                                                                                                                                                                                                                                                                                                                                                                              124 WKTLRKIMNSSIFSGNKLDGNQHLRSKKV-------QEL---IDYCQKC 162
                                                                                                                                                                                                                                                                                 217 PNLVDYFPFLEKIDPQGIKRRMTNNFTKFLGLISGLIDDRLKERNL----RDNANI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 --SVRTILGSGCLS--NLHDSSHKQRKKVIMRAFSREALECYVPVITEEVGSSLEQWLSC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 LFLAAIKLWDLYCVSG----RDRSCALPLPPGTMGFPFFGETLQMVLQRRKFLQMKRRKY 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 30-NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
FGGGLRSCVGKEFAKILLKIFTVELARHCDWQLLNG
                                          KVEEDVELSTYIIPKDSQVLVNVWAIGRNSDLWENPLVFKPERFWESEIDIRGRDFELIP
                                                                             VALKTFELNGYQIPKGWNVIYSICDTHDVAEIFTNKEEFNPDRFSAPHPEDASR-FSFIP 434
                                                                                                                                                   GLYPHVLQKVREELKSKGLLCKSNQDNKLDMEILEQLKYIGCVIKETLRLNPPVPGGF-R 375
                                                                                                                                                                                                                                         GLRASEAGQGCKDALQLLIEHSWERGERLDMQALKQSSTELLFGGHETTASAATSLITYL 316
                                                                                                                                                                                                                                                                                                                                                              AKNGEAY -- DIGRATEGTTLNLLSNTIFSKDLTNPESDSAKE ---- FKELVWNIMVEAGK 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GFIYKTHLFGRPTVRVMGADNVRRILLGDD-----RLV------SVHW-PA--- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILLGLFFTW--FLVNGLMSLRRRKISKKLPPGPFPLPIIGNLHLLGNHPHKSLAQLAKIH 63
                                                                                                                                                                                                   -----DVLDALLNISQENPEEIDRNQIEQLCLDLFAAGTDTTSNTLEWAMAEL
                                                                                                                                                                                                                                                                                                                                                                                                      GERGLLVYPEVKRLMFRIAMRILLGC--EPQLAGD-GDSEQQLVEAFEEMTRNL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPIMNLKLGQLNTVVISSSVVAREVLQKQDLTFSNRFVPDVVHVRNHSDFSVVWLPVNSR 123
                                                                                                                       LQNPHTLQKAQEELAQ--VIGKGKQVEEAD---VGRLPYLRCIVKETLRIHPAAPLLIPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.1%; Score 264.5; DB 1 24.4%; Pred. No. 2.5e-20;
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432 FGAGRRICPGLPLAMRMIPVALGSLLNSFNWKLYGG

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APPLICANT: Croteau, Rodney B
APPLICANT: Lupien, Shari L
APPLICANT: Karp, Frank
TITLE OF INVENTION: RECOMBINANT MATERIALS AN
TITLE OF INVENTION: LIMONENE HYDROXYLASES
FILE REFERENCE: WSU13463
CURRENT APPLICATION NUMBER: US/09/292,768
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: 08/881,784
EARLIER APPLICATION NUMBER: 08/881,784
EARLIER FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PATENTIN VET. 2.0
                 RESULT 15
US-09-292-768-70
Sequence 70, Application US/09292768
; Patent No. 6194185
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GENERAL INFORMATION:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.7%; Score 252.5; DB 4; Best Local Similarity 21.7%; Pred. No. 5.3e-19; Matches 114; Conservative 86; Mismatches 217;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFEEMTRNLFSLPIDVPFSGLYRGMKARNLI------HARIEQNIRAKICGLRASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VRRILLGDDRL----VSVHWPASVRTILGSGCLSNLHDSSHKORKKVIMRAFSREALECYV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QHALASVAKQYGPVAHVQLGEVFSVVLSSREATKEAMKLVDPACADRFESIGTKIMWYDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKFLQMKRRKYGFIYKTHL-------
                                                                                                                                                                                                                             ECEVNGYTIPNKARIMINVWSMGRNPLYWEKPETFWPERF-----DQVSRDFMGNDFEFI
                                                                                                                                                                                                                                                                     TFELNGYQIPKGWNVIYSICDTHDVAEIFTNKEEFNPDRFSAPHPEDASR-----FSFI 433
                                                                                                                                                                                                                                                                                                                                                      PHVLQKVREELKSKGLLCKSNQDNKLDMEILEQLKYIGCVIKETLRLNPPVPGGFRVALK 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISSAIIILVVTYTISLLIIKQW------RKPKPQENLPPGPPKLPLIGH-LHLLWGKLP 56
                                                                                                                                            PFGAGRRICPGLNFGLANVEVPLAQLLYHFDWKLAEGMNPSDMDMS
                                                                                                                                                                                    PFGGGLRSCVGKEFAKILLKIFTVELARHCDWQLLNG--PPTMKTS 477
                                                                                                                                                                                                                                                                                                              PEVMAKAQAEVRA---ALKGKTD--WDVDDVQELKYMKSVVKETMRMHPPIPLIPRSCRE
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Search completed: November Job time: 9918 sec

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Matches 114; Conserv
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Best Local
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APPLICANT: Lupien, Shari L
APPLICANT: Lupien, Shari L
APPLICANT: Karp, Frank
TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
TITLE OF INVENTION: LIMONENE HYDROXYLASES
FILE REFERENCE: WSU113463
CURRENT APPLICATION NUMBER: US/09/292,768
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: 08/881,784
EARLIER APPLICATION NUMBER: 08/881,784
EARLIER FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
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                                              PFGGGLRSCVGKEFAKILLKIFTVELARHCDWQLLNG--PPTMKTS 477
                                                                                                                           TFELNGYQIPKGWNVIYSICDTHDVAEIFTNKEEFNPDRFSAPHPEDASR-----FSFI 433
                                                                                                                                                                                                                                                                                                                                          AGQ-GCKDALQLLIEHSWERGERLDM--QALKQSSTELLFGGHETTASAATSLITYLGLY 319
                                                                                                                                                                                                                                          PHVLQKVREELKSKGLLCKSNQDNKLDMETLEQLKYIGCVIKETLRLNPPVPGGFRVALK 379
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                                                                                                 ECEVNGYTIPNKARIMINVWSMGRNPLYWEKPETFWPERF-----DQVSRDFMGNDFEFI 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISSAIIILVVTYTISLLIIKQW-----RKPKPQENLPPGPPKLPLIGH-LHLLWGKLP 56
PFGAGRRICPGLNFGLANVEVPLAQLLYHFDWKLAEGMNPSDMDMS
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OM protein - protein search, using sw model
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LIGNMENT

C;Species: Synechocystis sp.
A; Variety: PCC 6803
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: S75761
R; Kaneko, T.; Sato, S; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; R

N;Alternate names: protein slr0574
N;Contains: oxidoreductase (EC 1.-.-)

cytochrome P450 - Synechocystis sp. (strain PCC 6803)

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys

A; Reference number: S74322; MUID:97061201 A; Accession: S75761

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C;Genetics:
A;Gene: Cyp
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;251-413/Domain: cytochrome P450 homology <P45>
F;391/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-444 <KAN>
A;COSS-references: EMBL:D64003; GB:AB001339; NID:g1001200; PIDN:BAA10496.1; PID:g100
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 ALPLPPGTMGFPFFGETLQMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRI 100
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                                                                RGERLDMQALKQSSTELLFGGHETTASAATSLITYLGLYPHVLQKVREELKSKGLLCKSN 340
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NNQPLSLPELKDQILLLLFAGHETLTSALSSFCLLLGQHSDIRERVRQEQN-----KLQ
                                                                                                                                                                                                                          LFSLPIPLPNTLFGKSQRARALLLAELEKIIKAR-----QQQPPSEEDALGILLAARDD
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481

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R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID:20083487
A; Reference number: A84420; MUID:20083487
A; Recession: A84859
A; Status: preliminary A; Molecule type: DNA
A; Residues: 1-485 <STO>
A; Cross-references: GB:AE002093; NID:g4512670; PIDN:AAD21724.1; GSPDB:GN00139
C; Genetics: A:Gene: At2942850
A; Map position: 2
C; Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology C; Keywords: heme; iron; metalloprotein
F;432/Binding site: heme iron (Cys) (axial ligand) #status predicted
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 23-Mar-2001
C;Accession: A84859
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45
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                                                                                                                                                                                                                                                           VLEGVFALPVEFPCSKFARAKKARLEIETFLVGKVREK----RREMEKEGAEKPNTTLF-
                                                                                                                                        DTLLQEHAQIKANKGEGEYLTVEDVKKMKYSWQVVRETMRLSPPIFGSFRKAVADIDYGG
                                                                                                                                                                                                                         HSWERGERLDMQALKQSSTE------LLFGGHETTASAATSLITYLGLYPHVLQKVR
                                                                                                                                                                                                                                                                                          MTRNLFSLPIDVPFSGLYRGMKARNLIHARIEQNIRAKICGLRASEAGQGCKDALQLLIE
                                                                                                                                                                                                                                                                                                                                                           EEVGSSLE-OWLSCGERGLLVYPEVKRLMFRIAMRILLGCEPOLAGDGDSEQQLVEAFEE 216
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                                                    YTIPKGWKILWTTYGTHYNPEIFQDPMSFDPTRFDKP----IQAYTYLPFGGGPRLCAGH
                                                                                    YQIPKGWNVIYSICDTHDVAEIFTNKEEENPDRFSAPHPEDASRFSFIPFGGGLRSCVGK 445
                                                                                                                                                                                         -----SRLVEELIKGVITEEEVVDNMVLLVFAAHDTTSYAMSMTFKMLAQHP----TCR
                                                                                                                                                                                                                                                                                                                              DTVKFHHETEWR--GKEEISLYRSAKVLTFTVVFECLYGIKVEIG------MLEVFER
                                                                                                                                                                                                                                                                                                                                                                                               RLILSNEFSLVVSSWPSSSVQLMGMNCIMAKQGEKHRVLRGIVANSLSYIGLESLIPKLC
                                                                                                                                                                                                                                                                                                                                                                                                                             RRILLGDDRLVSVHWPASVRTILGSGCLSNLHDSSHKQRKKVIMRAFSREALECYVPVIT 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.9%; score 519.5; DB 2; 28.3%; Pred. No. 2.9e-32; tive 86; Mismatches 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436
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A; Accession: T05806
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A; Residues: 1-457 <BEV>
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A; Accession: T04444
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Best Local Similarity
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                                  401
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A;Map position: 4
A;Map position: 4
A;Map position: 4
A;Introns: 67/2; 173/3; 302/3; 358/1; 393/3
A;Introns: 67/2; 173/3; 302/3; 358/1; 393/3
A;Note: T18B16.200; T5K18.10
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 hom C;Superfamily: Synechocystis cytochrome P450 homology cp45>
F;272-433/Domain: cytochrome P450 homology cP45>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AL021687
A;Experimental source: cultivar Columbia; BAC clone T18B16
R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.;
submitted to the Protein Sequence Database, April 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytochrome P450 - Arabidopsis thaliana N;Alternate names: protein T18B16.200; protein T5K1 N;Contains: oxidoreductase (EC 1.-.-.) C:Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 C;Accession: T04444; T05806
                                                                                                                                                                                                                                                                         A; Experimental source: cultivar Columbia; BAC
                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 131-457 <BEW>
A; Cross references: EMBL: ALO22580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; submitted to the Protein Sequence Database, April 1998
                                                                                                                                                                                                                                                                         clone T5K18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T5K18
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                                                                                        cytochrome P450 homology
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                                                       oxidoreducta
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313 ITYLGLYPHVLQKVREELKSKGLLCKSNQDNKLDMEILEQLKYIGCVIKETLRLNPPVPG 18 LLLFLAAIKLWDLYCVSGRDR--SCALPLPPGTMGFPFFGETLQMVLQ-RRKFLQMKRRK 74 TFREAVEDVEYEGYLIPKGWKVLPLFRNIHHSADIFSNPGKFDPSRFEVAPKPN-----T KLRKLVLRAFMPESIRNMVPDIESIAQDSLRSW----EGTMINTYQEMKTYTFNVALLS 182 FMPFGNGTHSCPGNELAKLEMSIMIHHLTTKYRCVCVYYLL-FIPFGGGLRSCVGKEFAKILLKI----FTVELARHCDWQLLNGPPTMKTSPTVYPVDNLP LKYLAENPNVLEAVTEE--QMAIRKDKEEGESLTWGDTKKMPLTSRVIQETLRVASILSF ARI----LSERRQNGSSHNDLLGSFMGDKEELTDEQ-IADNIIGVIFAARDTTASVMSWI AKICGLRASEAGQGCKDALQLLIEHSWERGERLDMQALKQSSTELLFGGHETTASAATSL IFGKDEVL----YREDLKRCYYILEKGYNSMPVNLPGTLFHKSMKARKEL-----SQIL LLGCEPQLAGDGDSEQQLVEAFEEMTRNLFSLPIDVPFSGLYRGMKARNLIHARIEQNIR QRKKVIMRAFSREALECYVPVITEEVGSSLEQWLSCGERGLLV--YPEVKRLMFRIAMRI 192 YGSVFKTHVLGCPCVMISSPEAAKFVLVTKSHLFKPTFPASKERMLGKQAIFFHQGDYHA YGFIYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWPASVRTILGSGCLSNLHDSSHK 134 LTLFAGSLFLYFLRCLISQRRFGSSKLPLPPGTMGWPYVGETFQLYSQDPNVFFQSKQKR GFRVALKTFELNGYQIPKGWNVIYSICDTHDVAEIFTNKEEFNPDRFS-APHPEDASRFS 19.6%; Score 512; DB 2 29.6%; Pred. No. 1e-31; 84; Mismatches DB 2; 204; Length 457 Indels 54; TI Gaps 232 443 487 312 400 431 372 287 252 127 67 13;

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A:Map position: 2
A:Introns: 80/2; 187/3; 238/3; 321/3; 351/3; 413/3; 453/2
C:Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome F;291-453/Domain: cytochrome P450 homology <P45>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: T02739; D84692
R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.;
submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC T9I4 ger
A;Reference number: Z14710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable cytochrome P450 At2g29090 [imported] - Arabidopsis thaliana
N;Alternate names: cytochrome P450 homolog T914.17
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001
C;Accession: T02739; D84692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Talless, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vernature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
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A;Experimental source: cultivar Columbia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-482 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-482 <ROU>
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Best Local Similarity
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DRFS-APHPEDASRFSFIPFGGGLRSCVGKEFAKILLKIFTVELARHCDWQLLNGPPTMK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R-RKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWPASVRTILGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PALLASALCTFVLPLLLFLAAIKLWDLYCVSGRDRSCALPLPPGTMGFPFFGETLQMVLQ
                                                 TRVIQETLRAASVLSFTFREAVQDVEYDGYLIPKGWKVLPLFRRIHHSSEFFPDPEKFDP
                                                                                                                                                                            LFGGHETTASAATSLITYLGLYPHVLQKV-REELKSKGLLCKSNQDNKLDMETLEQLKYI
                                                                                                                                                                                                                                                                                                                                   RYAFDVAI -----MSAFGDKEEPTTIDVIKLLYQRLERGYNSMPLDLPGTLFHKSM
                                                                                                                                                                                                                                                                                                                                                                             RLMFRIAMRILLGCEPQLAGDGDSEQQ-----LVEAFEEMTRNLFSLPIDVPFSGLYRGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCLSNLHDSSHKQRKKVIMRAFSREALECYVPVITEEVGSSLEQWLSCGERGLLVYPEVK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NPNSFFATRQNKYGDIFKTHILGCPCVMISSPEAARMVLVSKAHLFKPTYPPSKERMIGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PALITLTIVVVVVVLLF-----KWWLHWKEQR-----LRLPPGSMGLPYIGETLRLYTE
                                                                                             GCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVAEIFTNKEEFNP 416
                                                                                                                                                                                                                                     KAR----IELSEELRKVIEKRRENGREEG--GLLGVLLGAKDQKRNGLSDSQIADNIIGV
                                                                                                                                                                                                                                                                                  KARNLIHARIEQNIRAKICGLRASEAGQGCKDALQLLIEHSWERGERLDMQALKQSSTEL
                                                                                                                                                                                                                                                                                                                                                                                                                            EALFFHQGPYHSTLKRLVQSSFMPSALRPTVSHIELLVLQTLSSWTSQKSINTLEY--MK
                                                                                                                                            IFAATDTTASVLTWLLKYLHDHPNLLQEVSREQFSIRQKIKKENR--RISWEDTRKMPLT
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Pred. No. 3.5e-30;
0; Mismatches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN: AAC33235.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSPDB:GN00139
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Tallon, L.
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A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; I Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Anthors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719
A; Accession: H86185
A, Status: preliminary
A; Molecule type: DNA
A, Residues: 1-490 (STO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: H86185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alo Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
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C; Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome
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Best Local S
Matches 132
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                                         435 FGGGLRSCVGKEFAKILLKIFTVELARHCDWQLLNGPPTMKTSPTVYPVDNLPARFTH 492
                                                                                     374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVIMRAFS-REALECYVPVITEEVGSSLEQWLSCGERGLLVYPEVKRLMFRIAMRILLGC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VNVWLYESSLGENRHY---LPPGDLGWPFIGNMLSFLRAFKTSDPDSFTRTLIKRYGPKG
                                                                                                                                                                           QEHPEVLQRAKAE----QEMILKSRPEGQKGLSLKETRKMEFLSQVVDETLRVITFSLTAF
                                                                                                                                                                                                                    GLYPHVLQKVREELKSKGLLCKSNQDNKLDMEILE--QLKYIGCVIKETLRLNPPVPGGF
                                                                                                                                                                                                                                                                                                          GLRASEAGQGCKDALQLLIEHSWERGERLDMQALKQSSTELLFGGHETTASAATSLITYL
                                                                                                                                                                                                                                                                                                                                                                                                                                            RLTAAPVNGHEALSTYIPYIEENVITVLDKWTKMGEFEFLTH--LRKLTFRIIMYIFLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWPASVRTILGSGCLSNLHDSSHKORK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IKLWDLYCVSGRDRSCALPLPPGTMGFPFFGETLQMVLQRR-----KFLQMKRRKYG--F 77
                                                                                                                   RVALKTFELNGYQIPKGWNVIYSICDTHDVAEIFTNKEEFNPDRFSAPHPEDASRFSFIP 434
                                                                                                                                                                                                                                                                NQRKQNILSNKKDMLDNLLNVKDEDGKTLDDEEIIDVLLMYLNAGHESSGHTIMWATVFL
                                                                                                                                                                                                                                                                                                                                                                                                EPQLAGDGDSEQQLVEAFEEMTRNLFSLPIDVPFSGLYRGMKARNLIHARIEQNIRAKIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IYKAHMFGNPSIIVTTSDTCRRVLTDDDAF-KPGWPTSTMELIGRKSFVGISFEEHKRLR 144
                                                                                                                                                                                                                                                                                                                                                      ESENVMDA-----LEREYTALNYGVRAMAVNIPGFAYHRALKARKTLVAAF-QSIVTERR
FGAGSHLCPGNDLAKLEISIFLHHFLLKYQVKRSNPECPVMYLPHTRPTDNCLARISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132;
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27.6%;
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Pred. No. 6.1e-28
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steroid 22-alpha-hydroxylase (DWF4) - Arabidopsis thaliana N;Alternate names: protein T3A5.40 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_chance C;Accession: T46143 R;Bloecker, H; Mewes, H,W; Mayer, K,F,X.; Lemcke, K.; Schuel submitted to the Protein Sequence Database, December 1999 A;Reference number: Z23024 A;Accession: T46143 A;Status: preliminary A;Molecule type: DNA A;Cross-references: EMBL:AL132979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: dwarf
C;Superfamily:
F;273-436/Doma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Cell 8, 959-969, 1996
A;Title: The tomato Dwarf gene isolated by A;Reference number: Z16181; MUID:96266705
A;Accession: T07859
A;Status: preliminary; translated from GB/E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T07859
cytochrome P450 homolog - tomato
cytochrome P450 homolog - tomato
cyspecies: Lycopersicon esculentum (tomato)
cybate: 14-May-1999 #sequence_revision 14-May-1999 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: T07859
R; Bishop, G.J.; Harrison, K.; Jones, J.D.
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A; Residues: 1-464 <BIS>
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                                                                                                                                                                                                                      T46143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGCE-PQLAGDGDSEQQLVEAFEEMTRNLFSLPIDVPFSGLYRGMKAR----NLIHARIE
                                                                                                                                                                                                                                                                                     --SFLVFGGGTRQCPGKELGVAEISTFLHYFVTKYRWEEIGGDKLMK 447
                                                                                                                                                                                                                                                                                                                                                      IVNGVLRKTTQDMEINGYIIPKGWRIYVYTRELNYDPRLYPDPYSFNPWRWMDKSLEHQN
                                                                                                                                                                                                                                                                                                                                                                                   PVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVAEIFTNKEEFNPDRFSAPHPEDAS
                                                                                                                                                                                                                                                                                                                                                                                                                      SMMAVKYLHDHPKVLEELRKE--HMAIREKKKPEDPIDYNDYRSMRFTRAVILETSRLAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATSLITYLGLYPHYLQKVREELKSKGLLCKSNQDNKLDMEILEQLKYIGCVIKETLRLNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QNIRAKICGLRASEAGQGCKDALQLLIEHSWERGERLDMQALKQSSTELLFGGHETTASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGIESTSLA-----QEFMSEFFNLVLGTLSLPINLPNTNYHRGFQARKIIVNLLRTLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GALLSLISPIMIRDQL---LPKIDEFMRSHLINW---DNKVIDIQEKINKMAFLSSLKQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVIMRAFS----REALECYVPVITEEVGSSLEQWLSCGERGLLVYPEVKRLMFRIAMRIL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FFKSHILGCPTIVSMDSELNRYILVNEAKGLVPGYPQSMIDILGKCNIAAVNGSAHKYMR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCIFCTALLRWNQVKYNQKN-----LPPGTMGWPLFGETTEFLKLGPSFMKNQRARYGS
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Se: strain GCR758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translated from GB/EMBL/DDBJ
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27.4%;
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P450 homology <P45>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 444; DB 2;
Pred. No. 1.8e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                      Lemcke, K.; Schueller,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIDN: AAB17070.1;
                                                                                                                                                     #text_change 16-Feb-2001
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                                                                                                                      Quetier,
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A;Map position: 3
A;Introns: 74/2; 182/3; 233/3; 338/3; 369/3; 396/1; 432/3
A;Introns: 73A5.40
A;Note: T3A5.40
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 c;Keywords: heme; iron; metalloprotein
F;308-484/Domain: cytochrome P450 homology <P45>
F;462/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: cultivar Columbia; C; Genetics:
                                                                                                                                                                                                                              R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fuj. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Teuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                               probable cytochrome P450 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: B84733
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
B84733
                                                                                                     A; Molecule type: I
a Residues: 1-489
                                                                                                                                                                  A; Reference number: A84420; A; Accession: B84733
A; Map position:
C; Superfamily:
                                       A; Gene: At2g32440
                                                                                   A; Cross-references:
                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                      A; Title: Sequence and analysis of chromosome 2 A; Reference number: A84420; MUID: 20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                               Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYRGMKARNLIHARIEQNIRAKICGLRASEAGQGCKDALQLLIEHSWE-----RGERL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GILGKWSMLVLVGDMHRDMRSISLNFLSHARLR---TILLKDVERHTLFVLDSWQQ--NS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TILGSGCLSNLHDSSHKQRKKVIMRAFSREALECYVPVITEEVGSS-----LEQWLSCGER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPLLLLPSL----LSLLLFLILLK------RRNRKTRFNLPPGKSGWPFLGETIGYLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHL
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Synechocystis
                                                                                                       BNA STO>
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                                                                                   GB:AE002093;
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  cytochrome
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                                                                                   NID:g3831452;
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Pred. No. 5e-26;
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    P450
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    slr0574;
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                                                                                        PIDN: AAC69934.1;
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                                                                                                                                                                                                                 the plant Arabidopsis
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  cytochrome
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                                                                                     GSPDB:GN00139
      P450
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    homotogy
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                                                                                                                                                                                                                 thaliana
                                                                                                                                                                                                                                                                                 Fujii, C.Y
L.; Tallon,
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Venter

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RESULT 9
$55379
cytochrome P450 CYP90 - Arabidopsis thaliana
N;Contains: oxidoreductase (EC 1.-.-)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change:
C;Accesion: $55379
C;Accession: $55379
R;Szekeres, M.; Nemeth, K.; Koncz, Z.; Nagy, F.; Koncz, C.
submitted to the EMBL Data Library, May 1995
A;Reference number: $55379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
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                                                                                                                                                                             A;Gene: CYP90
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
C;Reywords: cytochrome P450 homology <P45>
F;275-440/Domain: cytochrome P450 homology <P45>
F;418/Binding site: heme iron (Cys) (axial ligand) #status predicted
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C;Genetics:
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A; Residues: 1-472 <SZE>
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                                                                              Query Match
Best Local S
Matches 129
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYRGMKARNLIHARIEQNIRAKICGLRASEAGQGCKDALQLLIEHSWERGERLDMQALKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGLLVYPEVKRLMFRIAMRILLGCEPQLAGDGDSEQQLVEAFEEMTRNLFSLPIDVPFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASVRTILGSGCLSNLHDSSHKQRKKVIMRAFS-REALECYVPVITEEVGSSLEQWLSCGE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRAFKTSDPESFIQSYITRYGRTGIYKAHMFGYPCVLVTTPETCRRVLTDDDAF-HIGWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V-----LQRRKFLQMKRRKYG--FIYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGLPALLASALCTFVLPLLLFLAAIKLWDLYCVSGRDRSCALPLPPGTMGFPFFGETLQM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTMKTSPTVYPVDNLPARFT 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFNPDRFSAPHPEDASRFSFIPFGGGLRSCVGKEFAKILLKIFTVELARHCDWQLLN-GP 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVAEIFTNKE 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YHRALKARKKLVAAF-QSIVTNRRNQRKQNISSNRKDMLDNLIDVKDENGRVLDDEEIID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MWFPLII----LGLFYLKWY--LKRVNVWIYVSKLGEKKHY---LPPGDLGWPVIGNMWSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVM-FLPHNRPKDNCLARIT 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MVYLSQVIDETLRVITFSLTAFREAKSDVQMDGYIIPKGWKVLTWFRNVHLDPEIYPDPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KSTMKLIGRKSFVGISFEEHKRLRRLTSAPVNGPEALSVYIQFIEETVNTDLEKWSKMGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KFDPSRWEGYTPKAG---TFLPFGLGSHLCPGNDLAKLEISIFLHHFLLKYRVERSNPGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSTELLFGGHETTASAATSLITYLGLYPHVLQKVREELKSKGLLCKSNQDNKLDMEILEQ
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                           LLFLAAIKLWDLYCVSGRDRSCALPLPPGTMGFPFFGETLQMV-----LQRRKFLQMKRR 73
  LLLLSSIAAGFLLLLR-RTRYRRMGLPPGSLGLPLIGETFQLIGAYKTENPEPFIDERVA
                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.6%; Score 434; DB 2; 28.0%; Pred. No. 1.1e-25;
                                                                                                   16.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 08
                                                                                90;
                                                                              Score 433.5; DB 1
Pred. No. 1.2e-25;
0; Mismatches 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 248;
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                                                                                                                        DB 1;
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A; Molecule type: DNA
A; Residues: 1-457 <5T0>
A; Cross-references: GB:NC
C; GenetLcs:
A; Gene: A74936380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A;Reference number: A85001; MUID:20083488
A;Accession: D85429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 16-Feb-2001 #sequence_revision 16-Fe
C;Accession: D85429
R;anonymous, The European Union Arabidopsis
Nature 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytochrome P450 like protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_chang
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C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 C;Superfamily: Synechocystis cytochrome P450 C;Keywords: heme; iron; metalloprotein
E;396/Binding site: heme iron (Cys) (axial ligand) #status predicted
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Best Local
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                                       115 RITRDIEASVVLTLASWAQLPLVHVQDEIKKMTFEILVKVLMSTSP-----GEDMNILKL
                                                                          155 VITEEVGSSLEQWLSCGERGLLVY--PEVKRLMFRIAMRILLGCEPQLAGDGDSEQQLVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVVVMKRREEEEEGAERKKDMLAALLAADDGFSDEEIVDF-----LVALLVAGYETTST
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   AFEEMTRNLFSLPIDVPFSGLYRGMKARNLIHARIEQNIRAKICGLRASEAGQGCKDALQ
                                                                                                               VVLQNHGNTFVPAYPKSITELLGENSILSI-NGPHQKRLHTLIGAFLRS-----PHLKD
                                                                                                                                                  RILLGDDRLVSVHWPASVRTILGSGCLSNLHDSSHKQRKKVIMRAFSREALECYVP----
                                                                                                                                                                                       IPNGSLGWPVIGETLNFIACGYSSRPVTFMDKRKSLYGKVFKTNIIGTPIIISTDAEVNK
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                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                 15.5%;
26.7%;
                                                                                                                                                                                                                                                                   87;
                                                                                                                                                                                                                                                                                 Score 406; DB 2;
Pred. No. 1.5e-23;
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A,Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987
A;Accession: D70649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
D70649
Cytochrome P450 Rv3059 - Mycobacterium tuberculosis (strain H37RV)
N;Contains: oxidoreductase (EC 1....)
C;Species: Mycobacterium tuberculosis
C;Date: 10-Sep-1999 *sequence_revision 10-Sep-1999 *text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: Mycobacterium cytochrome P450 Rv3059; cytochrome P450 homology C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase F;300-461,Domain: cytochrome P450 homology <P459
F;439/Binding site: heme iron (Cys) (axial ligand) #status predicted
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A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-492 <COL>
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R; Cole, S.T.; Broscl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: nucleic acid sequence not shown; translation not shown
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Best Local Similarity
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311 SLITYLGLYPHVLQKVREELKSKGLLCKSNQDNKLDMEILEQLKYIGCVIKETLRLNPPV
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                                                                                                                                                                                                                                                                                MRAFSREALECYVPVITEEVGSSL-EQWLSCGERGLLVYPEVKRLMFRIAMRILLGCEPQ
                                                                                                                                                                                                                                                                                                                                 DSAVLPGVAALGPDAAQVIYSNRNKDYSQQGWVPVIGPFFHRG-LMLLDFEEHMFHRRIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRSCALPLPPGT-----MGFPFFGETLQMVLQRRKFLQMKRRKYGFIYKTH---LFG
                                                                                                                                                                                                                                                                                                                                                                                                                              EKKLAEP-PPGSGLKPVVGDAGLPILGHMIEMLRGGPDYLM-----FLYKTKGPVVFG
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                                                                                                                                                                                       LAGDGDSEQQLVEAFEEMTRN-----LFSLPIDVPFSGLYRGMKARNLIH-----ARIEQN
                                                                                                                                                                                                                                   QEAFVRSRLAGYLEQMDRVVSRVVADDWV-VNDARFLVYPAMKALTLDIASMVFMGHEP-
                                                                                                                                                                                                                                                                                                                                                                             ----RPTYRVMGADNVRRILLGDDRLVSVH-WPASVRTILGSGCLSNLHDSSHKQRKKVI 140
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                                                                                                                                           -GTDHELVTKVNKAFTITTRAGNAVIRTSVP---PFT-WWRGLRARELLENYFTARVKE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----NMEMKRRKLELGEEYKWTDYMSLSFTQNVINETLRMANIINGVWRKALKDVEIK
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                                                 ---NDLLTVLCQTEDDDGNRFSDADIVNHMIFLMMAAHDTSTSTAT
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Pred. No. 4.7e-23;
81; Mismatches 192;
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                   Qy
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Plant Cell 7, 1307-1317, 1995

A;Title: The maize dwarf3 gene encodes a cytochrome
A;Reference number: Z14648; MUID:96004534
A;Accession: T02263
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-519 <WINN
A;Residues: 1-519 <WINN
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C;Species: Zea mays (maize)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
C;Accession: T02263
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Best Local Sin
Matches 126;
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394 VIYSICDTHDVAEIFTNKEEFNPDRFSAPHPEDASRFSFIPFGGGLRSCVGKEFAKILLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                               \tt TELNYGMRAMAINLP-GFAYRGALRARRRLVA-VLQGVLDERRAARAKGVSGGGVDMMDR
                                                                                                                                                                                                                                                                                                      EEMTRNLFSLPIDVPFSGLYRG-MKARNLIHARIEQNIRAKICGLRASEAGQGCKDALQL
                                                                                                                                                                                                                                                                                                                                                       IDRTVTSSLRAWADHG--GSVEFLTELRRMTFKIIVQIFLG----GADQATTRALERSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CKQVLMDDDAFVT-GWPKATVALVGPRSFVAMPYDEHRRIRKLTAAPINGFDALTGYLPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRRILLGDDRLYSVHWPASVRTILGSGCLSNLHDSSHKQRKKVIMRAFSR-EALECYVPV
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                                                                                                                                                               LIEAQDERGRHLDDDEIIDVLVMYLNAGHESSGHITMWATVFLQENPDMFARAKAEQEAI 361
                                                                                                                                                                                                             LIEHSWERGERLDMQALKQSSTELLFGGHETTASAATSLITYLGLYPHVLQKVREELKSK
                                                                                                                                                                                                                                                                                                                                                                                                   ITEEVGSSLEQWLSCGERGLLVY-PEVKRLMFRIAMRILLGCEPQLAGDGDSEQQLVEAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 388; DB 1;
Pred. No. 4.3e-22;
6; Mismatches 216
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A;Cross-references: GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CAA18007.1; A;Experimental source: strain H37Rv C;Genetics: C;Genetics: A;Gene: Rv3685c C;Superfamily: Bacillus cytochrome P450 CYP106; cytochrome P450 homology C;Superfamily: Bacillus cytochrome P450 CYP106; cytochrome P450 homology C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase F;298-444/Domain: cytochrome P450 homology <P45> F;422/Binding site: heme iron (Cys) (axial ligand) #status predicted
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: F70791
C;Accession: F7
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: F70791
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probable steroid 22-alpha-hydroxylase T9L24.44 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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                                                                                                                                           H96759
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Best Local Similarity
Matches 102; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IFT-----VELARHCDWQLLNGPPTMKTSPTVYPVDNLPARFT 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VYPEVKRLMFRIAMRILLGCEPQLAGDGDSEQQLVEAFEEMTRNLFSLPIDVPFS----G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYRGMKARNLIHARIEQNIRAKICGLRASEAGQGCKDALQLLIEHSWERGERLDMQALKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRR-----ILLGDDRLVSVHWPASV 116
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                                                                                                                                                                                                                                                                                                                                                                                          EFNPDRFSAPHPEDASRFSFIPFGGGLRSCVGKEFAKILLKIFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAFTTAVINETLRVRPPAPLTARVAAQPLTIGGYRVEAGTRIVVHIIAINRSAEVYEHPH
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                                                                                                                                                                                                                                                                                                                  EFRPERFLGTRPQ---TYAWVPFGGGVKRCLGANFS--MRELITV
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Pred. No. 2.5e-
76; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178;
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R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Wh Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay, C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Wonder, J.C.; Davis, R.W.
A; Tritle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-512 <STO>
A; Cross-references: GB:
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A; Map position:
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Best Local Similarity
451
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GTRFCPGAELARLQIALF
                                       GLRSCYGKEFAKILLKIF 455
                                                                                    SYQDYVIPKGCFVVPFLSAVHLDESYYKESLSFNPWRWLDPETQQKRNWRTSPFYCPFGG
                                                                                                                              ELNGYQIPKGWNVIYSICDTHDVAEIFTNKEEFNPDRFSAPHPEDASRFS----FIPFGG
                                                                                                                                                                         EHDRLAGGML--TWQDYK-----TMDFTQCVIDETLRL----GGIAIWLMREAKEDV 390
                                                                                                                                                                                                   -VLGRLLEE-----ESLPNESMADFIINLLFAGNETTSKTMLFAVYFLTHCPKAMTQLLE
                                                                                                                                                                                                                                                                                                        DALQLLIEHSWERGERLDMQALKQSSTELLFGGHETTASAATSLITYLGLYPHVLQKVRE
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                                                                                                                                                                                                                                                                                                                                                                                             LVEAFEEMTRNLFSLPIDVPFSGLYRGMKARNLIHARIEQNIRAKICGLRASE-AGQGCK 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - VPVITEEVGSSLEQWLSCGERGLLVYPEVKRLMFRIAMRILLGCEPQLAG-DGDSE-QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FNRFIMQNEGKLFQSSYPKSFRDLVGKDGVITVHGDQQRRLHSIASSMMRHDQLKTHFLE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVRRILLGDDRLVSVHWPASVRTILGSGCLSNLHDSSHKQRKKVIMRAFSREALECY--- 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSHPSSFVEKQIKKFVSLLCSVLLLILKRPDNSGFNEIRYGRIFSCSLFGKWAVVSADPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSVSSSTTFLAFIIFLLA-----GIARRKRRAPHRLPPGSRGWPLIGDTFAWLNAVA
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468
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Maiti, R.;
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cytochrome P450 4D2 - fruit fly (Drosophila melanogaster)
N;Contains: oxidoreductase (EC 1.-.-)
C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: S41192; S34291
R;Frolov, M.V.; Alatortsev, V.E.
submitted to the EMBL Data Library, December 1993
A;Description: A cluster of cytochrome P450 genes in the X-chromosome of Dro

in the X-chromosome of Drosophila

RESULT S41192

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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 'A',31-496 <FRW>
A; Residues: 'A',31-496 <FRW>
A; Cross-references: EMBL: Z23005; NID: g312903; PIDN: CAA80549.1; PID: g312904
A; Experimental source: strain Oregon R
C; Genetics:
A; Gene: Cyp4d2
A; Cross-references: FlyBase: FBgn0011576
A; Map position: X
A; Androns: 53/1; 182/1; 205/2; 392/1
A; Introns: 53/1; 182/1; 205/2; 392/1
C; Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; oxidoreductase
F; 308-471/Domain: cytochrome P450 homology <P45>
F; 449/Binding site: heme iron (Cys) (axial ligand) #status predicted
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A; Accession: S41192
A; Molecule type: DNA
A; Residues: 1-496 <FRO>
A; Cross-references: EMBL:X75955; NID:g439650; PIDN:CAA53568.1; PID:g439651
A; Experimental source: strain Oregon R
R; Frolov, M.V.; Alatortsev, V.E.
submitted to the EMBL Data Library, June 1993
A; Description: Cluster of cytochrome P-450 genes on the X-chromosome in Drosophila melan
A; Reference number: S34291
A; Accession: S34291
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Search completed: November
Job time: 598 sec
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                                                                                                                                                                                                                                                                                                         407 IFTNKEEFNPDRFSAPHPEDASRFSFIPFGGGLRSCVGKEFAKILLKIFTVELARHCDWQ 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 ILLGCE-----PQLAGDGDSEQQLVEAFEEMTRN---LFSL--PIDVPFSGLYRGM 237
                                                                                                                                                  472 LLPLGPEPRHSMNIVCGRPTAF 493
                                                                                                                                                                                                              467 LLNGPPTMKTS-----PTVY 481
                                                                                                                                                                                                                                                                   415 YFESPDEFRPERFDADVPQ-IHPYAYIPFSAGPRNCIGQKFAMLEMKSTVSKLLRH--FE
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Petkovich M., van der Burg B., van der Burg B., van der Gells."; Cell Growth Differ. 9:629-637(1998) ISSUE SPECIFICITY. MEDLINE-99045433; PubMed-9826557; MEDLINE-99045433; PubMed-9826557; MEDLINE-99045433; PubMed-9826557; MEDLINE-99045433; PubMed-9826557; MEDLINE-99045433; PubMed-9826557; MEDLINE-99045433; PubMed-9826557; MEDLINE-SPORT ON ME., Juchau M.R. "Expression of cytochrome P450RAI (cephalic tissues."; Biochem. Biophys. Res. Commun. 252: -!- FUNCTION: PLAYS A KEY ROLE IN R. RETINOIDS, INCLUDING ALL-TRANSE-STEREOISOMER 9-CIS-RA. CAPABLE FOR FORMS OF RA, INCLUDING 4-OH-RA, -!- SUBCELLULAR LOCATION: MEMBRANE!- TISSUE SPECIFICITY: HIGHEST LEV PITUITARY GLAND, ADREMAL GLAND, -!- INDUCTION: BY RETINOIC ACIDS (R TISSUE SPECIFICITY: BELONGS TO THE CYTO	3C-199 3C-199 3C-199 3C-199 3C-199 3HROME SA1 OR SA	303 302.5 301 301 300 300 300 300 297.5 294.5 294.5 294.5 294.5 294.5 294.5
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    SEQUENCE FROM N.A.
STRAIN=C3H;
MEDLINE=97392446; |
Fujii H., Sato T.,
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055127;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CYTOCHROME P450 26 (EC 1.14.-.-) (RETINOIC ACID-METABOLIZING CYTOCHROME) (P450RA1) (RETINOIC ACID 4-HYDROXYLASE).

CYP26A1 OR CYP26 OR P450RA.
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Pfam; pF00067; p450; 1.
PRINTS; PRO0365; P450; 1.
PROSITE; PS00086; CYTOCCHROME_P450; 1.
Oxidoreductase; Monooxygenase; Membrane; Heme; Endoplasmic reticulum.
BINDING 42 42 HEME (POTENTIAL).
BEQUENCE 497 AA; 56162 MW; EAB6B84B24B2EAB3
                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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"Mouse p450RAI (CYP26) expression and retinoic acid-inducible retining acid metabolism in F9 cells are regulated by retinoic acid receptor retining and retinoid x receptor alpha.";

L J. Biol. Chem. 273:2409-2415(1998).

-! FUNCTION: PLAKS A KEY ROLE IN RETINOIC ACID METABOLISM. ACTS OF RETINOIDS, INCLUDING ALL-TRANS-RETINOIC ACID (RA) AND ITS STEREOISOMER 9-CIS-PA. CAPABLE OF BOTH 4-HYDROXYLATION AND 18-CHYDROXYLATION, RESPONSIBLE FOR GENERATION OF SEVERAL HYDROXYLATION: MEMBRANG-BOUND. ENDOPLASMIC RETICULUM.

C -!- SUBCELLULAR LOCATION: MEMBRANG-BOUND. ENDOPLASMIC RETICULUM.

C -!- SUBCELLULAR LOCATION ACIDS (RA).

-! SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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Interpro; IPR001128; -.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; 1.
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Endoplasmic reticulum.
BINDING 42 42 HEME (POTENTIAL).
SEQUENCE 497 AA; 56177 MW; 33B07D7C29134471 CRC64;
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"Metabolic inactivation of retinoic aci
differentially expressed in developing
EMBO J. 16:4163-4173(1997).
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X MEDIANE-97094702; Pubmed-8939936;

X MEDIANE-97094702; Pubmed-8939936;

X MADIANE-97094702; Pubmed-8939936;

X MADIANE-97094702; Pubmed-8939936;

X MADIANE-97094702; Pubmed-8939936;

X Hsu K.E., Dilworth F.J., Jones G., Petkovich M.;

Y Tacid 4-hydroxylase.";

Y Tacid 4-hydroxylase.";

Y J. Biol. Chem. 271:29922-29927(1996).

Y J. Biol. Chem. 271:29922-29927(1996).

Y FUNCTION: PLAYS A KEY ROLE IN RETINOIC ACID METABOLISM. ACTS ON RETINOIDS, INCLUDING ALL-TRANS-RETINOIC ACID (RA) AND ITS

Y J. BIOL. CHEM. 271:29927-29927(1996).

Y J. BIOL. CH
                                                                                                                                                                                        Query Match
Best Local S
Matches 338
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P79739;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYTOCHROME P450 26 (EC 1.14...) (RETINOIC ACID-METABOLIZING CYTOCHROME) (P450RAI) (RETINOIC ACID 4-HYDROXYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Verte
Actinopterygil; Neopterygil; Teleostel; Eutel
Cypriniformes; Cyprinidae; Rasborinae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                       BINDING
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PROSITE; PS00086; CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                           Endoplasmic reticulum
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Pred. No. 3.2e-11
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FD471435B2F30509 C
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                                                                                                                                                                                                                                        Length 492;
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C33051;
C23051;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYTOCHROME P450 88A3 (EC 1.14.--).
CYP88A3 OR YUPBH12.23.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstatic the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Theologis A., Osborne B.I., Vysotskaia V.S., Federspiel Toriumi M., Yu G., Oji O., Araujo R., Chung E., Dewar K. Ecker J.R., Marziali A., Oefner P., Davis R.W.; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
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                                                          Oxidoreductase; Monooxygenase; Transmembrane; TRANSMEM 6 26 POTENTIAL.
                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; 1200067; p450; 1. Pfam; PF00067; p450; 1. pfam; PF000385; p450.
                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                            Bishop G.J., Harrison K., Jones J.J.G.D.;
"The tomato Dwarf gene isolated by heterologous transposon
encodes the first member of a new cytochrome P450 family.";
Plant Cell 8:959-969(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYTOCHROME P450 85 (EC 1.14.-.-) (DWARF PROTE
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=CV. GCR758;
MEDLINE=96266705; PubMed=8672892;
                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum (Tomato).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
Solanales; Solanaceae; Solanum.
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Q43147;
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                                                                 EMBL; U54770;
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CYTOCHROME_P450;
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 use by modified entities
                                                                                                                            controlling cell elongation and de-etiolation in Arabi Cell 85:171-182(1996).
-i- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                           MEDLINE-96200769; PubMed-8612270;
Szekeres M., Nemeth K., Koncz-Kalman Z., Mathur J., Kauschmann
Altmann T., Redei G.P., Nagy F., Schell J., Koncz C.;
"Brassinosteroids rescue the deficiency of CYP90, a cytochrome
controlling cell elongation and de-etiolation in Arabidopsis.";
                                                                                                                                                                                                                                                                                                                    Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                   C901_ARATH STANDARD; PRT; 4
Q42569;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
CYTOCHROME P450 90A1 (EC 1.14.---).
CYP90A1 OR CYP90 OR CPD.
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BINDING 414 414 HEME (BY SIMILARITY).
SEQUENCE 464 AA; 53706 MW; D2B2lAAAB7B14E94 CRC64;
                                                    the European Bioinformatics Institute.
                                                                                                                                                                                                                                                             STRAIN-CV.
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                     SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMMAVKYLHDHPKVLEELRKE--HMAIREKKKPEDPIDYNDYRSMRFTRAVILETSRLAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWPASVRTILGSGCLSNLHDSSHKQRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
non-profit institutions as long and this statement is not removed. requires a license agreement (See
                                                                                                                                                                                                                                                           COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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27.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 444; DB 1;
Pred. No. 1.7e-23
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                                   There are no restrictions on ong as its content is in no
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RESULT 7
C136_MYCUD
ID C136_M
P95099
AC P95099
AC P9730-MAY
DT 30-MAY
DT 01-OCT
DE CYP136
GN CYP136
GN CYP136
OS MYCODA
OC ACTINO
OC ACTINO
OC ACTINO
CO NCBI.T
RN (1)
RP SEQUEN
RC STRAIN
RA COLE S
RA GORGON
RA Badcoc
                                                                                                                                                              D C136_MYCTU STANDARL,

D C136_MYCTU STANDARL,

C P95099;

77 30-MAY-2000 (Rel. 39, Created)

77 30-MAY-2000 (Rel. 39, Last sequence update)

77 30-MAY-2000 (Rel. 40, Last annotation update)

78 01-OCT-2000 (Rel. 40, Last annotation update)

79 PUTATIVE CYTOCHROME P450 136 (EC 1.14.-.-).

70 GN CYP136 OR RY3059 OR MTCY2D7.22C.

70 Mycobacterium tuberculosis.

70 Mycobacteria; Firmicutes; Actinobacteria; Actinobacteridae;

71 Antinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacteriacea
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BINDING 418 418 HEME (I
SEQUENCE 472 AA; 53785 MW; 41A7
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EMBL; X87368; CAA60794.1;
InterPro; IPR001128;
  MEDLINE-98295987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.
                                                                                                                                          SEQUENCE FROM N.A.
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TE; PS00086; CYTOCHROME_P450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               493
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Pred. No. 9.
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Mismatches 228;
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Interro; IPR002403; -.

R Interpro; IPR002403; -.

R Interpro; IPR002403; -.

R Pfam; PF00067; p450; 1.

DR PRINTS; PR00359; BP450.

DR PRINTS; PR00463; EP450I.

DR PRINTS; PR00465; EP450I.

DR PRINTS; PR00465; EP450I.

DR PRINTS; PR00465; CATOCHROME_P450; 1.

PROSITE; PS00086; CTTOCHROME_P450; 1.

PROSITE; PS00086; DATABASE; Heme.

PROSITE; PS00086; DATABASE; PS00086; DATABASE; Heme.

PROSITE; PS00086; DATABASE; PS000
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Best Local S
Matches 137
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-i- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                314
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                                                                                                                                                                                                                                                                                                                                                                                            265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211
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482
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                                                                                                                                                                                                                                                                                                                                                                                                                               IRAKICGLRASEAGOGCKDALQLLIEHSWERGERLDMQALKQSSTELLFGGHETTASAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAGDGDSEQQLVEAFEEMTRN-----LFSLPIDVPFSGLYRGMKARNLIH----ARIEQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----RPTVRVMGADNVRRILLGDDRLVSVH-WPASVRTILGSGCLSNLHDSSHKQRKKVI 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKKLAEP-PPGSGLKPVVGDAGLPILGHMIEMLRGGPDYLM-----FLYKTKGPVVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DRSCALPLPPGT-----MGFPFFGETLQMVLQRRKFLQMKRRKYGFIYKTH---LFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity
137; Conserv
                                                                                                                                                                                                               PGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVAEIFTNKEEFNPDRFSAPHPE-DASR
                                                                                                                                                                                                                                                                                TMAYQLAAHPEWQQRCRDESDRHG------DGPLDIESLEQLESLDLVMNESIRLVTPV
                                                                                                                                                                                                                                                                                                                                    SLITYLGLYPHVLQKVREELKSKGLLCKSNQDNKLDMEILEQLKYIGCVIKETLRLNPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GTDHELVTKVNKAFTITTRAGNAVIRTSVP---PFT-WWRGLRARELLENYFTARVKE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QEAFVRSRLAGYLEQMDRVVSRVVADDWV-VNDARFLVYPAMKALTLDIASMVFMGHEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSAVLPGVAALGPDAAQVIYSNRNKDYSQQGWVPVIGPFFHRG-LMLLDFEEHMFHRRIM
                                                    YAFTPFGGGVHKCIGMVFDQLEIKTILHRLLRRYRLELSRP-DYQ----
                                                                                                            FSFIPFGGGLRSCVGKEFAKI------LLKIFTVELARHCDWQLLNGPPTMKTSPTVY
                                                                                                                                                                 QWAMRQTVRDTELLGYYLPKGTNVIAYPGMNHRLPEIWTDPLTFDPERFTEPRNEHKRHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 400; DB 1;
Pred. No. 1.9e-20;
1; Mismatches 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 492;
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PMDGMP

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Best Local Similarity
Matches 126; Conser
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYTOCHROME P450 88A1 (EC 1.14.-.-) (DWARF3 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001128; --
Pfam; PF00067; p450; 1.
PROSITE; PS00086; CYTOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Winkler R.G., Helentjaris T.; "The maize Dwarf3 gene encodes a cytochrome P450-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays (Maize).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae;
Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductase; Monooxygenase; Transmembrane; Heme TRANSMEM 1 21 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U32579; AAC49067.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATHWAY: EARLY STED IN GIBBERELLIN BIOSYNTHESIS.
TISSUE SPECIFICITY: EXPRESSED IN ROOTS, DEVELOPING LEAVES,
VEGETATIVE MERISTEM, AND SUSPENSION CULTURE CELLS.
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
GLLCKSNQDNKLDMEILEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWN
                                                                                                                                                                                                                                                                                                                                               LPPGTMGFPFFGETLQMVLQRRK-----FLQMKRRKYG--FIYKTHLFGRPTVRVMGADN 96
                                                                                                                                                                                                                                          CKQVLMDDDAFVT-GWPKATVALVGPRSFVAMPYDEHRRIRKLTAAPINGFDALTGYLPF
                                                                                                                                                                                                                                                                                                              LPPGEMGWPLVGGMWAFLRAFKSGKPDAFIASFVRRFGRTGVYRSFMFSSPTVLVTTAEG
                                                                                                      TELNYGMRAMAINLP-GFAYRGALRARRRLVA-VLQGVLDERRAARAKGVSGGGVDMMDR
                                                                                                                                                                                                                                                                          VRRILLGDDRLVSVHWPASVRTILGSGCLSNLHDSSHKQRKKVIMRAFSR-EALECYVPV 155
                                  LIEAQDERGRHLDDDEIIDVLVMYLNAGHESSGHITMWATVFLQENPDMFARAKAEQEAI
                                                                  LIEHSWERGERLDMQALKQSSTELLFGGHETTASAATSLITYLGLYPHVLQKVREELKSK
                                                                                                                                       EEMTRNLFSLPIDVPFSGLYRG-MKARNLIHARIEQNIRAKICGLRASEAGQGCKDALQL
                                                                                                                                                                         IDRTVTSSLRAWADHG--GSVEFLTELRRMTFKIIVQIFLG----GADQATTRALERSY
                                                                                                                                                                                                         ITEEVGSSLEQWLSCGERGLLVY-PEVKRLMFRIAMRILLGCEPQLAGDGDSEQQLVEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      466
519 AA;
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      466 1
57906 MW;
                                                                                                                                                                                                                                                                                                                                                                                                 14.9%; Score 388; DB 1; 27.2%; Pred. No. 1.4e-19;
                                                                                                                                                                                                                                                                                                                                                                                   66;
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; 0F8977A024316D95 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 519
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 519;
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                                                                                                                                                                                                                                                                                                                                                                                   36;
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RESULT 9
cl37_MYCTU
ID Cl37_MYCTU
AC 068653;
DT 30-MAY-2000 (
DT 30-MAY-2000 (
DT 01-OCT-2000 (
DT 01-OCT-20
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                                                                                                                                 Query Match
Best Local S
Matches 102
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A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

A Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Hornsby T., Josels K., Krogh A., McLean J., Moule S., Murphy L.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Hornsby T., Josels K., Krogh A., McLean J., Moule S., Murphy L.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Narphy L.,

A Taylor K., Whitchead S., Skelton S., Squares S., Sqares R., Sulston J.E.,

The Topic F., Whitchead S., Barrell B.G.;

The Complete genome sequence.";

Nature 393:537-544(1998).

Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001128; -.
InterPro; IPR002397; -.
InterPro; IPR002397; -.
InterPro; IPR002401; -.
Pfam; PF00067; p450; 1.
PRINTS; PR00359; BP450.
PRINTS; PR00385; P450.
PRINTS; PR00385; E9450I.
PROSITE; PS00086; CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Oxidoreductase; Monooxygenase; BINDING 422 422 HEME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
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30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PUTATIVE CYTOCHROME P450 137 (EC 1.14.-.-).
CYP137 OR RY3685C OR MTY025.033C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TubercuList; Rv3685c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL022121; CAA18007.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinomycetales; Corynebacterineae; NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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8
                                                                65
                                                                                                                                                                     Local Similarity
                                                             RKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRR-----ILLGDDRLVSVHWPASV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IFT-----VELARHCDWQLLNGPPTMKTSPTVYPVDNLPARFT 491
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RRMLRLIRR-YGPIMTMPILSLGDVAIVSDSALAKEVFTAPTDVLLGGEGV----GPAA- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VFLHHFLLGYKLAR-----TNPRCRVRYLPHPRPVDNCLAKIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MRSIPSSQ-RGLTLRDFRKMEYLSQVIDETLRLVNISFVSFRQATRDVFVNGYLIPKGWK
                                                                                                                                                                                                                                                                                                          476 AA;
                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                              52265 MW;
                                                                                                                                                                  13.0%;
                                                                                                                                 76;
                                                                                                                                 Score 338.5; DB 1;
Pred. No. 3.1e-16;
6; Mismatches 178;
                                                                                                                                                                                                                                                                                                              4FF0DBC89D8D0548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         476
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                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                      Length 476;
                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium.
                                                                                                                                 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           collaboration
- outstation
                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20196011; PubMed=10731137;

Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,

Benos P.V., Gatt M.K., Ashburner M., Murphy L., Demailles J., Cadieu F

Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu F

Barrell B.G., Ferraz C., Vidal S., Brun C., Galibert F., Borkova

Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,

Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,

Modolell J., Peter A., Schottler P., Werner M., Mourkioti F.,

Beinert N., Dowe G., Schafer U., Jackle H., Bucheton A.,

Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,

Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,

McMillan P.J., Salles C., Tait E.A., Valenti P., Saunder R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C4D2_DROME STANDARD; PRT; 501 AA. (27589; Q27588; O46053; O18651; O18674; O9W51. 15-DEC-1998 (Rel. 37, Created) 01-OCT-2000 (Rel. 40, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) CYTOCHROME P450 4D2 (EC 1.14.-.) (CYPIVD2). CYP4D2 OR EG:152A3.4 OR CG3466. Drosophila melanogaster (Fruit fly.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DROME
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J. Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle George R.A., Lewis S.E., Richards S., Ashburner M., Henderso Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X. Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "From sequence
melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-OREGON-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 melanogaster."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Frolov M.V., Alatortsev V.E.;
"Cluster of cytochrome P450 genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94296569; PubMed=8024706;
                                                                                                                                                                                                                       MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                      Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLITLVLAGHETTATTLAWAFDLLLHHPDALRRVRAEAVGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYRGMKARNLIHARIEQNIRAKICGLRASEAGQGCKDALQLLIEHSWERGERLDMQALKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VYPEVKRLMERIAMRILLGCEPQLAGDGDSEQQLVEAFEEMTRNLFSLPIDVPFS----G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTILGSGCLSNLHDSSHKQRKKVIMRAFSREALECYVPVITEEVGSSLEQWLSCGERGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVAEIFTNKE
: || || || || || || || || || : : || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALRVWPARARANTEIDDVVMALIAQRRADPRLGERHDVLSLLVSARGESGEQLSDSEIRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -AIYGSGSMFVQEEPEHLRRRKLLTPPLHGAALDRYVPIIENSTRAAMHTWPV--DRPFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFRPERFLGTRPQ - - - TYAWVPFGGGVKRCLGANFS - - MRELITV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFNPDRFSAPHPEDASRFSFIPFGGGLRSCVGKEFAKILLKIFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAFTTAVINETLRVRPPAPLTARVAAQPLTIGGYRVEAGTRIVVHIIAINRSAEVYEHPH
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                                                                                                                                                                                                                                                                                                                                                                                                                      287:2220-2222(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome: the tip of the X chromosome of D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPEEVRRLGRPFERLLNLGVSEQLTVRYALRRLG
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                                                                                      Henderson
              Pfeiffer B.D.,
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                                                                                               S.N.,
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EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL;

AF017008; AF0170109; AF017011; AF017011; AF017012; AF017013; AF017014; AF017015; AF017016; AF0170116;

EMBL; EMBL;

AAB71169.1;
AAB71170.1;
AAB71171.1;
AAB71172.1;
AAB71173.1;
AAB71174.1;
AAB71175.1;
AAB71176.1;
AAB71177.1;

EMBL;

AL009194;

AAF45741 CAA15698

EMBL;

AE003423; AF017006; AF017007;

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RA Durbin K.J. Downes M., Dunkov B.C., Fleischmann W., RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Ralcok N., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C., Ralali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kunlp D., Lai Z., Liang Y., Lin X., Rak Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Syiers E., Spradling A.C., Stapleton M., Strong R., Sun E., RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., RA Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wan K.H., Doyle C., Baxter E.(
Abril J.F., Agbayani A., An H.
                                EMBL;
                                                                                                  use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or, send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC
                                                                                                                                                                                                                                        European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
X75955; CAA53568.1;
Z23005; CAA80549.1;
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                                                                                                                                          (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                               as its content
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Best Local
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                                                  RABIT STANDARD; PRT; 5
P14579; PRT: 5
O1-JAN-1990 (Rel. 13, Created)
O1-JAN-1990 (Rel. 13, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
CYTOCHROME P450 4A5 PRECURSOR (EC 1.14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002402; ... Pfam; PF00067; p450; 1. PRINTS; PR00385; P450. PRINTS; PR00464; EP450II.
                Oryctolagus
                               CYP4A5
                                         OMEGA-HYDROXYLASE).
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Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0011576;
     Eukaryota;
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                                                                                                                                                                                     PLGPEP 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KORKKVIMRAFSREALECYVPVITEEVGSSLEQWLS--CGERGLLVYPEVKRLMFRIAMR
                                                                                                                                                                                                                                                                                                                MEILEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KYGFIYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWPASVRTILGSGCLSNLHDSSH
                                                                                                                                                                                                                                     YFESPDEFRPERFDADVPQ-IHPYAYIPFSAGPRNCIGQKFAMLEMKSTVSKLLRHFELL
                                                                                                                                                                                                                                                            IFTNKEEFNPDRFSAPHPEDASRFSFIPFGGGLRSCVGKEFAKILLKIFTVELARHCDWQ
                                                                                                                                                                                                                                                                                       LRDLGELKFMENVIKESLRLHPPVPMIGRWFAEDVEIRGKHIPAGTNFTMGIFVLLRDPE
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                                                                                                                                                                                                                                                                                                                                                                MOALKOSSTELLFGGHETTASAATSLITYLGLYPHVLOKVREELKSKGLLCKSNODNKLD
                                                                                                                                                                                                                                                                                                                                                                                           KAIKVMHDFTENIIRERRETLVNNSKETTPEEEVNFLGQKRRMALLDVLLQSTIDGAPLS
                                                                                                                                                                                                                                                                                                                                                                                                                  KARNLIHARIEQNIRAKICGL-------RASEAGQGCKDALQLLIEHSWERGERLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
     Metazoa;
cuniculus (Rappir
Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    501 AA;
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487
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163
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160
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24.7%;
                (Rabbit)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 331; DB 1;
Pred. No. 1.1e-15;
9; Mismatches 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN REF. 2).
I -> A (IN CAA80549).
A -> R (IN REF. 1).
LRSANGVHLGLKPRA -> CGRPTAFILA
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    Craniata;
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                                                      tion update)
1.14.15.3)
                                                                               update)
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    Vertebrata;
                                                                                                                     A
                                                      (CYPIVA5) (LAURIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 501;
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     Euteleostomi;
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                                                                                            Вр
                                                                                                                                                             Matches 137;
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Best Local
                                                                                                                                                                                                                                          CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00385; P450.

PRINTS; PR00464; EP450II.

PROSITE; PS00086; CYTOCHROME_P450; Oxidoreductase; Monooxygenase; Elec
                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A34260; A34260.
InterPro; IPR001128; -.
InterPro; IPR002402; -.
Pfam; PF00067; p450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBICTICS.

-!- CATALYTIC ACTIVITY: OCTANE + REDUCED RUBREDOXIN + O(2) = 1-OCTANOL + OXIDIZED RUBREDOXIN + H(2)O.

-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.

-!- INDUCTION: 9450 CAN BE INDUCED TO HIGH LEVELS IN LIVER AND OTHER -
-!- INDUCTION: 9450 CAN BE INDUCED TO HIGH LEVELS IN LIVER AND OTHER -
-!- TISSUES BY VARIOUS FOREIGN COMPOUNDS, INCLUDING DRUGS, PESTICIDES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "cDNA cloning and expression of the mRNA for cytochrome P-450kd which shows a fatty acid omega-hydroxylating activity."; eur. J. Biochem. 196:531-536(1991).

-!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN ANDEH-DEPENDENT ELECTRON TRANSPORT BATHWAY. IT OXIDIZES A VARIETY OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M28655; AAA31229.1; EMBL; X57209; CAA40493.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yokotani N., Kusunose E., Sogawa K., Kawashima H., Kusunose M., Fujii-Kuriyama Y.;
                                                                                                                                                                                                                                                                                          BINDING
                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
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Biochemistry 29:873-879(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johnson E.F., Walker D.L.,
Meurhoff A.S., Masters B.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90254128; PubMed=2340280; Johnson E.F., Walker D.L., Griffin
                                                                                                                                                                                                                                                                                                                            PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91192021; PubMed=2013275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
107
                                56
                                                                                              11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND CARCINOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
LVSVHWPASVRTILGSGCLSNLHDSSHKQRKKVIMRAFSREALECYVPVITEEVGSSLEQ
                                                                                                                            LPALLASALCTFVL--PLLLFLAAIKL-----WDLYCVSGRDRSCALPLPPGTMGFPFFG
                                --FHWLLGHSREFQMNQELQQILKWVEKFPRACPHWIGGNKVRVQLYDPDYMKVILGRSD
                                                                                            LPGSLSGLLQVAALLGLLLLLLKAAQLYLRRQWLLRALQ-----QFPCPP-----
                                                             ETLQMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVR---
                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                          Endoplasmic
                                                                                                                                                                                                                                                             458
435
477
                                                                                                                                                             Conservative
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458
435
477
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26.2%;
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HEME (BY SIMILARITY).
G -> S (IN REF. 2).
V -> L (IN REF. 2).
'; 11D174BFC8BFA268 CRC64;
                                                                                                                                                                           Score 325.5; DB
Pred. No. 2.6e-1
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                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                           transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clark J.E.,
                                                                                                                                                                                            DB 1;
                                                                                                                                                               Indels
                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                             Membrane;
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166
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CYTOCHROME P450 51 (EC 1.14.14.1) (CYPLI) (P450L1)
DEMETRYLASE) (LANOSTEROL 14-ALPHA DEMETRYLASE) (LDN
                        lanosterol 14-alpha demethylase.";

Gene 161:243-248(1995).

-i- FUNCTION: CATALYSES C14-DEMETHYLATION OF LANOSTE
LANOSTEROL INTO 4,4'-DIMETHYL CHOLESTA-8,14,24-T
-i- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN +
                                                                                                                                                                                                                                            MEDLINE=98158318; PubMed=9498553;
Noshiro M., Aoyama Y., Kawamoto T., Gotoh O.,
"Structural and evolutionary studies on sterol
                                                                                                                                                                                                                                                                                                                                  Aoyama Y., Funae Y., Noshiro M., Horiuchi T., Yoshida "Occurrence of a P450 showing high homology to yeast demethylase (P450(14DM)) in the rat liver."; Biochem. Biophys. Res. Commun. 201:1320-1326(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
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                                                                                                                 Swinney D
                                                                                                                               Sloane D.L., So
                                                                                                                                             MEDLINE=95394364; PubMed=7665087;
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functional expression
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                                           LANOSTEROL; IT TRANSFOF, 14, 24-TRIENE-3-BETA-OL.
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M) (P450-14DM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLLVYPEVKRLMFRIAMRILLGCEPQLAGDGDSEQQLVEAFEEMTRNL--
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                                                                                                                                                                                                    DNKLDMEILEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDT
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U17697; AAA87074.1;
  HCDWQLLNGP-PTMKTSPTVYPVDNLPARF
                                                    QRLKDSWVERLDFNPDRYLQDNPASGEKFAYVPFGAGRHRCIGENFAYVQIKTIWSTMLR
                                                                                                                                                       P-PLTYEQLKDLNLLDRCIKETLRLRPPIMTMMRMAKTPQTVAGYTIPPGHQVCVSPTVN
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AB004092; BAA20354.1;
AB004093; BAA20354.1;
                                                                                                   HDVAEIFTNKEEFNPDRFSAPHPEDASRFSFIPFGGGLRSCVGKEFAKILLKIFTVELAR
                                                                                                                                                                                                                                                      GRPLTDDEIAGMLIGLLLAGQHTSSTTSAWMGFFLARDKPLQDKCYLEQKT---VCGEDL
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0067; p450;
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Pred. No. 2.8e-15;
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Baybayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guann P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
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Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D., Cadieu E Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D., Cadieu E Benos P.V., Gatt M.K., Ashburner M., Murphy L., Demailles J., Cadieu E Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E Dreano S., Gloux S., Lelaure V., Mottler S., Galibert F., Borkova Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S., Papagjannakis G., Spanos L., Cox S., Madueno E., de pablos B., Modolell J., Peter A., Schottler P., Warner M., Mourkioti F., Beinert N., Dowe G., Schafer U., Jackle H., Bucheton A., Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S., McMillan P.J., Salles C., Tait E.A., Valenti P., Saunder R.D., Glover D.M.,
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p33269; O18664; O18644; O18653; Q9W515; Q9W516;
O1-FEB-1994 (Rel. 28, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
O1-OCT-2000 (Rel. 40, Last annotation update)
CYTOCHROME P450 4D1 (EC 1.14.--) (CYPUD1),
CYP4D1 OR CYT-P450-D1 OR EG:87B1.1 OR CG3656.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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STRAIN-OREGON-R; TISSUE-Embryo;
MEDLINE-9229716; PubMed=1605861;
Gandhi R., Varak E., Goldberg M.L.;
"Molecular analysis of a cytochrome P450 gene of family 4 on Drosophila X chromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (LONG STRAIN=BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phillips K.S., Begun D.J., Aquadro C.F.; Evidence for non-neutral evolution around the cytochrome cluster on the Drosophila melanogaster X chromosome."; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20196006; PubMed=10731132;
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STRAIN=VARIOUS STRAINS;
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RA Merkulov G., Milshina N.V., Mobarry C., McDeherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Ra Melson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Ra Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
CC I- FUNCTION: INVOLVED IN THE METABOLISM OF INSECT HORMONES AND IN THE
Science 287:2185-2195(2000).
CC I- SUBCELIJITAR TOZATTON. MENDALOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
-SHORT FORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
-!- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT DEVELOPMENT, WITH THE
HIGHEST LEVELS OCCURRING DURING LATE LARVAL STAGES, THEN FALLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jalali M., Kalush F., Karpen G.H., Ke Z., Kenni
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRASTICALLY DURING PUPARIATION.
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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Lin X.,
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EMBL; EMBL; X67645; CAA47887.1; Z98269; CAB10972.1;

EMBL; EMBL; EMBL; EMBL; PRINTS; PRO0385; P450.
PRINTS; PR00464; EP450II.
PROSITE; PS00086; CYTOCHI EMBL; EMBL; EMBL; EMBL; EMBL; Endoplasmic reticulum; Oxidoreductase; Monooxygenase; Membrane; Heme; Pfam; PF00067; InterPro; IPR001128; FlyBase; FBgn0005670; Cyp4d1. EMBL; S25707; S25707 AF016996; AF016997; AF016999; AF017000; AF017000; AF017001; AF017003; AF017003; AF017004; AF017004; AF016994; AF016995; AF016992; AF016993; AE003423; IPR002402; p450; AAB71155.1;
AAB71156.1;
AAB71157.1;
AAB71159.1;
AAB71160.1;
AAB71161.1;
AAB71162.1;
AAB71163.1;
AAB71164.1;
AAB71165.1;
AAB71165.1;
AAB71166.1;
AAB71166.1;
AAB71167.1;
AAF45736.1;
AAF45737.1; CYTOCHROME_P450; 1

Alternative splicing; Polymorphism.
HEME (BY SIMILARITY).
MELVIGAILASALFYGLLLYHLKFKRLIDLISYMPGPPVLP GRKWHKRRKIITPAFHFKILDQFVEVFEKGSRDLLRNMEQD RLKHGESGFSLYDWINLCTMDT -> MWLLLSLVLLLAIIA $LVGHGHHF\\ IGKPPHEMVKK\\ IFEFMETYSKDQVLKVWLGPEL\\ NVLMGNPKDVEVVLGTLRFNDKAGEYKALEPWLKEGLLVSR$

Microsome;

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                                                                         CP84_ARATH STANDARD; PRT; 520 AA. 042600; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) CYTOCHROME P450 48A1 (FERULATE-5-HYDROXYLASE) CYP84A1 OR FAHI OR AT4G36220 OR F23E13.110. Arabidopsis thaliana (Mouse-ear cress).
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                                              Eukaryota; Viridiplantae; Embryophyta; Trache Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                   427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALLASALCTFVLPLLLFLAAIKLWDLYCVSGRDRSCALPLPPGTMGFPFFGETLQMVLQR 64
                                                                                                                                                                                                                                                                      ASRFSFIPFGGGLRSCVGKEFAKILLKIFTVELARHCDWQLL---NGPPTM 474 : :::||| | | :||:|| : || : : || :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F -- \texttt{EKGSRDLLRNMEQDRLKHGESGFSLYDWINLCTMDTICETAMGVSINAQSNADSEYV}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVEVVLGTLRFNDKAGEYKALEPWLKEGLLVSRGRKWHK-RRKIITPAFHFKILDQFVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVRTILGS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AILASAL--FYGLLLYHLKFKRLIDL------ISYMPGPPVLPLVG------
                                                                                                                                                                                                                                                                                                                                                                                                                                    EGSSQESSNDDADVGAKRKMAFLDILLQSTVD--ERPLSNLDIREEVDTFMFEGHDTTSS
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                                                                                                                                                                                                                                                       LNPYAYIPFSAGPRNCIGQKFAMLEIKAIVANVLRHYEVDFVGDSSEPPVL
                                                                                                                                                                                                                                                                                                                PSVPLLGRKVLEDCEINGKLIPAGTNIGISPLYLGRREELFSEPNSFKPERFDVVTTAEK
                                                                                                                                                                                                                                                                                                                                           PPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVAEIFTNKEEFNPDRFS-APHPED
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316
468
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                                   Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----HGHHFIGKPPHEMVKKIFEFMETYSKDQVLKVWLGPELNVLMGNPK
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509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83;
                                 Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 324.5; DB 1
Pred. No. 3.1e-15;
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E -> PSWPMCSGTTRLTLWATSFGTTRADRRTYSAYQGPL
SSRCG (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y -> I (IN REF. 1).
E -> K (IN REF. 1).
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QEYSSLGRWINEGLIKSNGRKWHRRKIITPAFHFRILEPY
VEIFDRQSLRLVEELALRISRQOERINLGEAIHLCALDA
(IN SHORT ISOFORM)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 209;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IN STRAINS
                                                  Tracheophyta; S
dicots; Rosidae;
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                                                  Spermatophyta;
e; eurosids II;
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RA MOOIJMAN P., Klein Lanknorst K., Kose M., Lamberth S., Van den Daele H.,
RA Berneiser S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Clark L., Dogdett J., Warse A., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Granderth K., Dauner D., Herzl A.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Schnah J., Hasse D., Lemcke K., Mewes H.-W., Stocker S.,
RA Schnah M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Schnah J., Bertley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.;
Till S.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.;
Till S.,
RA Chen E., Scholler P., Couther S., Geisel C., Layman D.,
RA Chen E., Marra M., Martiensen R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volcka
Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terr
Harris B., Ansorge W., Brandt P., Grivell L., Rieger M.,
Weichselgartner M., de Simone V., Obermaier B., Mache R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Meyer K., Cusumano J.C., Somerville C.R., Chapple C.C.S., "Ferulate-5-hydroxylase from Arabidopsis thaliana defines family of cytochrome P450-dependent monooxygenases."; Proc. Natl. Acad. Sci. U.S.A. 93:6869-6874(1996).
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Langham S.-A., McCullagh B., Bilham L., Robben J.,
Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche
Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor
                                                                                                                                                                                                                                                                                                                MEDLINE-99097044; PubMed-9880351;
Ruegger M., Meyer K., Cusumano J.C., Chapple C.;
"The regulation of ferulate-5-hydroxylase expression the context of sinapate ester biosynthesis.";
Plant Physiol. 119:101-110(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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InterPro; IPR001128; ...

R pfam; pF00067; p450; 1.

R PRINTS; PR00385; P450, 1.

OR PROSITE; PS00086; CYTOCHROME_P450; 1.

OXIdocreductase; Monooxygenase; Membrane; Heme.

YNDING 458 458 HEME (BY SIMILARITY).

**TNDING **70 AA; 58720 MW; E812779AF5BF01BC CRC64;
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Matches 129
                                                                                  CP51_PIG STANDARD;
CP51_PIG STANDARD;
046420;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CYTOCHROME P450 51 (EC 1.14.14.1) (CYPL1) (P450L1)
CYTOCHROME P450 51 (EC 1.14.14.1) (CYPL1) (P450L1)
                           Sus scrofa (Pig).
Eukaryota; Metazoa; (Mammalia; Eutheria; (NCBI_TaxID=9823;
                                                                                                                                                                                                             PIG
   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVSLFIFISFI-----TRRRRPPYPPGPRGWPIIGNMLMMDQLTHRGLANLAKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL022141; CAA18128.1; -. AF068574; AAD11580.1; -. AL161589; CAB80293.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----HKQRKKVIMRAFSREALECYVPV-----ITEEVGSSLEQWLSCGERGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                           Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.3%;
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Pred. No. 4.7e-15
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                                                                                                 )L1) (STEROL 14-ALPHA (LDM) (P450-14DM).
                                           Euteleostomi;
Sus.
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Best Local S
Matches 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KOjima M., Morozumi T., Hamasima N., Okamoto T.;

"Cloning of a pig lanosterol 14-demethylase CNA.";

Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: CATALYSES C14-DEMETHYLATION OF LANOSTEROL; IT TRANSFOLLANOSTEROL INTO 4,4'-DIMETHYL CHOLESTA-8,14,24-TRIENE-3-BETA-OL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001128;
InterPro; IPR002403;
Pfam; PF00067; p450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00465; EP450IV.
PROSITE; PS00086; CYTOCHROME_P450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OXIDIZED FLAVOPROTEIN + H(2)O.

-!- PATHWAY: CHOLESTEROL BIOSYNTHESIS.

-!- SUBCELLULAR LOCATION: MICROSOMAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase; Monooxygenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB009988; BAA24134.1; -.
 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: MICROSOMAL (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         +
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CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2)
                                QLLNGP-PTMKTSPTVYPVDNLPARF
DLIDGYFPTVNYTTMIHTPENPVIRY
                                                            DSWVERLDFNPDRYLQDNPASGEKFAYVPFGAGRHRCIGENFAYVQIKTIWSTMLRLYEF
                                                                             DMEILEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVA 405
                                                                                                                                                                                                                                                                             IDVPFSGLYRGMKARNLIHARIEQNIRAKICGLRASEAGQGCKDALQLLIEHSWERGERL
:| | | | | | : :::: | |
                                                                                                                           TYDQLKDLNLLDRCIKETLRLRPPIMTMMRMAKTPQTVAGYTIPPGHQVCVSPTVNQRLK 412
                                                                                                                                                                                           TDDEVAGMLIGLLLAGQHTSSTTSAWMGFFLARDKTLQEKCYLEQKT---VCGEDLP-PL
                                                                                                                                                                                                                                                              GWLPLPSFRR---
                                                                                                                                                                                                                                                                                                                          NL--FEALSELIILTASHCLHGKE-----IRSQLNEKVAQLYADLDGGFSHAAWLLP
                                                                                                                                                                                                                                                                                                                                                         GLLVYPEVKRLMFRIAMRILLGCEPQLAGDGDSEQQLVEAFEEMTRNL---FS-----LP
                                                                                                                                                                                                                                                                                                                                                                                       RLTTPVFGKGVAYDVPNPVFLEQKKMLKSGLNIAHFRQHVSIIEKETKEYFQSWGESGER
                                                                                                                                                                                                                                                                                                                                                                                                                        ASVRTILGSGCLSNLHDSSHKQRKKVIMRAFSREALECYVPVITEEVGSSLEQWLSCGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETLQMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRIL--LGDDRLVSVHWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLSSLLLACAFTLILVYLFRQAI -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLASAL -- CTFVLPLL - LFLAAIKLWDLYCVSGRDRSCALPLPPGTMG-----FPFFG
                                                                                                                                                                                                                          DMQALKQSSTELLFGGHETTASAATSLITYLGLYPHVLQKVREELKSKGLLCKSNQDNKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HATAFGKSPIEFLENAYEKYGPVFSFTMVGKTFTYLLGSDAAALLFNSKNEDLNAEDVYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 12.3%;
Similarity 23.9%;
21; Conservative 8'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     503 AA;
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449
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                                                                                                                                                                                                                                                            -RDRAHREIKNIFYKAIQKRRQSE--EKIDDILQTLLDSTYKDGRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56866 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87;
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Pred. No. 5.2e
87; Mismatches
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HEME (BY SIMILARITY).
; 0302949CE461AFD6 CRC64;
                                490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --GHLAPLPAGAKSPPYIFSPIPFLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
.2e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane;
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Search completed: November 6, 2001, 13:39:40 Job time: 243 sec

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Result
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Maximum Match 100%
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                              2434
2030.5
1739.5
1041.5
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Gapop 10.0 , Gapext 0.5
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2611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425026 seqs, 132305027 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGLPALLASALCTFVLPLLL......PTVYPVDNLPARFTHFHGEI 497
                                                                                                                                                                                                                                                                                               sp_organelle:*
sp_phage:*
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sp_vertebrate:*
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  10
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 SUMMARIES
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Q9r1f4 mus musculu
Q9pnb4 gallus gall
Q93323 xenopus lae
Q9nr63 homo sapien
Q9np41 homo sapien
Q5990 synechocyst
Q91vy7 arabidopsis
Q9pug2 gallus gall
Q9sjh2 arabidopsis
Q9fh76 arabidopsis
Q9fh77 arabidopsis
Q9fm85 arabidopsis
Q9fm85 arabidopsis
Q9fm85 arabidopsis
Q9fm87 arabidopsis
Q9scq9 arabidopsis
Q9scq9 arabidopsis
Q9scq9 arabidopsis
Q9scq9 arabidopsis
Q9lk7 phaseolus a
Q9ln73 arabidopsis
                                                                                                                                                                          Description
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45	44	43	42	41	40	39	38	37	36	3 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
312.5	313.5	313.5	317.5	318	318.5	326	327	328.5	332	333	333.5	334	335.5	338	344	347	347	348.5	377	391.5	406	406	409	411.5	417.5
12.0	12.0	12.0	12.2	12.2	12.2	12.5		12.6	12.7	12.8	12.8	12.8	12.8	12.9	13.2	13.3	13.3	13.3	14.4	15.0	15.5	15.5	15.7	15.8	16.0
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Q9ngk3 tribolium c	Q9sbp8 populus tri	Q9saa9 arabidopsis	Q9lg17 arabidopsis	Q21424 caenorhabdi	048786 arabidopsis	004949 arabidopsis	016806 drosophila	Q9shy7 arabidopsis	Q9fvb9 brassica na	Q9fvc0 brassica na	Q9fx29 arabidopsis		Q9fvb8 brassica na	Q9xfm2 lycopersico			Q9jiy3 mus musculu	Q9swrl liquidambar	Q9x7g9 myxococcus	Q9lic5 arabidopsis	023242 arabidopsis	Q9m066 arabidopsis	Q9sng3 oryza sativ		Q9fqy4 cucurbita m

ALIGNMENTS

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	1 MGLPALLASALCTFVLPLLLFLAAIKLWDLYCVSGRDRSCALPLPPGTMGFPFFGETLQM 60	Query Match 93.2%; Score 2434; DB 11; Length 497; Best Local Similarity 93.2%; Pred. No. 1.4e-190; Matches 463; Conservative 15; Mismatches 19; Indels 0; Gaps 0;	SEQUENCE 497 AA; 56191 MW; 67CB167A997842C1 CRC64;	Electron transport; Endoplasmic reticulum; Heme; Membrane; Microsome;	PIANTS; PROUCUST; P450; L. PRINTS; PROOCHES P450; INKNOWN 1.	InterPro; IPR001128;		-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM (BY SIMILARITY).	OXIDIZED FLAVOPROTEIN + H(2)O (BY SIMILARITY).	-!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +	the yeast two-hybrid system.";	"Identification of tuftelin- and amelogenin-interacting proteins using	PubMed=11063033;		SECULENCE EDON N P		Eukaryota; metazoa; Chordata; Cidhiata; vertebiada; Eutecostomi, Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.).	P450 RETINOIC ACI	01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)	-2000 (TrEMBLrel. 13, Creat	QYKLE4 PRELIMINARY; PRI; 49/ AA. Q9R1F4;	1

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SIMILARITY).

SIMILARITY: BELONGS TO THE CYTOCHROME P450 |
EMBL; AF199462; AAF09250.1; -.
Interpro; IPR001128; -.
Interpro; IPR001128; -.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450; 0.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Electron transport; Endoplasmic reticulum; Heme
Monocxygenase; Oxidoreductase.
SEQUENCE 492 AA; 55264 MW; 7F28B72E75C232FB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9PUB4 PRELIMINARY; PKT; 492 AA.
Q9PUB4;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CYTOCHROME P450 26 (EC 1.14.-.-) (RETINOIC ACID METABOLIZING
CYTOCHROME) (P450RAI) (RETINOIC ACID 4-HYDROXYLASE).
                                                                                                                                                                                                                  "Complementary Domains of Retinoic Acid Production and Degr
the Early Chick Embryo.";
Dev. Biol. 0:0-0(2000).
-!- CATALTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) =
OXIDIZED FLAVOPROTEIN + H(2)0 (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                            Eichele G.;
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                            E.C.,
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                                                                                                                                                                                                                                                                                                                                                                               N.A.
Thaller C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Chordata; Craniata; Vertebrata; Euteleostomi; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                 Sockanathan
    7F28B72E75C232FB
                                                                                                                                                                                                                                                                                                                                                                               s.,
                                                                                                                                                                               P450 FAMILY
                                              Heme; Membrane; Microsome;
                                                                                                                                                                                                                                                                                                                                                                            Petkovich M.,
      CRC64
                                                                                                                                                                                                                         RETICULUM
                                                                                                                                                                                                                                                                                                                                 Degradation
                                                                                                                                                                                                                                                                                                                                                                            Jessell T.M.
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Query Match Best Local

Similarity

77.8%; 78.9%;

Score Pred.

2030.5 No. 1.

.5; DB 13; 1.3e-157;

Length

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MGLPALLASALCTFVLPLLLFLAAIKLWDLYCVSGRDRSCALPLPPGTMGFPFFGETLQM

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  Query Match
Best Local S
Matches 334
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                                                                                                                                         Chen J.L., Grunz H., Panitz F., Pieler T., Hollemann T.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.

1. SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY. EMBL; AF057566; AAC25158.1; ...

InterPro; IPR001128; ...
Pfam; PF00067; p450; 1.
PRINTS; PR000385; P450.
PROSITE; PS00086; CYTOCHROME P450; UNKNOWN_1.
Heme: Monooxygenase; Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                     O93323 PRELIMINARY; PRT; 492 AA.
O93323;
O1-NOV-1998 (TrEMBLrel. 08, Created)
O1-NOV-1998 (TrEMBLrel. 08, Last sequence update)
O1-NAR-2001 (TrEMBLrel. 16, Last annotation update)
CYTOCHROME P450 26 (EC 1.14.-.) (RETINOIC ACID 4-METABOLIZING
CYTOCHROME) (P450RAI) (RETINOIC ACID 4-HYDROXYLASE).
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Xenopodinae; Xenopus.
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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  Local Similarity nes 334; Conserv
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                                                                                                                       Monooxygenase; Oxidoreductase
NCE 492 AA; 55459 MW; D1D41
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    Conservative
                        66.6%;
  68;
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                        Score 1739.5;
Pred. No. 7.56
                                                                                                                       D1D4BB7651BF2D3E CRC64;
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    Mismatches
                        .5e-134;
                                            DB 13; Length
    , 68
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MDLYTLLTSALCTLALPLLLLLTAAKLWEVYCLRRKDAACANPLPPGTMGLPFFGETLQM

60

Best Local Similarity 44.7 Matches 219; Conservative

44.28;

Pred.

88;

Mismatches 165;

Indels

23;

Gaps

9

No. 8.4e-77;

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                                                                                                                                                                        White J.A., Ramshaw H., Taimi M., Stangle W., Zhang A., Everingham Creighton S., Tam S.-P., Jones G., Petkovich M.; "Identification of the human cytochrome P450, P450RAI-2, which is predominantly expressed in the adult cerebellum and is responsible all-trans-retinoic acid metabolism.";
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CYTOCHROME P450 RETINOID METABOLIZING PROTEIN P450RAI-2.
                                                                                                                                                                                                                                                                                                                                                                                                  Q9NR63
                                                                                                                                                                                                                                                                                                                                                                                        Q9NR63;
                                                 InterPro; IPR001128; -. Pfam; PF00067; p450; 2. PRINTS; PR00385; P450.
                                                                                                                                     all-trans-retinoic acid metabolism.";

Proc. Natl. Acad. Sci. U.S.A. 97:6403-6408(2000).

-i-CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) =

OXIDIZED FLAVOPROTEIN + H(2)0 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
  Monooxygenase;
SEQUENCE 512
                       PROSITE; PS00086; CYTOCHROME_P450; Electron transport; Endoplasmic re
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE~20300913; PubMed=10823918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               475
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                                                                                                                         SUBCELLULAR LOCATION: MEMBRANE-BOUND.
                                                                                                 SIMILARITY:
                                                                                                               SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKRLMFRIAMRILLGCEPQLAGDGDSBQQLVEAFEEMTRNLFSLPIDVPFSGLYRGMKAR:||:||:|||||||::||
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                                                                                    MILARITY: BELONGS TO THE CYTOCHROME AF252297; AAF76003.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
  Oxidoreductase. AA; 57512 MW;
                                                                                                                                                                                                                                                                                      Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               492
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                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
   A06D1D9944E6726F
                         50; UNKNOWN_1. reticulum; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                   512
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                                                                                                  P450 FAMILY
                                                                                                                         ENDOPLASMIC
                                                                                                                                                                                                                                                                                        Hominidae;
   CRC64;
                           Membrane;
                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                        Homo
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                            Microsome;
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Query

Match

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Score 1041.5;

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Length

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                                                WUGSC:H_NHU4>>--
HOMO sapiens (Human).
Homo sapiens (Human).
Tharyota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2001 (TrEMBLrel. 16, WUGSC: H_NH0493L16.1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9NP41;
Q9NP41;
                                                                                                                                                                                                                                                                                                                                 MEDLINE=99063792; PubMed=9847074; Sulston J.E., Waterston R.; "Toward a complete human genome s Genome Res. 8:1097-1108(1998).
  SIMILARITY).
-!- SIMILARITY:
EMBL; AC007002;
                                                                                                                                                                                                                                                "The
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Bourne S., Bauer C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; NCBI_TaxID=9606;
                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                         Submitted (MAR-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   476
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ne S., Bauer C., Pape K., Jones T.;
sequence of Homo sapiens BAC clone RP11-493L16.";
sequence of Homo sapiens BAC clone RP11-493L16.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HETTASAATSLITYLGLYPHYLQKVREELKSKGLL----CKSNQDNKLDMEILEQLKYIG
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  BELONGS TO
AAF65576.1;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                           CYTOCHROME
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                                                                       ENDOPLASMIC RETICULUM
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Best Loc
Matches
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence upda
01-MAR-2001 (TrEMBLrel. 16, Last annotation up
PUTATIVE CYTOCHROME P450 120.
CYP120 OR CYP OR SLR0574.
Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synech
NCBL_TaxID-1148;
Kaneko T., Tanaka A., Sato S.,
Sugiura M., Tabata S.;
"Sequence analysis of the genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00385; P450.

PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.

Electron transport; Endoplasmic reticulum; He
Monooxygenase; Oxidoreductase.

SEQUENCE 525 AA; 59124 MW; 71D47B6752A603
                                                                SEQUENCE FROM N.A. MEDLINE=96127529; Pubmed=8590279;
                                                                                                                                                Submitted
                                                                                                                                                                                           STRAIN-PCC6803
                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q59990
                                                                                                                                                                   Tabata S.;
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::| | : : | | | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGERGLLVYPEVKRLMFRIAMRILLGCE-PQLAGDGDSEQQLVEAFEEMTRNLFSLPIDV | : | | | ::: |:||||:|::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFELATRTEPRITLVPVLHPVDGLSVKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VHWPASVRTILGSGCLSNLHDSSHKQRKKVIMRAFSREALECYVPVITEEVGSSLEQWLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QKCTLRETRVWLPQGSGFQSSRREKYGNVFKTHLLGRPLIRVTGAENVRKILMGEHHLVS
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                                                                                                                                         (AUG-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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    genome
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Pred. No. 9
                                                Kotani H.,
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    of.
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    unicellular
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                                             Sazuka T.,
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                                                Miyajima
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AC Q0
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DT C
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Best Local
                                                                                  Q9LVY7;
Q9LVY7;
01-OCT-2000
              01-OCT-2000 (TIEMBLITE1. 15, Created)
01-OCT-2000 (TIEMBLITE1. 15, Last sequei
01-MAR-2001 (TIEMBLITE1. 16, Last annott
CYTOCHROME P450-LIKE.
Arabidopsis thallana (Mouse-ear cress)
Eukaryota, Viridiplantae; Embryophyta;
Magnoliophyta; eudicotyledons; core euc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.", DNA Res. 3:109-136(1996).

-I- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; D64003; BAA10496.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97061201; PubMed-8905231;
MEDLINE-97061201; PubMed-8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamu Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T. Miyajima N., Matsuno A., Muraki A., Nakazaki N., Naruo K., C. Hosouchi T., Matsuno A., Mada T., Watanabe A., Yamada M., Yas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synechocystis sp. strain PCC6803. region from map positions 64% to DNA Res. 2:153-166(1995).

[3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam: PF00067; p450; 1.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Hypothetical protein; Heme; Monooxygenase; Oxido
SEQUENCE 444 AA; 50578 MW; 8F62A9EED3B54BDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shimpo S., Takeuchi C., Wada T., Watanabe A.,
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                                                                                                                                                                                                  406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                  VELARHCDWQLLNGPP-TMKTSPTVYPVDNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNQPLSLPELKDQILLLLFAGHETLTSALSSFCLLLGQHSDIRERVRQEQN-----KLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIPIPPGDEGLPWIGETINF-INDGDEGKKRQQQEGPIFKTRIEGKNVIFISGALANREL
                                                                                                                                                                                                  TRLIQQFDWTLLPGQNLELVVTPSPRPKDNL
                                                                                                                                                                                                                                                       THADPDLYPDPEKFDPERFTPDGSATHNPP----FAHVPFGGGLRECLGKEFARLEMKLFA
                                                                                                                                                                                                                                                                                  THDVAEIFTNKEEFNPDRE----SAPHPEDASRESFIPFGGGLRSCVGKEFAKILLKIFT
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                                                                                                                                                                                                                                                                                                                                                                                     LFSLPIPLPNTLFGKSQRARALLLAELEKIIKAR-----QQQPPSEEDALGILLAARDD
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                                                                                                                              PRELIMINARY;
  Brassicaceae;
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  Arabidopsis
                                                                     Created)
Last sequence up
Last annotation
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Pred.
                                                                                                                              PRT;
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                 core eudicots;
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(ygenase; Oxidoreductase.
מיייים 154BDC CRC64;
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                              Tracheophyta;
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                                                                                    update)
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                  Rosidae;
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                 Spermatophyta;
e; eurosids II;
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RESULT
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Best Local Similarity
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 Q9PUG2;
Q9PUG2;
01-MAY-2000
01-MAY-2000
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EMBL; AB018112; BAA96885.1; -.

InterPro; IPRO01128; -.

Pfam; PF00067; p450; 1.

PRINTS; PR00385; P450.

PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.

Electron transport; Endoplasmic reticulum; Heme; Membrane; Microsome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monooxygenase;
SEQUENCE 477
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CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = OXIDIZED FLAVOPROTEIN + H(2)O (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
                                                                   œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHDSSHKQRKKVIMRAFSR-EALECYVPVITEEVGSSLE-QWLSCGERGLLVYPEVKRLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRKY----GFIYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWPASVRTILGSGCLSN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IILFLSSILLSLLLLLRKHLSHFSYPNLPPGNTGLPLIGESFSFLSAGRQGHPEKFITDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLLFLAAIKLWDLYCVSGRDRSCALP-LPPGTMGFPFFGETLQMVLQRR-----KFLQMK 71
                                                                                                                            SPTVYPVDNLPAR 489
                                                                                                                                                                                                                                                                                                                                  EVSAIVRQRKEELKAGKA--
                                                                                                                                                                                                                                                                                                                                                                                                                                              SKEEARKLR--MLLSQFMKPEALRRYVGVMDETAQRHFETEW--ANQDQVTVFPLTKKFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRRFSSSSSCVFKTHLFGSPTAVVTGASGNKFLFTNENKLVVSWWPDSVNKIFPSSMQTS
                                                                                                                                                                                                                                        IKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVAEIFTNKEEENPDRF
                                                                                                                                                                                                                                                                                                    GGHETTASAATSLITYLGLYPHVLQKVREELKSKGLLCKSNQDNKLDMEILEQLKYIGCV
                                                                                                                                                                                                                                                                                                                                                            RIEQNIRAKICGLRASEAGQGCKDALQLLIEHS-----WERGERLDMQALKQSSTELLF
                                                                                                                                                                                                                                                                                                                                                                                         FSIACRSFLSME-----DPARVRQLEEQFNTVAVGIFSIPIDLPGTRFNRAIKASRLLRK
                                                                                                                                                                                                                                                                                                                                                                                                                    FRIAMRILLGCEPQLAGDGDSEQQLVEAFEEMTRNLFSLPIDVPFSGLYRGMKARNLIHA
                                                                                                             DPLPIPDKGLPIR
                                                                                                                                                                                           --SAPHPEDASRFSFIPFGGGLRSCVGKEFAKILLKIFTVELARHCDWQ-LLNGPPTMKT 476
                                                                                                                                                                                                                      ACEVMRIVPPLSGTFREAIDHFSFKGFYIPKGWKLYWSATATHMNPDYFPEPERFEPNRF
                                                                                                                                                                                                                                                                           GGHDTASIVCTFVVNYLAEFPHVYQRVLQE--QKEILKEKKEKEGLRWEDIEKMRYSWNV
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 (TrEMBLrel. (TrEMBLrel.
                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase. AA; 54850 MW;
                                                                                                                                                                 -YTYVPFGGGPRMCPGKEYARLEILIFMHNLVNRFKWEKVFPNENKIVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=10718197;
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 13,
13,
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Pred.
  Last sequence update)
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                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                  -LEEHDILSHMLMNIGETKD-EDLADKIIGLLI
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No. 6.4e-38;
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Q9SJH2;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Martinez-Ceballos E., Burdsal C.A.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) =
OXIDIZED FLAVOPROTEIN + H(2)O (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., Vanaken S.E., Umayam L., Talion L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome II of Arabidopsis thaliana."; "sequence and analysis of chromosome II of Arabidopsis thaliana."; "sature 402:761-768(1999)
-i- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + OXIDIZED FLAVOPROTEIN + H(2)O (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
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CYP26 (FRAGMENT).
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Pfam; PF00067; p450; 1.

PRINTS; PR00385; P450.

PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_PS00086; CYTOCHROME_P450; UNKNOWN_PS0008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16, PUTATIVE CYTOCHROME P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Electron transport; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF185266; AAD56546.1; HSSP; P14779; 1BU7.
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                                                                                                                                                                                                                                                                                                                                                STRAIN=CV. COLUMBIA; MEDLINE=20083487; PubMed=10617197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monooxygenase; Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 IPFGGGLRSCVGKEFAKVLLKIFTVELARSCDWQLLNGPPTMKTSPT
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107 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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12009
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Last annotation updat
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; Galliformes; Phasianidae; Phasianinae;
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RESULT
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Q9FH76;
01-MAR-2001 (TrEMBLrel. 16, C
01-MAR-2001 (TrEMBLrel. 16, L
01-MAR-2001 (TrEMBLrel. 16, L
CYTOCHROME P450.
    clones.";
clones.";
clones.7:31-63(2000)
                                                                                                                   Sato S.,
Tabata S.
                                                                                                                                      Sato
                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sp
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Brassicales; Brassicaceae; Arabidopsis.
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InterPro; IPR001128; -.
Pfam; PF00067; p450; 2.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.
Electron transport; Endoplasmic reticulum; Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 485 AA; 55405 MW; 08B0B16474620F82 C
                                                                                                                                                              STRAIN=COLUMBIA;
MEDLINE=20181125;
                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                      features of the
                                                                                            "Structural
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132; Conservative
  AB020744;
                                                                                                                                         Nakamura
                                                                  analysis of
the regions
  BAB10255.1;
                                                                                                                                    PubMed=10718197;
Y., Kaneko T., K
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Pred. No. 3.4e
86; Mismatches
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065624;
01-AUG-1998 (TrEMBLrel. 07, C:
01-AUG-1998 (TrEMBLrel. 10, L:
01-MAR-2001 (TrEMBLrel. 16, L:
CYTOCHROME P450.
T18B16.200 OR AT4G19230.
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Best Local
                                                                                                                                      Benes V.,
Mayer K.F.
                                                                                                                                                                                                             SEQUENCE FROM N.A.

Bevan M., Benes V., Rechmann S., Bo

Bevan M., Mayer K., Schueller C.;

Mewes H.W., Mayer K., Schueller C.;

Submitted (JAN-1998) to the EMBL/Ger

[2]
                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Symagnoliophyta; eudicotyledons; core eudicots; Rosidae; Brassicales; Brassicaceae; Arabidopsis.
Van Der Schueren J., Chuang Y.J., Volckaert G., Mewes H.W., Lemcke Submitted (MAR-2000) to the EMBL/
                                                                     SEQUENCE OF 131-457 FROM N.A.
                                                                                                                     Submitted
                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
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EMBL/GenBank/DDBJ
                                                                                                                  EMBL/GenBank/DDBJ
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Pred. No. 4.7e-34;
2; Mismatches 220
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K., Mayer
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Best Local S
Matches 144
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O1-NOV-1998 (TrEMBLrel. 08, C1
O1-NOV-1998 (TrEMBLrel. 16, L1
O1-MAR-2001 (TrEMBLrel. 16, L1
O1-MAR-TVE CYTOCHROME P450.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ d
--- SIMILARITY: BELONGS TO THE CYTOCHROME P450
EMBL; AL021687; CAA16713.1; -.
EMBL; AL161550; CAB78925.1; -.
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PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1
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SEQUENCE FROM N.A.
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                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                                                                                                                                                                           PUTATIVE CYTOCHROME T914.17.
                                                                                 Magnoliophyta; eudicotyled
Brassicales; Brassicaceae;
        SEQUENCE FROM N.A
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01-MAR-2001 (TrEMBLrel. 16, I
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-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AC005315; AAC33235.1; -.
InterPro; IPR001128; -.
InterPro; IPR001128; -.
Pfam; Pf00067; P450; 1.
ProSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 482 AA; 55175 MW; AB6A07AB2778DD3B CRC64;
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                                                                                                                                                                                         Magnoliophyta; eudicotyledons; core eudicots; Brassicales; Brassicaceae; Arabidopsis NCBI_TaxID=3702
    MEDLINE=98290546; P
Sato S., Kaneko T.,
                                                                              SEQUENCE FROM N.A. STRAIN-COLUMBIA;
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Local Similarity 28.4%;
nes 141; Conservative 9
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                                             PubMed=9628582;
        Kotani
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Last annotation update)
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01-AUG-1998 (Tremblrel. 07, C
01-AUG-1998 (Tremblrel. 07, L
01-MAR-2001 (Tremblrel. 16, I
STEROID 22-ALPHA-HYDROXYLASE.
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"Structural analysis of Arabidopsis thaliana chromosome "Structural analysis of the regions of 1,456,315 bp covered Sequence features of the regions of 1,456,315 bp covered physically assigned Pl and TAC clones.";
DNA Res. 5:41-54(1998).
DNA Res. 5:41-54(1998).
EMBL; AB009040; BAB08653.1; ...
EMBL; AB009040; BAB08653.1; ...
                                                                                                                                                                            DWF4.
       Plant Cell 10:0-0(1998).
-I- SIMILARITY: BELONGS TO THE CYTOCHROME EMBL; AF044216; AAC05093.1; -.
                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sy
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Brassicales; Brassicaceae; Arabidopsis.
                                               Choe S., Dilkes B.P., Feldmann K.A.;
                                                                          STRAIN-WS-2
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                                                                                    SEQUENCE FROM N.A.
InterPro;
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27.8%;
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07, Last sequence update)
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Pred. No. 1.4e-28;
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Q9SCQ9;
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-MAY-2000 (TrEMBLrel. 16,
Q1-MAR-2001 (TrEMBLrel. 16,
         EU Arabidopsis sequencing project;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450
EMBL; AL132979; CAB62435.1; -.
                                                                                                       SEQUENCE FROM N.A. Bloecker H., Mewes Salanoubat M.;
                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Trachec
Magnoliophyta; eudicotyledons; core eudicots;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                          Submitted
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PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1
Heme; Monoxygenase; Oxidoreductase.
SEQUENCE 513 AA; 58867 MW; B1639BDD9A4DA
                                                                SEQUENCE FROM N.A.
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  InterPro;
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PRINTS; PR00385; P450;
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 513 AA; 58867 MW; B1639BDD9A5D7C93 CRC64;
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                 443 VGKEFAKILLKIFTVELARHCDWOLLNGPPTMKTSPTVYPVDNLP 487
                                                            403 WKYLPYISAVHLDNSRYDOPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLC
                                                                                             392 WNVIYSICDTHDVAEIFTNKEEFNPDRFSAPHPEDASRFS-----FIPFGGGLRSC 442
                                                                                                                               343 EIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSG
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463 AGSELAKLEMAVFIHHLVLKFNWELAE-----DDKPFAFPFVDFP 502
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Search completed: November 6, 2001, 13:38:27 Job time: 255 sec

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9b_p12:ATCHRIV50
9b_p11:AB020744
9b_p12:AF139532
9b_r01:AF166266
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Query length: 497
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Database length: -856060004
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gb_p14:SLU54770
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-Q=/cgn2_1/USPf0_spco1/US09668482/runat_05112001_13353_10884/app_query.fasta_1.1680
-Q=/cgn2_1/USPf0_spco1/US09668482/runat_05112001_13353_10884/app_query.fasta_1.1680
-DB=cenEmbl - QFMT=fastap - SUFFIX=ye -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000 -FGAPOP=6.000
-QGAPEXT=0.050 -XGAPED=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MIN=0
-ALIGN=15 -MODE-LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=200000000 -USER=US09668482_@CGN1_1_8677 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1
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1726 ! AF115769 Mu;
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475 | AB018112 Arabidopsis thaliana
44 | AF326277 Hordeum vulgare ent-k
0331 | AC007002 Homo sapiens BAC cl
24 | U32579 Zea mays DWARF3 (dwarf3
81 | AJ232955 Myxococcus xanthus cy
574 | AL021087 Arabidopsis thaliana
9382 | AL161550 Arabidopsis thaliana
                         AF139532 Liquidambar styracifi
0 i AF162366 Mus musculus lanoster
125 i AL022121 Mycobacterium tuber
7 i AB056457 Mus musculus Cyp4v3 m
9 i AF150881 Lycopersicon esculent
1 AF214009 Brassica napus cytoch
1 AF214008 Brassica napus cytoch
1 AF214008 Brassica napus cytoch
1 AF214008 Brassica napus cytoch
1 M28655 Rabbit cytochrome P4501
1 M28657 Rabbit mRNA for omega-H
                                                                                                                                                                                                                                                                                                                                                                                                                                         56 | AF252297 Homo sapiens cytochro

564 | D64003 Synechocystis sp. PCC

564 | D64003 Synechocystis sp. PCC

675 | AF185266 Gallus gallus CYP26 (C

676 | AF318211 Taxus cuspidata 5-alg

676 | AC006931 Arabidopsis thalian
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1 AF3158613 Homo sapiens chromo
1 AF199462 Gallus gallus retinoi
1 AF057566 Xenopus laevis retino
                                                                                                                                                                                                                                                                                                                    AF279252 Vigna radiata cytochu
AF212991 Cucurbita maxima ent
AB008097 Arabidopsis thaliana
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AF318501 Arabidopsis thaliana
AR074363 Sequence 1 from pater
X87367 A.thaliana mRNA for cyt
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              Rabbit mRNA for omega-
Rattus sp. mRNA for cy
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gb_in3:DMCTP450A
gb_pat1:AR085702
gb_p13:ATU38416
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CDNA cloning of human retinoic acid-metabolizing enzyme (hP450RAI)
identifies a novel family of cytochromes P450
J. Biol. Chem. 272 (30), 18538-18541 (1997)
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White, J.A., Beckett Jones, B., Guo, Y.D., Dilworth, F.J., Bonasoro, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (26-MAY-1997) Cancer Research Labs, Queen's University, Botterell Hall, Rm 355, Kingston, Ont K7L 3N6, Canada Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              White, J.A., Beckett-Jones, B., Guo, Y., Dilworth, F.J., Bonasoro, J., Jones, G. and Petkovich, M.
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POTTMOEPFECETLOWIQARKELQMKRKYGFIYKTHLEGRPTVRVMGADNVRRILL
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4442 C 477 g 401 t
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                                                                                                                                                                                                                                                       Fujii, H., Sato, T., Kaneko, S., Gotoh, O., Fujii-Kuriyama, Y., Osawa, K., Kato, S. and Hamada, H. Metabolic inactivation of retinoic acid by a novel P450 differentially expressed in developing mouse embryos
                                                                                                                                                                                                                                                                                                                                                   house mouse.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                   MMP450RA 1756 bp
M.musculus mRNA for
                                                                                                                                                                           Submitted (17-APR-1997) H. Hamada, Osaka University, Institute Mol. & Cell. Biol., 1-3 Yamada-oka, Suita, Osaka, 565, JAPAN
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1756)
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P450RA gene.
                                                                                                                                                                                                      Hamada,H.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 eLeuGlnMetLysArgArgLysTyrGlyPheIleTyrLysThrHisLeuP 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 PheproPhePheGlyGluThrLeuGlnMetValLeuGlnArgArgLySPh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 erGlyArgAspArgSerCysAlaLeuProLeuProProGlyThrMetGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACCATCCTGGGCGCTGCCTGCCTCCAACCTGCACGATTCCTCGCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         408
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REFERENCE
AUTHORS
TITLE
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AUTHORS
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VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS AF115769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
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                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AF115769 from: 1 to: 1726
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
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                                                                       127
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                                                                77
                                                                                                                                                                                         17 oLeuLeuPheLeuAlaAlaIleLysLeuTrpAspLeuTyrCysValS 34
                           51
                                                                                                                                                                                                                                                              27 ATGGGGCTCCCGGCGCTGCTGCCACTCGCGCTCTGCACCTTCGTGCTGCC
                                                                                                                                                                                                                                                                                       1 MetGlyLeuProAlaLeuLeuAlaSerAlaLeuCysThrPheValLeuPr 17
PheProPhePheGlyGluThrLeuGlnMetValLeuGlnArgArgLysPh 67
                                                                                                                                                                GCTGCTGCTCTTCCTGGCGCGCGCTCAAGCTCTGGGACCTGTACTGTGA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus cytochrome P450 retinoic acid metabolizing enzyme P450RA mRNA, complete cds. AF115769.1 GI:4324987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 1726)
Paine,C.T., Paine,M.L. and Snead,M.L. Identification of amelogenin and tuftelin-interacting proteins using the yeast two-hybrid system Connect. Tissue Res. 38, 257-267 (1998)
2 (bases 1 to 1726)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (21-DEC-1998) CCMB, University of Southern California, 2250 Alcazar Street, CSA103, Los Angeles, CA 90033, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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Location/Qualifiers
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15 a 428 c 476 g 417 t
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5.029
97.384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="cytochrome P450 retinoic acid metabolizing enzyme P450RA"
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Percent Identity: 93.159
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351 1077	GluGlnLeuLysTyrIleGlyCysValIleLysGluThrLeuArgLeuAs 3 	12

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SOURCE
ORGANISM
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LOCUS AL358613 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         snGlyTyrGlnIleProLysGlyTrpAsnVallIeTyrSerIleCysAsp 400
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Homo sapiens chromosome 10 clone RP11-348J12,
PROGRESS ***, 14 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (13-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Apr 17, 2001 this sequence version replaced gi:13625010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 166337)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code:
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NOTE: This is a 'working draft' sequence.
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      It currently
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SEQUENCING
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* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105296 105395: gap of 100 bp in length 105396 129702: contig of 24307 bp in length 129703 129802: gap of 100 bp 129803 132462: contig of 2660 bp in length 132463 132562: gap of 100 bp 132563 137099: contig of 4537 bp in length 137100 137199: gap of 100 bp in length 137200 158409: contig of 21110 bp in length 158310 158409: gap of 100 bp 158410 158409: gap of 100 bp 158410 166337: contig of 7928 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32410 32509: gap of 100 bp
32510 52913: contig of 20404 bp in length
52914 53013: gap of 100 bp
53014 55817: contig of 2804 bp in length
55818 55917: gap of 100 bp
55818 55917: contig of 18595 bp in length
74513 74612: gap of 100 bp
74613 83833: contig of 9221 bp in length
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83934 8700
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83934. .8
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74613. .8
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105396. .129702
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                                                                                                                                                            100684.
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123 GlyCysLeuSerAsnLeuHisAspSerSerHisLysGlnArgLys.Lys. 138 	106 rgLeuValSerValHisTrpProAlaSerValArgThrIleLeuGlySer 122 	89 largValMetGlyAlaAspAsnValArgArgIleLeuLeuGlyAspAspA 106 	73 ArgLysTyrGlyPheIleTyrLysThrHisLeuPheGlyArgProThrVa 89 	64ArgArgLysPheLeuGlnMetLysArg 72	rccccec	63 63	55164 GCTGAAGTCGGGGTAGGCCCCCCGGGAGGCATGCTATTGCGGCTAGGAG 552	- - TOLLOPSINGLORDSONS OF THE TANK THE T	63	51 PheProPhePheGlyGluThrLeuGlnMetValLeu.Gln	34 erGlyArgAspArgSerCysAlaLeuProLeuProProGlyThrMetGly 50	17 oLeuLeuPheLeuAlaAlaIleLysLeuTrpAspLeuTyrCysVals 34 	1 MetGlyLeuProAlaLeuLeuAlaSerAlaLeuCysThrPheValLeuPr 17 	Align seg 1/1 to: AL358613 from: 1 to: 166337	alignment_block: US-09-668-482-4 x AL358613	tio: 4.221 Gaps: ity: 42.196 Percent Identity: 41.	tv: 2076.50 Length: 116		<pre>fragment_chain:3 clone_end:SP6 vector_side:right"</pre>	fragment	". fragment	/note="assembly_fragment:02005
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300		288
288	euIleGluHisSerTrpGluArgGlyGluArgLeuAspMetGln + + + + + + + + + + + + + + + +	274 56364
56363	YLeuArgAlaSerGluAlaGlyGlnGlyCysLysAspAlaLeuGlnLeuL 	257 56314
1 257 3 56313	AsnLeuIleHisAlaArgIleGluGlnAsnIleArgAlaLysIleCysGl 	241 56264
y 240 56263	Gly.MetLysalaarg	236 56214
. 235 3 56213	Tyrarg Accegetaaagegcecaaacegectecegactagegececegeacctegetecegecegececegecegececegecegecegecegecegecegecegecegecegececege	234 56164
233 1 3 56163	etThrargAsnLeuPheSerLeuProIleAspValProPheSerGlyLeu 	217 56114
M 217 N 56113	UAlaGlyAspGlyAspSerGluGlnGlnLeuValGluAlaPheGluGluM 	200 56064
e 200 56063	LeuMetPheArgIleAlaMetArgIleLeuLeuGlyCysGluProGlnLe 	184 56014
9 183 1 5 56013	rpLeuSerCysGlyGluArgGlyLeuLeuValTyrProGluValLysArg	167 55964
r 167 r 55963	TyrValProValI1eThrGluGluValGlySerSerLeuGluGlnT 	152 55914
N 55913	NINNINNINNINNINNINNINNINNINNINNINNINNIN	55864
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N 55863	CCGANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	55814
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UI I	GGGCGGATGGAGGCTTTTAACGCTGTCCCCTCCTCGGGACTCAGGTGA	
1 140	GGTGTCTGGAAGGG	139
138		13
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T 55613	GAATTCCGGCTGATGGATGCTAGGCGCGGGCTAGCAGCTTGAGGTGGGCT	55564
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G 55563	GGGGGCAGGAGGCGACGGCTGGACAGGGAGGGGGACCCCATTTATGAGCG	55514
. 138		138

56414	AGCAGCTTCAGACCAGGCACTGCGGAGTTTGGTCCCCTGGCTTTCCAAGC 5	6463
288		888
56464	GCTGTTCCTGGGGCCCCCAAAGCGCGCGCCTGGGGCCCAGCTTTCTGGAG 5	6513
288		883
56514	TGGGCGGCCGGCTCAGACTACAGCTATGGAATCCCGAAGGAAG	56563
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56564	CACCCGGTCAGGAGAGCTGCGGAAGGGGCTGCGGCGGAACTGGGAGCATC 5	56613
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56614	CCCTAGCCTTTCCAGGTTTCAAAGGGAAAGTTGGAATTTGCAAAAATGTT 5	56663
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56664	AATAAAGAACCTTGCGATTTTAATAAAACTAAGACTTTAACTCAGGAGTT 5	56713
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56714	TCCGGTAGAGCGGGGTCGTACTCGCCTTACTGCTCCAGCTGAACTAAAGG 5	56763
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56764	GACGTTGCATTTTGTTTAAAGATATTGCTTTCCTTGACTTTCTGTCAGCA	56813
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56814	AAACATTTAGCCCTTCTAGTCTTCCCTCCAGAACTCTCAGTTCGATTCTG	56863
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56864	AGTAATCCTTCTGTCAAACCGCAGGCAGACTTGTGAGAATGTGGGTCTCA	56913
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301 56964	yHisGluThrThrAlaSerAlaAlaThrSerLeuIleThrTyrLeuGlyL 	318 57013
318 57014	euTyrProHisValLeuGlnLysValArgGluGluLeuLysSerLys 	333 57063
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57064	GGGAGACTGGGTCTGGGGGTGTCCTTATTAGCTTAGGAAATTCAGCTGCT	57113
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57114	4 CCCTAGCCAACTTCCGAATAAGTCAGTGTGCCTGCCTTCATGGAGTATTTT	57163
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57164	4 GAAAGTGCAAGGCCCAGGGCTGCGTGGGCCAGTGGGCAGAATTAGCTTTG	57213
33:		333
57214	4 TGAATAAACAGGATGGAGTCTTGAGCTGTGAGCCCACTTGGGCAGGGTTT	57263
333		333
5726	4 GACCTTGTATTCCTACCCCTCCTCCACCTTTTGCTGAACCGTGGAGATTC	57313
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451 5826	TGCTG G1yG1 	
eProP 435 TCCAT 58213	418 gPhes	
AspAr 418 ACCG 58163	402 HisaspValalaGluIlePheThrAsnLysGluGluPheAsnProAspAr 	
spThr 401 ATACT 58113	386TyrGlnIleProLysGlyTrpAsnValileTyrSerIleCysAspThr 	
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Gly 385	385	
STTGA 58013	57964 TTAGCTCATAATTTCCCCCAAAGATATCAGTGACTGCTTTTTGTTG	
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yGly 373 AGGG 57763	357 lyCysVallleLysGluThrLeuArgLeuAsnProProValProGlyGly	
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J 57	64 TTAAGCCCTGTTT	
w	:	
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GGTT 57413	TGAATAGCT	
333	333	
PAGT 57363	57314 TCAGATAGGTTCCACTTTCTTGAATTGGTGTGTCCAAGGGCATACATA	_

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REFERENCE
AUTHORS
                                                           alignment_block:
US-09-668-482-4 x AF199462
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LOCUS AF199462
                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
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   Align seg 1/1 to: AF199462
                                                                                                                                                                    Percent Similarity:
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                                                                                                                                                                 Quality: 2030.50
Ratio: 4.463
milarity: 91.549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Swindell,E.C., Thaller,C., Sockanathan,S., Petkovich,M., Dessell,T.M. and Eichele,G. Complementary Domains of Retinoic Acid Production and Dein the Early Chick Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 1479)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Swindell, E.C., Thaller, C., Jessell, T.M. and Eichele, G.
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//prodein_flam_har09250.1"
/prodein_id="har09250.1"
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/db_xref="taxon:9031"
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 ${\tt MetGlyLeuProAlaLeuLeuAlaSerAlaLeuCysThrPheValLeuPr}$

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SOURCE
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MEDLINE
REFERENCE
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LOCUS AF057566
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ACCESSION
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                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.

1 (bases 1 to 1479)

1 (Chen,Y., Grunz,H. and Pieler,T. Hellemann,T., Chen,Y., Grunz,H. and Pieler,T. Regionalized metabolic activity establishes boundaries of retinoic regionalized metabolic activity establishes
                                                                                                                                                                                                                                                                                               African clawed frog. Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis retinoic
AF057566
                                               Chen,J.L., Grunz,H., Panitz,F., Pieler,T. and Hollemann,T. Direct Submission
Submitted (05-APR-1998) Developmental Biochemistry, University of Goettingen, Humboldtallee 23, Goettingen, Lower Saxony 37073,
                                                                                                                                                      acid signalling
EMBO J. 17 (24), 7361-7372 (1998)
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Location/Qualifiers
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                                                                                          CysTyrValProValIleThrGluGluValGlySerSerLeuGluGlnTr
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                    pLeuSerCysGlyGluArgGlyLeuLeuValTyrProGluValLysArgL
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/db_xref="GI:3283172"
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                                                                                                                                           GACACCCACGGTGAGGCCGATCTGTTTCCCGACACGGACAAATTCAACCC
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                                                                                                                                                                                                                                                                                                                  TAAATGGCTATCAGATTCCCCAAGGGCTGGAATGTTATATACAGCATTGCT 1182
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alignment_block:
US-09-668-482-4 x DRU68234
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Ratio: 4.080
milarity: 85.714
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J. Biol. Chem. 271 (47), 29922-29927 (1996)
97094702
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1 (bases 1 to 1479)
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Danio rerio all-trans-retinoic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (28-AUG-1996) Cancer Research Labs, Botterell Hall, Kingston, ON K7L 3N6, Canada
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/note="all-trans-retinoic acid 4*-hydroxylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="p450RAI"
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4-hydroxylase (p450RAI) mRNA,
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CATGTTTCTGGGTCTGAACACAGAAGTGGTGCAGAAGGTCAGAGAGGAGGAGG
           eThrTyrLeuGlyLeuTyrProHisValLeuGlnLysValArgGluGluL
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                                                      LeuLeuPheGlyGlyHisGluThrThrAlaSerAlaAlaThrSerLeuIl 313
                                                                                                                                  CGAACAGAAATACAAAGACGCCCTTCAGCTGTTGATCGAGAACAGCAGAA
                                           CTTCTATTTGGAGGTCATGAAACCACCGCCAGCACTGCAACCTCACTTGT
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MEDLINE
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LOCUS AF252297
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Homo sapiens cytochrome P450 retinoid metabolizing
P450RAI-2 mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4445)
White, J.A., Ramshaw, H., Taimi, M., Stangle, W., Zhang, A., Everingham, S., Creighton, S., Tam, S.P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S.P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S.P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S.P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S.P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S.P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S.P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S.P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S.P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S.P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S.P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S.P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S.P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S.P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S.P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S.P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S.P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S.P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S.P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S.P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S., P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S., P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S., P., Jones, G. and Petkovich, M. Everingham, S., Tam, S., P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S., P., Jones, G. and Petkovich, M. Everingham, S., Creighton, S., Tam, S., P., Jones, G. and Petkovich, M. Everingham, S., Tam, S
                                                                                                                          Submitted (04-APR-2000) Cytochroma Inc., 116 Barrie Street, Bioscience Complex, Suite 2424, Kingston, ONT K7L 3N6, Cana Location/Qualifiers
                                                                                                                                                                                                                      White, J.A., Ramshaw, H., Taimi, M., Stangle, W., Zhang, A., Everingham, S., Creighton, S., Tam, S.-P., Jones, G. and Pe Direct Submission
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/db_xref="taxon:9606"
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                                                                                               1. .4445
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ORIGIN
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Ratio: 2.838
Percent Similarity: 74.141
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                                                                                                                                                                                                                                                                                                                                                                                               522 CCACCCCGAG...GCCATCAACGTGTACCAGGAGGCGCAGAAGCTGACCT 568
                                                                                                                                          153 ValProValIleThrGluGluValGlySerSerLeuGluGlnTrpLeuSe 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 GGCCGCTGATACGCGTGACCGGCGCGGAGAACGTGCGCAAGATCCTCATG 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 rgProThrValArgValMetGlyAlaAspAsnValArgArgIleLeuLeu 102
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222 GTCGCGGAGGAAGTATGGCAACGTGTTCAAGACGCATTTGTTGGGGC 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 LeuAlaSerAlaLeuCysThrPheValLeuProLeu.....Le 19
                                                                                                                                                                                                                                                                                                GCTGGGCCCCAACACGGTGTCCAATTCCATTGGCGACATCCACCGCAACA
                                                                                                                                                                                                                                                                                                                            eLeuGlySerGlyCysLeuSerAsnLeuHisAspSerSerHisLysGlnA 136
                              rCysGlyGluArgGlyLeuLeuValTyrProGluValLysArgLeuMetP 186
                                                                                                                                                                                              AGCGCAAGGTCTTCTCCAAGATCTTCAGCCACGAGGCCCTGGAGAGTTAC
                                                                                                                                                                                                                                            rgLysLysValIleMetArgAlaPheSerArgGluAlaLeuGluCysTyr 152
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(KLPIPRGSMGFPLIGETGHMILQGSGFQSSRREKYGNVFKYHLIGRPLIRYTGAENV
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P450RAI-2"
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Gaps: 9
Percent Identity: 44.242
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122

36

72

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169

479 hrValTyrProValAspAsnLeuProAlaArgPhe 490

422 136 372 119

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Synechocystis sp. (strain:PCC6803) DNA.
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Synechocystis sp. PCC6803 complete genome,
D64003 AB001339
D64003.1 GI:1001200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome DNA Res. 2 (4), 153-166 (1995) 96127529
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1 (bases 1 to 113064)
Kaneko,T., Tanaka,A., Sato,S., Kotani,H., Sazuka,T., Miyajima,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                     Potential protein coding regions were assigned on the basis of similarity search of the ORFs and GeneMark analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (30-AUG-1995) to the DDBJ/EMBL/GenBank databases. Satoshi Tabata, Kazusa DNA Research Institute, Gene Structure 2; 1532-3 Yanauchino, Kisarazu, Chiba 292, Japan (E-mail:tabata@kazusa.or.jp, Tel:0438-52-3933, Fax:0438-52-3934)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Res. 3 (3), 109-136 (1996) 97061201
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                                                                                                                                                                       complement(1. .3960)
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                                                                                                                                                                                                                                                                                                                                                   .113064
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22/27, 2755703-2868766.
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Quality:
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41 AlaLeuProLeuProProGlyThrMetGlyPheProPhePheGlyGluTh :::|||||:::|||| :::||||
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Gaps: 8
Percent Identity: 33.703
                                                                                                                                                   to: 113064
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91 62334	ValMetGlyAlaAspAsnValArgArgIleLeuLeuGlyAspAspArgLe:::: :::::: ::::::	107 62383
107 62384	UValSerValHisTrpProAlaSerValArgThrIleLeuGlySerGlyC 1 :::::	124 52433
124 62434	YSLEUSERASDLEUHISASPSERSERHISLYSG1DARGLYSLYSVAIIle 1 :: :::: ::: ::::	L40 52483
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341 63024	GlnAspAsnLysLeuAspMetGluIleLeuGluGlnLeuLysTyrIleGl 3 :::::::	57 3073

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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                           REFERENCE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus CYP26 (AF185266
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasiani Phasianiane; Gallus; Loses 1 to 322)

1 (bases 1 to 322)

Martines-Ceballos, E. and Burdsal, C.A.
                                                                                                                                                                                                                                                                             Direct Submission
Submitted (09-SEP-1999) Cell and
University, 2000 Stern Hall 6400
                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus
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/db_xref="taxon:9031"
                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                              enzyme"
                                                                                  /codon_start=2
                                                                                                                 /note="contains
                                                                                                                                  /gene="CYP26"
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; (СҮР26) п
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Freret St., New Orleans,
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                                                                                                                                                                                                                                                                                                                  KEYWORDS
SOURCE
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VERSION
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Quality:
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                                                                                                                                                                                                                                                                                                        Taxus cuspidata.
Taxus cuspidata
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
                                                                                                                                                                                                 Schoendorf, A., Rithner, C.D., Williams, R.M. and Croteau, R.B. Molecular cloning of a cytochrome P450 taxane 10beta-hydroxylase cDNA from Taxus and functional expression in yeast proc. Natl. Acad. Sci. U.S.A. 98 (4), 1501-1506 (2001)
                                                                                                                                                                                                                                                                                                                                                                         AF318211
AF318211.1 GI:12656591
                                                                                                                                                                                                                                                                                                                                                                                                                          Taxus cuspidata
                                                                                  Direct Submission
Submitted (30-CCT-2000) Institute of I
Submitted National State University, Pullman,
Location/Qualifiers
                                                                                                                                                                                                                                                                        Coniferopsida; Coniferales; Taxaceae; 1 (bases 1 to 1494)
                                                                                                                                                                                                                                                                                                                                                                                                          complete cds.
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Schoendorf, A. and Croteau, R.
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97.196
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5-alpha-taxadienol-10-beta-hydroxylase mRNA,
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Gaps:
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                                                                                                         of Biological Chemistry,
man, WA 99164, USA
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alignment_block:
US-09-668-482-4 x AF318211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 ProAlaLeuLeuAlaSerAlaLeuCysThrPheValLeuProLeuLeuLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAGAGGGCTTATCTTCTCCATTGCAAGCACCCTGTTTTTCGAT.....
                                  alLysArgLeuMetPheArgIleAlaMetArgIleLeuLeuGlyCysGlu 197
                                                                                                                                                                                 TTACAAAATTATCTGGGTAGAATGAGTTCAGAAATAGGACACCATTTCAA
                                                                                                                                                                                                                             LeuGluCysTyrValProValIleThrGluGluValGlySerSerLeu..
                                                                                                                                                                                                                                                                                                                    erHisLysGlnArgLysLysVallleMetArgAlaPheSerArgGluAla 148
                                                                                                                                                                                                                                                                                                                                                                                                                 rValArgThrIleLeuGlySerGlyCysLeuSerAsnLeuHisAspSerS 132
                                                                                                 TGAAAAATGGAAG
                                                                                                                                                                                                                                                                             ATCATCGCATCTTACGCACTGCACTTGCTCGGTTTTTGGGCGCTCAAGCT
                                                                                                                                                                                                                                                                                                                                                                     TTTCATGAAACTGATTGGGGAAGATTCCATTGTTGCTAAAAGAGGCGAGG
                                                                                                                                   .GluGlnTrpLeuSerCysGlyGluArgGlyLeuLeuValTyrProGluV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCACCGATCCTCTTAAACTTCCCCCTGGAAAGTTAGGTTTTCCTCTC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spargSerCysalaLeuProLeuProProGlyThrMetGlyPheProPhe 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAGTTTTTTGATGATAGATTGAAGAAATTCGGTCCTGTTTACATGACTT 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysPheLeuGlnMetLysArgArgLysTyrGlyPheIleTyrLysThrH 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTGCTATTCTTTCCCTTACCCTCGCACCTATTCTCGCCATTATTCTTCT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
Ratio:
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315 c 314 g 436 t
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/protein_id="AAK00946.1"
/db_xref="GI:12656592"
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	TATCAGATCACTACCTCCTCCCTGCC 1458	476 1430
176 429	uAlaArgHisCysAspTrpGlnLeuLeuAsnGlyProProThrMetLysT 4 ::::::::::::::::::::::::::::::::::::	a ப
159 1379	ValGlyLysGluPheAlaLysIleLeuLeuLysIlePheThrValGluLe 4	443 1330
142 1329	PheSerPheIleProPheGlyGlyGlyLeuArgSerCys 4	430 1280
129 1279	uPheAsnProAspArgPheSerAlaProHisProGluAspAlaSerArg. 4 ::: ::: ATTCAGGCCTTCAAGATTT	413 1245
413 1244	SerileCysAspThrHisAspValalaGluIlePheThrAsnLysGluGl 4	397 1195
396 119 4	hrPheGluLeuAsnGlyTyrGlnIleProLysGlyTrpAsnValIleTyr 3 ::::::::::::::	380 11 4 5
380 1144	rLeuArgLeuAsnProProValProGlyGlyPheArgValAlaLeuLysT: :::	363 1095
363 1094	MetGluIleLeuGluGlnLeuLysTyrIleGlyCysValIleLysGluTh : :::	347 1045
346 1044	euLysSerLysGlyLeuLeuCysLysSerAsnGlnAspAsnLysLeuAsp ::::::::::::::::::::::::::::::::::	330 1004
330 1003	rTyrLeuGlyLeuTyrProHisValLeuGlnLysValArgGluGluL ::: ::: ::: ::: GCTTCTATACTCCAATCCTGAATACCATGAAAAAGTATTTCAAGAGCAGT	314 954
314 953	LeuPheGlyGlyHisGluThrThrAlaSerAlaAlaThrSerLeuIleTh 	298 904
297 903	rgGlyGluArgLeuAspMetGlnAlaLeuLysGlnSerSerThrGluLeu :: :::	281 854
281 853	yGlnGlyCysLysAspAlaLeuGlnLeuLeuIleGluHisSerTrpGluA ::::	26 4 807
264 806	3 GluGlnAsnIleArgAlaLysIleCysGlyLeuArgAlaSerGluAlaGl ::::: :::	248 75:
247 756	<pre>l erGlyLeuTyrArgGlyMetLysAlaArgAsnLeuIleHisAlaArgIle :: ::: :::: / CTCGTTATCGTAAAGGGCTTCAGGCGCGGCTGAAGCTTGATGAAATTCTC</pre>	231 707
231 706	4 eGluGluMetThrArgAsnLeuPhoSerLeuProIleAspValProPheS : ::: ::: : GGAAACTATTCTTGTGGGAAGTTTGTCAGTCCCGCTGGACTTTCCAGGAA	214 657
21 4 656	8 ProGlnLeuAlaGlyAspGlyAspSerGluGlnGlnLeuValGluAlaPh :::::: :::::: 6GTAAATGATGGACACCCAACAGAAGCAACTTCATCATCTTCT	19

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 2050, USA On Dec 17. 1999 this sequence version replaced gi:4512656. The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE). Simple repeats were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for the latest are named to indicate the level of evidence for the latest are named to indicate the level of evidence for the latest are named to indicate the level of evidence for the latest are named to indicate the level of evidence for the latest are named to indicate the l
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                                                                                                                                                                                                                                                                                                                                              F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy peterson, Michael Holmes, and Delwood Richardson for software and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genes were identified by a combination of three methods: Gene
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20083487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      We thank the CSHL/WashU/ABI consortium for sequencing BAC clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are
numbered from the top to bottom of the chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10617197
                                                                                                         This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.
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Address all correspondence to:
                                                                                                                                                                                                                                                                                                                                  Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, F
Peterson, Michael Holmes, and Delwood Richardson
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           at@tigr.org
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<1226. .>2344
/gene="At2g42650"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(7700, .7818
8844. 8989,9294. 9396))
/gene="ktzg42670"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="F7D19.34; predicted by genscan"
complement(join(2761. .2943,3035. .3164,3258. .3372,
3450. .3489,3570. .3646,3732. .3954))
/gene="AtJq42660"
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Sequence from clone F7D19"
complement(join(<2761. .2943,3035.
3450. .3489,3570. .3646,3732. .>395
/gene="At2942660"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Translation="msrvspktyddavkalvkegneksrtekpolleedgeffluval
kkipornftnayriplphplinttedspelcliiddreesglipedakkniksenipi
rkvvklsklkedygspeskrkicdsydmefsbrrviphkligkkffgskffpval
lkhnnwkeqiekacgaamffmrtgscsaikvaklsmesddivenvtatlngvvdylps
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<1226. .>2344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(<7700...78
8844...8989,9294...>9396))
/gene="At2g42670"
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5756. .5806
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KTKKKNGKIHEVRYMDSNVSETLGDDEFDRSVGEDEVADDLNASGDKKKRKKMSSSKS
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/db_xref="GI:6598642"
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/gene="At2g42650"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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TNLGGNFLMRPSSWFSGLCRNDRDSTENKTLPLLEIRKKNNEKRVRDEEVSSVKRLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAD21740.1"
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/db_xref="GI:4512686"
/translation="MAGRSSPGKCSTWLDLNREETVEKNNEEESSVEDEDQITNNVRQ
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/note="F7F17
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                                                                                                                                                                                                                                                /translation="mpyfaqrlyntckasfssdgpitedalekvrnvlekiresdvgi
Eqdaqlarshggplanrngsbysppairylhhecdsfsigiromppssmiplhnhpg
MTVLSKLYVGSMHVKSYDMLEPQLTBPEDEPSGEARPAKIVKOTEMTAGSPVTTLYPKS
GGNIHCFKAITHCAILDILAPPYSSEHDRHCTYFRKSRREDLPGELEVDGEVVTDVTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(<7700. .>9396)
/gene="At2g42670"
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                                                                                                                                            10075
                                                                                                                                                                                           LEEFOPPDDFVIRRIPYRGPVIRT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAD21739.1"
/db_xref="GI:4512685"
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                                                                                  /rpt_family="(GAA)n"
                                                                                                                                                  .1015
                                   .10809,11165. .11248,11522. .11604,11693. .11994)
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alignment_scores:
Quality:
Ratio:
Percent Similarity:
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US-09-668-482-4 x AC006931
                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AC006931
                                                                                                                                   67490 CTTCTTCCTGGAGAAATGGGGCTTCCATGGATTGGTGAAACAATGGATTT 67539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
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                                                                                                                                                                                                                                                                       44 LeuProProGlyThrMetGlyPheProPhePheGlyGluThrLeuGlnMe 60
60 tValLeuGlnArgArgLys......PheLeuGlnMetL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /PIOTEIN_id="AAD21736.1"
/POTEIN_id="AAD21736.1"
/POTEIN_id="AAD21736"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative lipase"
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/product="putative lipase"
/product="gi:4512683"
/farsiation="MATTTTSWEELLGSKNWDTILDPLDQSLRELILRCGDFCQATYD
AfVNNDONSKYCGASRYGKSSFPDKVMLENASDYEVNWFLYATARVSLDEGLLLQSQSR
DSWDRESNWFGYIAVTSDEERSKALGRREIYILLRGTSRNYEWVNLGARPTSADPLLH
GPEQDDGSGGVVEGTTFDSDSEDEEGCKVMLGWLTIYTSNHPESKFTKLSLRSQLLAKI
GPEQDDGSGGVVEGTTFDSDSEDEEGCKVMLGWLTIYTSNHPESKFTKLSLRSQLLAKI
GECHLLKYKDEKPSIVLTGHSLGATEAVLAAVDIAENGSDDVPVTAIVFGCPQVGNKE
FRDEVMSHKNLKLILHVRNTIDLLTRYPGGLGYVENGGLINFVIDTKKSFPLSDRNPGD
WHNLQAMLHVVAGWNGKKGEFKLMYKRSIALVNKSCEFLKAECLVPGSWWVEKNKGLI
KNEDGEWYLAPVEEEBPVPEF"
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1.683
52.852
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GNLKFLNGLTEELEGRLNRLKSEETKEIPSDDQLDIDALDDDPWGKWGDEEEEEVDNS
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/POODUL_5-GAD21738.1"
/POODUL_5-GAD21738
/POODUL5-GAD21738
/POODUL5-GA
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15513. .15664,15832. .17384,17446. .17514,17602. .17730)
/gene="At2g42700"
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/gene="At2g42690"
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/gene="At2g42690"
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/gene="At2g42700"
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/gene="At2g42680"
/note="unknown protein"
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3. .15664,15832. .17364,17446. .17514,17602. .17786)</pre>
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Gaps: 14
Percent Identity: 26.046
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336	sValArgGluGluLeuLysSerLysGlyLeuL	325
68376	CAAGGTAACAATCAACTGAATATCAGAATGTTCTCTTCCTATCAGCAAAA	68327
325	HisValLeuGlnLy	321
68326	TGACTTTCAAGATGTTAGCTCAGCACCCAACTTGTCGTGACACTCTCCTT	68277
2	9510111	
311 68276	LeuLeuPheGlyGlyHisGluThrThrAlaSerAlaAlaThrS	297 68227
80 (GAAGAGTTGATCAAAGGTGTGATAA	
96	MetGlnAlaLeuLvsGlnSerSerThrGlu	28
286 68176	laLeuGlnLeuIleGluHisSerTrpGluArgGlyGluArgLeuAsp	270 68148
270 681 4 7	aLysIleCysGlyLeuArgAlaSerGluAlaGlyGlnGlyCy:	253 68110
253 68109	'MetLysAlaArgAsnLeuIleHisAlaArgIleGluGlnAsnIleArgAl ::::: AAGAAAGCAAGGCTAGAGATAGAGACATTTCTAGTTGGGAAGGTCAGGGA	237 68060
236 68059	snLeuPheSerLeuProIleAspValProPheSerGlyLeuTyrArgGly :::: ::: ::: ::: :::	220 68010
220 68009	pGlyAspSerGluGlnGlnLeuValGluAlaPheGluGluMetThrArgA 	203 67979
203 67978	ArgIleAlaMetArgIleLeuLeuGlyCysGluProGlnLeuAlaGlyAs	187 67934
186 67933	ysGlyGluArgGl ::::: GGCAAGGAAGA	170 67886
170 67885	OVALIIEThrGluGluValGlySerSerLeuGluGlnTrpLeuSerC ::	154 67840
154 67839	LysVallleMetArgAlaPheSerArgGluAlaLeuGluCysTyrValPr 	138 67790
137 67789	lySerGlyCysLeuSerAsnLeuHisAspSerSerHisLysGlnArgLys 	121 67740
121 67739	paspargLeuValSerValHisTrpProAlaSerValArgThrIleLeuG 	104 67690
104 67689	ThrValArgValMetGlyAlaAspAsnValArgArgIleLeuLeuGlyAs	88 67640
87 67639	ysArgArgLysTyrGlyPheIleTyrLysThrHisLeuPheGlyArgPro 	71 67590
67589	: : : : : : : : : : : : : : : : : : :	67540

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MEDLINE
REFERENCE
AUTHORS
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KEYWORDS
                                                                                                                                                                                                                                                                                                                        DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                              seq_name:
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                                                                                        TITLE
                                                                                                                           AUTHORS
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                                                      JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leProPheGlyGlyGlyLeuArgSerCysValGlyLysGluPheAlaLys 449
                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCTTGGAATGCCAATCAAAATTTCT 68990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alAspAsnLeuProAlaArgPheThr 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTAGTCTACCCAGATGAGACAATTAGCATGGATCCTCTCCCATTTCCGT 68964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACCATTTGGAGGTGGACCAAGGCTTTGTGCAGGTCACCAACTAGCCAAA 68864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAATAAACCTCTGCTTCTTTGTTTGAATGCAGATACTCTGGACCACTTAT 68726
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                                                                                                                                                                                                                                                                                          Arabidopsis thaliana complete cds.
                                                    Peacock, W.J.
The CYP88A cytochrome P450, ent-kaurenoic acid oxidase, catalyzes three steps of the gibberellin biosynthesis pathway proc. Natl. Acad. Sci. U.S.A. 98 (4), 2065-2070 (2001)
                                                                                                                                        Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaces; Arabidopsis.

1 (bases 1 to 1487)
                                                                                                                                                                                                                 Arabidopsis thaliana
                                                                                                                      Helliwell, C.A., Chandler, P.M., Poole, A., Dennis, E.S. and
                                                                                                                                                                                                                                  thale cress.
                                                                                                                                                                                                                                                                      AF318500.1 GI:13021852
 2 (bases 1 to 1487)
Helliwell,C.A., Peacock,J. and Dennis,L
                                                                                                                                                                                                                                                                                                                              ent-kaurenoic acid
                                                                                                                                                                                                                                                                                                                                             mRNA
                                                                                                                                                                                                                                                                                                                            hydroxylase (KAO1) mRNA,
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alignment_block:
US-09-668-482-4 x AF318500
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Quality:
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                                    sGlnArgLysLysValIleMetArgAlaPheSer...ArgGluAlaLeuG
                                                                                                                                                                                                              euLeuGlyAspAspArgLeuValSerValHisTrpProAlaSerValArg 117
                                                                                                                                                                                                                                                                                                      eGlyArgProThrValArgValMetGlyAlaAspAsnValArgArgIleL 101
GCGGCTCAGGCGTTTGACTGCTGCTCCAGTCAATGGCCATGAAGCCCTCT
                                                                                       GAACTCATTGGAAGGAAATCATTCGTTGGTATCTCTTTCGAGGAACACAA
                                                                                                                              ThrIleLeuGlySerGlyCysLeuSerAsnLeuHisAspSerSerHisLy
                                                                                                                                                                         TGACAGACGATGATGCGTTC...AAGCCAGGTTGGCCAACATCTACAATG
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Submitted (02-NOV-2000) Plant Industry, CSIRO, Clunie Ross Street,
Canberra, ACT 2601, Australia
Cantherra, ACT 2601, Australia
1. .1487
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DTCRRVLTDDDAFKPGWPTSTMELIGRKSFVGISFEEHKRLRELTAAPVNGHEALSTY
IPYIBENVITVLDKWIKMGEFEFLTHLRKLTFRIIMYIFLSSESENVMDALEREYTAL
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/protein_id="AAK11564.1"
/db_xref="GI:13021853"
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15. .1487
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/db_xref="taxon:3702"
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                       rPheIleProPheGlyGlyGlyLeuArgSerCysValGlyLysGluPheA 448
                                                                         GATCCTGCTAGATGGGATAATGGTTTTGTACCAAAAGCTGGT.....GC 1297
                                                                                                                                                                                     leCysAspThrHisAspValAlaGluIlePheThrAsnLysGluGluPhe 414
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                                                                                                          AsnProAspArgPheSerAlaProHisProGluAspAlaSerArgPheSe 431
                                                                                                                                                  TTAGGGATGTCCACATCGACCCTGAAGTCTTTCCAGATCCAAGAAAATTT 1253
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alignment_block:
US-09-668-482-4 x SLU54770
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AUTHORS
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                                                                                                                          Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l (bases 1 to 1395)
Bishop,G.J., Harrison,K. and Jones,J.D.
The tomato Dwarf gene isolated by heterologous transposon
encodes the first member of a new cytochrome P450 family
Plant Cell 8 (6), 959-969 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Solanum lycopersicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (11-APR-1996) Gerard Bishop, Sainsbury Innes Centre, Colney Lane, Norwich, Norfolk, NR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bishop,G.
Direct Submission
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U54770.1 GI:1421740
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    to: SLU54770
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                                                                                                                                                                                                                                                                 /product="cytochrome P450 homolog"
/product="cytochrome P450 homolog"
/protein_id="AABI7070.1"
/db_xref="gi:1421741"
/db_xref="gi:1421741"
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KVIDIOEKTNKNAFLSSLKQIAGIESTSLAQEEWSEFNLVLGTISLPINLDHTNYHR
KVIDIOEKTNKNAFLSSLKQIAGIESTSLAQEEWSEFNLVLGTISLPINLDHTNYHR
GFQARKIIVNLLRTLIEERRASKEIQHDMLGYLMNEAATRFKLTDDEMIDLITTILYS
GYETYSTTSMMAVKYLHDHPKYLEELRKEHMAIREKKEDEPIDYNDYRSMRSTRAVI
LETSRLATIVNGVLRKTTQDMEINGYIIPKGWRIYYTRELNYDPRLYDDPYSFNPWR
WMDKSLEHQNSFLYFGGGTRQCPGKELGVAEISTFLHYFVTKYRWEEIGGDKLMKFPR
VALPMGLRINVSAH"
                                                                                                    444.00
1.620
58.672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="dwarf"
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/strain="GCR758"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="dwarf"
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REFERENCE
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TITLE
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LOCUS AF318501
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                                                                                                                                                                                                       1 (bases 1 to 1740)
Helliwell, C.A., Chandler, P.M., Poole, A., Dennis, E.S. Peacock, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                        AF318501
                                                    Submitted (02-NOV-2000) Plant Canberra, ACT 2601, Australia Location/Qualifiers
                                                                                                            2 (bases 1 to 1740)
Helliwell,C.A., Peac
Direct Submission
                                                                                                                                                                                    The CYP88A cytochrome P450, ent-kaurenoic acid oxidase, three steps of the gibberellin biosynthesis pathway
                                                                                                                                                                                                                                                                                                                                                                 thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                              complete
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                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                   Brassicales; Brassicaceae; Arabidopsis.
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                                          1. .1740
/organism="Arabidopsis
/db_xref="taxon:3702"
                                                                                                                                    Peacock, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ent-kaurenoic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
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                                                                                                                                      Dennis, L.
                      thaliana"
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hydroxylase (KAO2) mRNA,
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140 IleMetArgAlaPheSer...ArgGluAlaLeuGluCysTyrValProVa 155
                                                                                                                                           458 AGTCCTTTGTTGGTATCTCCTTTGAAGAACACAAGAGGCTCAGGCGTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
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                                                                                                                                                                                                                       lyCysLeuSerAsnLeuHisAspSerSerHisLysGlnArgLysLysVal 139
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239 787	INILEARGALALYSIL	255 833
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	THE THE CONTRACT OF THE CONTRA	32/
422 328	roHisProGluAspAlaSerArgPheSerPheIleProPheGlyGlyGly 4	368
439	rgSerCysValGlyLysGluPheAlaLysIleLeuLeuLysIleP	55
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                                                     This nucleotide sequence encodes the human cytochrome P450RAI. Its expression is dependent on the presence of retinoic acid (RA). The retinoid-regulated genes such as the inducible cytochrome P450RAI gene specifically metabolises a derivative of the RA. The cytochrome P450 gene in general produces enzymes involved in the oxidative metabolism of endogenous and exogenous compounds. The cytochrome P450 nucleotide sequence can be used to induce or suppress the expression of its protein. P450RAI is highly induced by RA in cell lines and tissues. This allows for development of a drug screen using promoters and nucleotide sequences to identify drugs which are useful for reducing the catabolism of RA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Retinoid regulated gene; cytochrome P450 oxidative metabolism; P450RAI; retinoic a
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P-PSDB; AAW37734.
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                                                                                             Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid; human; inhibitor; antisense; cancer; actinic keratosis; oral leukoplakia; head tumour; neck tumour; non-small cell lung carcinoma; basal cell carcinoma; acute promyelocytic leukaemia; skin cancer; acne; psoriasis; acute promyelocytic leukaemia; skin cancer; acne; psoriasis;
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                                                                                                                                                                                                                                                                           /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV12204
                                                                                                                                                                                                                                           1494
                                                                                    skin cancer; acne; psoriasis;
screening; cytochrome P450;
                                                                                                                                                                                                                                                                                                    1491
                                                                                                                                                                                                                                                                                                                          497
                                                                                                                                                                                                                                                                                                                                                                                                                      467
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23-JUN-1997;

97WO-CA00440

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alignment_block:
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CC laimed
                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 2611.00
Ratio: 5.254
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AAV12204
                                                                                                                                                                                                                                                                                                                                                                                                 US-09-668-482-4 x AAV12204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Retinoid metabolising protein - useful to develop products to treat, e.g. cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-077178/07.
P-PSDB; AAW44160.
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21-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1494 BP;
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                                                                                                                                                                          GCTGCTGCTCTTCCTGGCTGCGATCAAGCTCTGGGACCTGTACTGCGTGA
                                                                                                                                                                                                                                                        ATGGGGCTCCCGGCGCTGCTGCCAGTGCGCTCTGCACCTTCGTGCTGCC
                                                                                                                                                                                                                                                                                                                       MetGlyLeuProAlaLeuLeuAlaSerAlaLeuCysThrPheValLeuPr 17
heGlyArgProThrValArgValMetGlyAlaAspAsnValArgArgIle
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96US-0667546.
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGCTCGGAGACGACCGGCTGGTCTCGGTCCACTGGCCAGCGTCGGTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCGGGCGGCCCACCGTACGGGTGATGGGCGCGCGCACAATGTGCGGCGCATC
                                                                                                                                                                                                                                                                                                                                                                                  TCATGTTCCGAATCGCCATGCGCATCCTACTGGGCTGCGAACCCCCAACTG
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                                                                                                                                                                                          GCGGGCGACGGGACTCCGAGCAGCAGCTTGTGGAGGCCTTCGAGGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaGlyAspGlyAspSerGluGlnGlnLeuValGluAlaPheGluGluMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGAGCTGCGGCGAGCGCGCCTCCTGGTCTACCCCGAGGTGAAGCGCC
                                                                                                                                                    SLysAspAlaLeuGlnLeuLeuIleGluHisSerTrpGluArgGlyGluA 284
GAACAACTTAAATACATCGGGTGTGTTATTAAGGAGACCCTTCGACTGAA
                                                                                      GluGlnLeuLysTyrIleGlyCysValIleLysGluThrLeuArgLeuAs
                                                                                                                CAAAGACGCGCTGCAGCTGTTGATCGAGCACTCGTGGGAGAGGGGGAGAGC
                                                                                                                                                                                                                                                                                                          ATTCGCGCCAAGATCTGCGGGCTGCGGGCCATCCGAGGCGGGCCAGGGCTG
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seq_documentation_block:
ID AAA60752 standard; cDNA; 21
XX
AC AAA60752;
XX
DT 31-OCT-2000 (first entry)
XX
DF 31-OCT-2000 (first entry)
XX
DF 31-OCT-2000 (first entry)
XX
DF Human PSEC64 encoding nucle
XX
CS Homo sapiens.

I Location/Qu
FH Key 46..696
FT CDS 46..696
FT CDS /*tag= a
FT //product= "pro
XX
FH Key JP2000152790-A.
XX
PD 06-JUN-2000.
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PD 06-JUN-2000.
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PP 19-NOV-1998; 98JP-0329989
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PP 19-NOV-199
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                                                              The present sequence encodes a human protein, designated PSEC64, which is related to neuron growth. The PSEC64 protein and its gene can be used for the development of a preventive agent for use in the treatment of diseases in which nerves are involved.
                                                                                                                                                                                                                Claim 2; Page 8-10; 13pp; Japanese.
                                                                                                                                                                                                                                                                                    A protein related to the growth of neuron and a gene encoding protein \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HERI-) HERIKKUSU KENKYUSHO KK
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/product= "PSEC64"
/note= "protein related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
      509 A; 510 C;
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      547 G;
      558 T; 0 other;
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alignment_scores:

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Align seg 1/1 to: AAA60752
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ATTCGCGCCAAGATCTGCGGGCTGCGGGCATCCGAGGCGGGCCAGGGCTG
                                                                              AlaGlyAspGlyAspSerGluGlnGlnLeuValGluAlaPheGluGluMe
                                                                                                                                                                                                                                                                                     IleArgAlaLysIleCysGlyLeuArgAlaSerGluAlaGlyGlnGlyCy
                                                 pLeuSerCysGlyGluArgGlyLeuLeuValTyrProGluValLysArgL
                                                                                                                                                                                                                                             heGlyArgProThrValArgValMetGlyAlaAspAsnValArgArgIle
                                      ACCGGGGCATGAAGGCGCGGAACCTCATTCACGCGCGCATCGAGCAGAAC
                                                                                                                      GCGGGCGACGGGACTCCGAGCAGCAGCTTGTGGAGGCCTTCGAGGA.AT
                                                                                                                                                               TCATGTTCCGAATCGCCATGCGCATCCTACTGGGCTGCGAACCCCAACTG
                                                                                                                                                                                                       GCTGAGCTGCGGCGAGCGCCGCCTCCTGGTCTACCCCGAGGTGAAGCGCC
                                                                                                                                                                                                                                                                                                                                         gThrIleLeuGlySerGlyCysLeuSerAsnLeuHisAspSerSerHisL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PheProPhePheGlyGluThrLeuGlnMetValLeuGlnArgArgLysPh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTGCAGATGAAGCGCAGGAAATACGGCTTCATCTACAAGACGCATCTGT
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Ratio:
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Gaps: 0
Percent Identity: 99.195
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AAV09252 standard;
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                                     Retinoid regulated gene; cytochrome P450 gene; enzyme; oxidative metabolism; P450RAI; retinoic acid; RA; prom
Synthetic
                                                                             Cytochrome
                                                                                                      07-JUL-1998
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                                                                             P450RAI isoform cDNA sequence
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                                        promoter;
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alignment_block:
US-09-668-482-4 x AAV09252
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                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      This nucleotide sequence encoding an isoform of cytochrome P450RAI. Its expression is dependent on the presence of retinoic acid (RA). The retinoid-regulated genes such as the inducible cytochrome P450RAI gene specifically metabolises a derivative of the RA. The cytochrome P450 gene in general produces enzymes involved in the oxidative metabolism of endogenous and exogenous compounds. The cytochrome P450 nucleotide sequence can be used to induce or suppress the expression of its protein. P450RAI is highly induced by RA in cell lines and tissues. This allows for development of a drug screen using promoters and nucleotide sequences to identify drugs which are useful for reducing the catabolism of RA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying DNA encoding inducible or suppressible cytochrome P450 by screening for drugs which reduce the catabolism of retinoic acid, useful in cancer chemotherapy and the treatment of acne and
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P-PSDB; AAW37735.
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21-JUN-1996;
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                                                                                                                          erGlyArgAspArgSerCysAlaLeuProLeuProProGlyThrMetGly
                                                                                                                                                                  TTCCCATTCTTTGGGGAAACATTGCAGATGGTGCTTCAGCGGAGGAAGTT
                                                                                                              GCAGCCGCGATCGCAGCTGCGCCCTCCCCTTGCCCCCGGTACCATGGGC
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96US-0667546.
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Gaps: 0
Percent Identity: 93.360
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                                                                                                                                          AlaGlyAspGlyAspSerGluGlnGlnLeuValGluAlaPheGluGluMe
                                                                      GluGlnLeuLysTyrIleGlyCysValIleLysGluThrLeuArgLeuAs 367
                                                                                                              lyLeuLeuCysLysSerAsnGlnAspAsnLysLeuAspMetGluIleLeu
                                                                                                                                                                                                                                                                snGlyTyrGlnIleProLysGlyTrpAsnValIleTyrSerIleCysAsp 400
                                nProProValProGlyGlyPheArgValAlaLeuLysThrPheGluLeuA 384
                                                            GAACAGCTTAAATACATTGGGTGTGTCATTAAGGAGACCCTGCGATTGAA
                                                                                                    GCTTACTTTGCAAGAGCAATCAAGACAACAAGTTAGACATGGAAACTTTG
                                                                                                                                                                                   GGTCATGAAACTACAGCCAGTGCTGCGACATCACTGATCACTTACCTAGG
                                                                                                                                                                                             GlyHisGluThrThrAlaSerAlaAlaThrSerLeuIleThrTyrLeuGl 317
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              Claim 15; Page 62-64; 110pp; English
                                      Retinoid metabolising e.g. cancer, actinic lichthyosis
                                                                                                                                                                                                                                                                                                                                                                Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid; mouse; inhibitor; antisense; cancer; actinic keratosis; oral leukoplakia; head tumour; neck tumour; non-small cell lung carcinoma; basal cell carcinoma; acute promyelocytic leukaemia; skin cancer; acne; psoriasis; acute promyelocytic leukaemia; skin cancer; acne; psoriasis;
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                                                 products to treat, acne, psoriasis or
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alignment_block:
US-09-668-482-4 x AAV12205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This cDNA clone codes for a novel mouse retinoid metabolising protein (see AAW44160) designated mp450RAI. The encoded protein is a retinoid oxidase that has the ability to hydroxylate retinoic acid at the 4 position of the beta-ionone ring and is inducible in cepithelial cells exposed to retinoic acid. The clone was isolated from a retinoic acid-treated p19 teratocarcinoma CDNA library using human p450RAI cDNA (see AAV12204) as probe. Zebrafish, human acid mouse p450RAI cDNA clones (see AAV12203-05) are claimed. They can be used in the recombinant production of p450RAI proteins. Antisense nucleic acids can be used in a claimed method for cancer extinoic acid hydroxylation for the treatment of cancer, and/or neck, non-small ceil lung carcinomas, basal cell carcinomas, cacute promyelocytic leukaemia, skin cancer, and premalignancy associated with actinic keratosis, acne, psoriasis and/or the P450RAI cacute passociated with actinic keratosis, acne, psoriasis and/or the P450RAI cacute passociated sequences (see AAV12206-08) for the P450RAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AAV12205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PheProPhePheGlyGluThrLeuGlnMetValLeuGlnArgArgLysPh
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                                                            CysTyrValProValIleThrGluGluValGlySerSerLeuGluGlnTr 167
                                                                                                                                                                                                                                                                              TTGCTGGGAGAGCACCGGTTGGTCTCGGTGCACTGGCCCGCGTCGGTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCCCATTCTTTGGGGAAACATTGCAGATGGTGCTTCAGCGGAGGAAGTT
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                                                                                                                                        ysGlnArgLysLysVallleMetArgAlaPheSerArgGluAlaLeuGlu 150
                                                                                                                                                                                                  CACCATCCTGGGCGCTGCCTCTCCAACCTGCACGATTCCTCGCACA
                                                                                                                                                                                                                 gThrIleLeuGlySerGlyCysLeuSerAsnLeuHlsAspSerSerHisL 134
                                   pLeuSerCysGlyGluArgGlyLeuLeuValTyrProGluValLysArgL
                                                                                                                     AGCAGCGAAAGAAGGTGATTATGCAGGCCTTCAGCCGCGAGGCACTCCAG
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Ratio: 5.035
milarity: 97.384
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||TCATGTTCCGCATCGCCATGCGCATCCTGCTGGGCTGCGAGCCGGGTCCA
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                                                                                                                         lyLeuLeuCysLysSerAsnGlnAspAsnLysLeuAspMetGluIleLeu
                                                                                                                                                                                                                                                                                                                                                                                  ACTCTACCCACATGTCCTCCAGAAAGTTCGAGAAGAGATAAAAGAGCAAGG
                                                                                                                                                                                                                                                                                                                                                                                            LeuLeuLysIlePheThrValGluLeuAlaArgHisCysAspTrpGlnLe 467
                                                                                                                                                                                ThrHisAspValAlaGluIlePheThrAsnLysGluGluPheAsnProAs
                                                                                                                                                                                                                      TCTAAATGGACCTCCTACAATGAAGACAAGCCCCACTGTGTACCCTGTGG
          uLeuAsnGlyProProThrMetLysThrSerProThrValTyrProValA 484
                                        CTTCTTAAGATATTTACAGTGGAGCTGGCTAGGCACTGTGATTGGCAGCT
                                                                                 roPheGlyGlyGlyLeuArgSerCysValGlyLysGluPheAlaLysIle 450
                                                                                                                                                                    ACCCACGATGTGGCAGATATCTTCACTAACAAGGAGGAATTTAATCCCGA
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497

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alignment_block:
US-09-668-482-4 x AAV09251
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                                            Percent Similarity:
                                                                                                                                                     This nucleotide sequence encodes the cytochrome zP450RAI of the zebra fish. Its expression is dependent on the presence of retinoic acid (RA). The retinoid-regulated genes such as the inducible cytochrome P450RAI gene specifically metabolises a derivative of the RA. The cytochrome P450 gene in general produces enzymes involved in the oxidative metabolism of endogenous and exogenous compounds. The cytochrome P450 nucleotide sequence can be used to induce or suppress the expression of its protein. P450RAI is highly induced by RA in cell lines and tissues. This allows for development of a drug screen using promoters and nucleotide sequences to identify drugs which are useful for reducing the catabolism of RA.
                                                                                                                              Sequence 1850 BP; 519 A; 391 C; 454 G; 486 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                               Identifying DNA encoding inducible or suppressible cytochrome E by screening for drugs which reduce the catabolism of retinoic useful in cancer chemotherapy and the treatment of acne and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Retinoid regulated gene; cytochrome P450 gene; enzyme; oxidative metabolism; P450RAI; retinoic acid; RA; promoter;
                                                                                                                                                                                                                                                                                                                                     Disclosure; Pages 59B-59D; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytochrome zP450RAI cDNA sequence
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Ratio: 4.080
milarity: 85.714
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96US-0667546
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68.008
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Align seg 1/1

to: AAV09251

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767
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GAAGTGACGAACCTTTTAGTTTGCAGGCGATGAAAGAAGCAGCTACAGAG
                 aGlyGlnGlyCysLysAspAlaLeuGlnLeuLeuIleGluHisSerTrpG
                                                                                                                                             IleGluGlnAsnIleArgAlaLysIleCysGlyLeuArgAlaSerGluAl 263
                                                                                                                                                                                    TTTTGAGGAAATGATCAAAAACTTGTTCTCCTTGCCAATCGACGTTCCTT
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                                                                                                                       ATTGAGGAAAACATCAGGAAGAAATTCAAGAT...GACGACAATGAAAA
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seq_documentation_block:
ID AAV12203 standard; cf
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AC AAV12203;
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Retinoid metabolising
KW retinoic acid; zebrafi
KW retinic keratosis; oi
KW ron-small cell lung c
KW acute promyelocytic l
KW acute promyelocytic l
KW ichthyosis; therapy;
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PN Key Banio rerio.
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                                                                                                                                   retinoic acid; zebrafish; inhibitor; antisense; cancer; actinic keratosis; oral leukoplakia; head tumour; neck tumou non-small cell lung carcinoma; basal cell carcinoma; acute promyelocytic leukaemia; skin cancer; acne; psoriasis;
                                                                                                                                                                                            Retinoid metabolising protein; P450RAI; retinoid oxidase;
                                                                                                                                                                                                                            Zebrafish retinoid metabolising protein zP450RAI cDNA
                                                                                                                      ichthyosis; therapy;
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                               Location/Qualifiers
88..1566
/*tag= a
                                                                                                                      diagnosis;
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                                                                                                                                                                     neck tumour;
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alignment_block:
US-09-668-482-4 x AAV12203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cepithelial cells exposed to retinoic acid. To isolate the clone, transcripts present in fin tissue regenerating in the presence or absence of retinoic acid were compared using a differential display pCR technique, and an isolated clone (see AAV12213) was used to screen a D. rerio 6-18 hr embryo cDNA library. Human (see AAV12204) and mouse (see AAV12205) p450RAI clones have also been identified. The isolated clones can be used in the recombinant production of later p450RAI proteins. Antisense nucleic acids can be used in a claimed method for inhibiting retinoic acid hydroxylation for the treatment of cancer, actinic keratosis, oral leukoplakia, secondary tumours of the head and/or neck, non-small cell lung carcinomas, basal cell carcinomas, acute promyelocytic leukaemia, skin cancer, psoriasis and/or ichthyosis. Promoter sequences (see AAV12206-08) are also
                                                                                                                                                                                                                                                                                                              Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Retinoid metabolising protein - e.g. cancer, actinic keratosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996;
21-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       retinoid oxidase that has the ability to hydroxylate retinoic acid at the 4 position of the beta-lonone ring and is inducible in epithelial cells exposed to retinoic acid. To isolate the clone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This cDNA clone codes for a novel zebrafish retinoid metabolising protein (see AAW44159) designated zP450RAI. The encoded protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 15; Page 52-54; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB;
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| CGTTTTACTCTCTCGCCGCGGTGAAGTTGTGGGAAGTGTTAATGATCC
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eLeuGlnMetLysArgArgLysTyrGlyPheIleTyrLysThrHisLeuP
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|TTTGAGGAAATGATCAAAAACTTGTTCTCCTTGCCAATCGACGTTCCTT
                                                                                           TTCAGGAGAAGGTTGAAATGGGCATGTATACACCTGGAAAGGGCTTGAGT
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seq_documentation_block:
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This sequence comprises a genomic clone of a novel mouse retinoid metabolising protein designated mP450RAI. A cDNA clone (see AAV12205) that includes a coding sequence for the full-length mP450RAI protein (see AAW44161) is also provided. The encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1364
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                                                                                                                                                         Page 69-70;
                                                                                                                                                                                                                                                                                                                                                                                     Jones G,
                                                                                                                                                                                                                                                                                                                                                                                                                                              QUEENS KINGSTON
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96US-0667546
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alignment_block: US-09-668-482-4 x AAV12216 alignment_scores:
Quality: 1712.00
Ratio: 4.019
Percent Similarity: 40.727 Align seg 1/1 to: AAV12216 from: 1. protein is a retinoid oxidase that has the ability to hydroxylate retinoic acid at the 4 position of the beta-ionone ring and is inducible in epithelial cells exposed to retinoic acid. Zebrafish, human and mouse p450RAI cDNA clones (see AAV12203-05) are claimed. They can be used in the recombinant production of p450RAI. Antisense sequences can be used in a claimed method for inhibiting retinoic acid hydroxylation for the treatment of cancer, actinic keratosis, oral leukoplakia, secondary tumours of the head and/or neck, non-small cell lung carcinomas, basal cell carcinomas, acute promyelocytic leukeemia, kin cancer, and premalignancy associated with actinic keratosis, acne, psoriasis and/or ichthyosis. Promotes sequences (see AAV12206-08) for the P450RAI genes are also claimed. Sequence 4164 BP; 997 A; 975 C; 1071 G; 1121 T; 0 other; 181 123 106 131 138 331 AGGGTGAGCTGGCAACTCCTTGGCTGGCAGGGAGACCTCATCCTATGGCT 380 138 281 231 139ValileMetArgAlaPheSerArgGluAlaLeuGl 150
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581 CTGGGGGGTGCTCAGGTGATTATGCAGGCCTTCAGCCGCGAGGCACTCCA 630 481 TGGGTTAGTCCTGGGGGGGGACTGAAATTCTTGAAAGGGTACTCGGAAAGG 530 381 TGGTTCAGGCAAAATAGAATGCGGGGGGGGGGGGTAGTCCTATGTGGTGGG 430 40 CysAlaLeuProLeuProProGlyThrMetGlyPheProPhePheGlyGl 56 531 CGAAGGGGGGGGGCTGAGGGAAAGTAGAGGATTGTAACACTCTCTGCTC 580 90 73 TGCGGTCTCTCCTCCACCTCCCTCT........... GACCAGGACCCTCTCTATCTGAGATCCACTTTAGCTTTCTGCTAGCACG 480 Length: 1046 Gaps: 10 Percent Identity: 38.815 to: 4164

153(ol movectorectarcancadatementaranaggeraaggerenteracaaa	1
288	88	N
1480	31 AACCGTATTAAAGGGTGGCATTGGTCTAGAGAGCTGTGGAAGGGGGTGGC	14
288	88	2
1430	81 GAAGTAGCAACAAAGATAATTTTATCGTTGGGGGGTCACCACAACACGAGG	13
288	88	21
1380	31 ATATCCGATATTTACATCAAGAAACATAACAGTAGCAAAATTACCGTTAT	13:
288	88	2
1330	81 CTTCACGGAGCCAAACAACCCTTTCAGAAGGGTCGCCTAAGAGCATCTGC	128
288	88	22
1280	31 GTGGGCGGCGATGCTAGGTCTAGAGCTTTTCAACCTGTGGGTCGTGACCC	12:
288	88	28
1230	1 CACACTTTCTGGGGTCTCCAAAGCCCTGTCAAGGCCCCAGCTACTTCCAA	118
288	60 	28
1180	1 AGCAATTTCAAAAGGTGCCCAAGGGCCGGGGAGTGCCTCTGACTTTCCAGA	113
288		28
288 1130	4 eulleGluHisserTrpGluArgGlyGluArgLeuAspMetGln	27 108
274 1080	7 yLeuArgAlaSerGluAlaGlyGlnGlyCysLysAspAlaLeuGlnLeuL ::: ::: GCTTCAGGCTACAGAGCCGGATGGGGGTTGCAAGGACGCGCTGCAGCTCC	25 103
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257	1 AsnLeuIleHisAlaArgIleGluGlnAsnIleArgAlaLysIleCysGl	4
240 980	6	23 93
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235	4 Tyrarg	23
880	1 TGACCCGCAATCTCTTCTCTCCCATTGACGTGCCCTTTAGCGGCCTG	
233	7 etThrArgAsnLeuPheSerLeuProIleAspValProPheSerGlyLeu	ï
217 830	0 uAlaGlyAspGlyAspSerGluGlnGlnLeuValGluAlaPheGluGluM 2 ::::::	20 78
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183 730	7 rpLeuSerCysGlyGluArgGlyLeuLeuValTyrProGluValLysArg 1	16
580	GTCTGGAGCAGT 6	63:
167	nCvsTvrValProValTleThrGluGluValGlvSerSerLeuGluGlnT	

350	.GlyLeuLeuCysLysSerAsnGlnAspAsnLysLeuAspMetGluIleL :	334
2430	TTTTTGGAGTGCCCAGGGATCCATCACTCACTTTTTTATCTGTTTCCATA	2381
333	Lys.	333
2380	CAGACGCCTTCAGGTTTAGTTAACAGGTGAGTCCTGCTGGGCTGACTTTT :	2331
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2280	CCTGATAAGCAACATTGTCTGGATAATGGGTTTAGGCTGAGGAAGTGTGG	2231
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332		332
2180	TTCTCCTTTCCCTGACCAAGAACATGAATAATGTGATTAGAGCCAATAGC	2131
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332		332
1880	AGATAAAGAGC	1831
332	luLeuLysSe	329
329 1830	UleThrTyrLeuGlyLeuTyrProHisValLeuGlnLysValArgGluG	312 1781
312 1780	GluLeuLeuPheGLyGlyHisGluThrThrAlaSerAlaAlaThrSerLe	1731
7	TCTGTATAAACTTCCGTTTTTATCCTTAGGCACTAAAACAATCGTCA	· 60
295	· ·····AlaLeuLvsGlnSerSerT	289
1680	CAATATTCTCAGGTCAGGTCTTTGTAACAGTGCTATAAACTGCACTCAGA	1631
288		288
1630	TCTTTGACTTTCTATGAACAAAACGGATTTTACCCTTGAAGTCTTCCGTG	1581
288		288
1580	GGTTAAAGCGGAAGAGCAGGATTAAGGGAGTTTTGCGTTTTTGTTGTGG	1531
288		288

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                                                                                454 IlePheThrValGluLeuAlaArgHisCysAspTrpGlnLeuLeuAsnGl 470
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                                   ACCTCCTACAATGAAGACAAGCCCCACTGTGTACCCTGTGGACAATCTCC
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV12214

2677 BP

seq_documentation_block:
ID AAV12214 standard; DNA;

AAV12214;

22-JUN-1998 (first entry)

Human retinoid metabolising protein hP450RAI genomic DNA

Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid; human; inhibitor; antisense; cancer; actinic keratosis; oral leukoplakia; head tumour; neck tumour;

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This sequence comprises a genomic clone of a novel human retinoid cometabolising protein designated hP450RAI. Another genomic clone (see AAV12215) is also provided, as well as a cDNA clone (see AAV12204) that includes a coding sequence for the full-length hP450RAI composed to retinoid subject that includes a coding sequence for the full-length hP450RAI composed to highly to hydroxylate retinoid actid at the 4 position composed to retinoic acid. The hP450RAI gene has been localised to composed to retinoic acid. The hP450RAI gene has been localised to composed to retinoic acid. The hP450RAI gene has been localised to composed to retinoic acid. The hP450RAI gene has been localised to composed to retinoic acid. They can be used in the recombinant composed to are claimed. They can be used in the recombinant composed to a composed to a composed to a composed to acid med method for inhibiting retinoic acid hydroxylation for the composed to cancer, actinic keratosis, oral leukoplakia, secondary the composed to compose acid with actinic keratosis, acne, composed to compose acid with actinic keratosis, acne, composed to compose acid composed to composed to compose acid composed to composed to compose acid composed to compose acid composed to compose
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US-09-668-482-4 x AAV12214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 1365.00
Ratio: 4.320
Percent Similarity: 47.235
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21-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Retinoid metabolising protein - useful to develop products to treat, e.g. cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
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                                                                                                                                                                             776
                                                                                                        34 erGlyArgAspArgSerCysAlaLeuProLeuProProGlyThrMetGly 50
GCGGCCGCGACTGCTGTGTGCCCTTCCCATTGCCCCCGGGACTATSGGS
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96US-0667546.
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826	TTCCCCTTCTTTGGGGAAACCTTGCAGATGNTACTNCAGGTAAGGGAGGG 8	75
63	6	ω
876	TGGGGCGGGACAGGCTGCTTCCCCGGAGCCCGGCGCGCGC	925
63		ū
926	GCTGAAGTCGGGGTAGGCGCCCCCGGGAGGCATGCTATTGCGGCTAGGAG 9	75
63		ũ
976	CAGGGCTGGCGGAGCGCGCGCTCCCCGGMKYMCSCTCAWGCSCRCWWK 1	025
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1026	I NOMINGE LOSSINGCOC	
73 1076	ArgLysTyrGlyPheIleTyrLysThrHisLeuPheGlyArgProThrVa 8	125
89	ArgValMetGlyAlaAspAsnValArgArgIleLeuLeuGlyAspAspA	L06
106 1176	GG UV	1225
123	GlyCysLeuSerAsnLeuHisAspSerSerHisLysGlnArgLysLys. 1	138 1275
138		138
1276	GGGGCAGGAGGCGACGGCTGGACAGGGAGGGGGACCCCATTTATGAGCG	1325
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1326	GAATTCCGGCTGATGGATGCTAGGCGCGGGCTAGCAGCTTGAGGTGGGCT	1375
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1376	AGGACCCTCTGCCAGCTCCAGGTTAGCTTTCCCAGCTCGGAGAGTGCCAT	1425
138		138
1426	GTGTCTGGCAGGACTGGGGGTGTCTGGAAGGGGACGGCGGTAGACGAGAG	1475
139	valIl	0
1476	TGA	
141 1526	MetargalaPheSerArgGluAlaLeuGluCysTyrValProValIleTh 	157 1575
157 1576	rGluGluValGlySerSerLeuGluGlnTrpLeuSerCysGlyGluArgG 	174 1625
174 1626	lyLeuLeuValTyrProGluValLysArgLeuMetPheArgIleAlaMet	190 167
191 1676	ArgIleLeuLeuGlyCysGluProGlnLeuAlaGlyAspGlyAspSerGl	207 172
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LysGlnSerSerThrGluLeuLeuPheGlyGlyHisGluThrThrAlaSe
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                rAlaAlaThrSerLeuIleThrTyrLeuGlyLeuTyrProHisValLeuG
                                                         AAGCAATCTTCAACCGAACTCCTCTTTGGAGGACACGAAACCACGGCCAG
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15 ValLeuPro...LeuLeuLeuPheLeuAlaAlaIleLysLeuTrpAspLe

30

אק קר את הקר התקופה המונים להתקופה המו

18-JUN-1999
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916	uGlnLeuLeuIleGluHisSerTrpGluArgGlyGluArgLeuAspMetG 2	71
271 866	IleCysGlyLeuArgAlaSerGluAlaGlyGlnGlyCysLysAspAlaLe 2	23
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129 479	3 ProAlaSerValArgThrIleLeuGlySerGlyCysLeuSerAsnLeuHi :: :::: ::::: :: ::	113
112 429	6 snValArgArgIleLeuLeuGlyAspAspArgLeuValSerValHisTrp 	96 380
96 379	9 rLysThrHisLeuPheGlyArgProThrValArgValMetGlyAlaAspA	7 <u>9</u> 33(
79 329	4 ArgArgLysPheLeuGlnMetLysArgArgLysTyrGlyPheIleTy ::: ::: ::: ::: ::: 0 AACCCCAATGTTTCTTCACCTCCAAGCAAAAGAGATATGGAGAGATATT	64 280
63 279	7 lyThrMetGlyPheProPhePheGlyGluThrLeuGlnMetValLeuGln ::: ::: ::::	47 230
47 229	0 uTyrCysValSerGlyArgAspArgSerCysAlaLeuProLeuProProG 	3(184
183	::: ::: 2 GTTGTACCAATCCTCATCTTATGCTTGCTTTT	142

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EB-1999; AR-1999; AR-1999; AR-1999;	вв-2000; ;	EP-2000.	33405-A2.	idopsis t	sation ident ic pat	idopsis t	T-2000	8714;	entation_ 8714 stan	/SIDS1/gcgdat	spAsnLeuProAlaAr :::: ACGGTCTTCCCGCTAC	uLeuAsnGlyProProThrMe : ::: GAAGGGAGGAGAAAGGAAT	LeuLeuLys ;;; CAAATTCTT	roPheGlyGlyGl ::: CTTTTGGAAGTGG	gPheSerAl ::::: ATTCGAGGT	HisAspVal	lyTyrGlnI GATATTTGA	OProValPr ;;; CATCATATC	GlnLeuLys :::::: AATATGCCA	euCysLysSer :::::: ATGAAGAAAAC	SValLeuGlnLys TGATGATCAGAAA	ACAGCTAGT
-SD66 -SD66 -SD66 -SD66	2000EP-			haliana	assay; ificati hway; p	haliana	(first		n_block: andard; D	a	roalaar CCGCTAC	yProPro AGAGAAP	IlePhen ATATTTC	AG - Y	a : AAA1	AlaGlu: ::: 'CCGAAA	leProLysG	oGlyGl CTTCAC	Tyr11 CTGAC	AsnG :::: AGTA	LnLysValAr ::: GAAACTTCT	TGCTIA
.0121825. .0123180. .0123548. .0125788.	0301439.			•	; genetic mapping; gene ex ion; signal transduction p promoter; termination sequ	DNA fragment SEQ ID NO:	entry)		NA; 1398 BP.	geneseq/geneseqn/NA2000.D	99Phe 490 ATTT 1509	roProThrMetLysThrSerProThrValTyrProValA :::::: AGAAAGGAATACAGTACAGTCCATTTCCAATACCTCAAA	euLeuLys1lePheThrValGluLeuAlaArgHisCysAspTrpGlnL ::: AAATTCTTATATTTCTCCACCATTTAGTTTCCAATTTCCGATGGGAAG	euArgSerCysValGlyLysGluPheAlaLys :::::::: ::: :: TTCATGCTTGTCCCGGGAACGAACTCGCCAAG	HisProGluAspAlaSerArgPh ::: AAGCCGAAT	ValAlaGluIlePheThrAsnLysGluGluPheAsnP ::: ::: AATCCGAAATATTTTCAAACCCTGAGGTTTTCGACC	.IleProLysGlyTrpAsnValIleTyrSerIleCysAsp ::: ::: ATACCTAAGGGATGGAAAGTGATGCCACTGTTTCGGAAT	yPheArgValAlaLeuLysThrPheGluL Alli ATTCAGAGAAGCAGTGGTTGATGTTGAAT	lyCysVallleLysGluThrLeu ATAAGGTTATAGTTGAAAGCTTG	nAspAsnLysLeuAspMetGl :::::: aGAGAAGAAACCTTTAACATGGAG	gGluGluLeuLysSer ::: ::: AGAAGCTGTTAAGGCTGAGC	TIAACITGGATICITAAGTACITA
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					ontrol;					4.		484 1489	467 1439	450 1389	434 1339	418 1304	401 1254	385 1204	368 1154	351 1104	336 1054	1004

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                                                                                                                                                                                                                                   89 CCAAGAATGGT......CTTCCTCCTGGAACC
                                                                                                                                                                                                                                                         32 ysValSerGlyArgAspArgSerCysAlaLeuProLeuProProGlyThr 48
                                                                                                                                                                                                                                                                                      55
                                                                                                                                                                                                                                                                                                17 oLeuLeuPheLeuAlaAlaIleLysLeuTrpAsp.....LeuTyrC::::|||::::|||
                                                                                                                                                                                                                                                                                                                               22 ATGGGTCTTCTCTTGATCATCGTGTCT...CTCTGT.........
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                                                                                          ATCTTCTAGGTTGTCCAACGTTAATCTCAATGGACTCAGAAGTAAACAGA 264
GATGCTTGATATACTTGGGACTTGTAACATGGCTGCGGTTCACGGTTCGA 364
                                                                                                                                                                                                                                                                                 .....TCCGCTCTCCTTCGATGGAATCAGATGCGATATA 88
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::: :::::::::::::::::::::::::::::::	ATGTATACACGAGG	1102
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eGluLeuAsnGlyTyrGlnIleProLysGlyTrp 392 : :::	luI - -	376 1052
ATTGGCAACGATCGTTAATGGGGTCCTAAG	ATTTATGAGACATCAAC	1002
gLeuAsnProProValProGlyGly	LysGluThrLeuAı	359
LULIEHEUGINGINHEULYSTYTILEGIYCYSVA 359 :::::::::: ::: AGGACGTGAAGTCAATGAAGTTCACTCGAGCTGT 1001	Ω <u>1</u>	952
THE TAXABLE PROPERTY OF THE PR		
SSETLYSGLYLeuLeuCysLysSerAsnGlnAsp 342 :::::: ::::::: CATTTTGGCATTTCAGGGAAAGGAAAAGGACAGGAC 051	٠ <u>- ۲</u> ۸	326 908
TACCTTCATGATCACCCAAAAGCTCTTCAAGAAC 907	TTAAGTA	858
yrLeuGlyLeuTyrProHisValLeu	rSerLeuIleThrTy	309
TCGGGTTACGAAACTGTCTCTACGACCTC 8	::: :: ::: ::: :::: CAAGTTGTGACGATTTTGTAT	0
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uArgGlyGluArgLeuAspMetGlnAlaLeuLysGln 292 :	<pre>luHisSerTrpGluArgGlyG :: :::::: aGAAGGAAGGTAACCGATACCG</pre>	276 761
CATGTTAGGTTACTTGATG	GAGATTCTGGAGAA	\vdash
lnGlyCysLysAspAlaLeuGlr ;;	rGluAlaGly	259
::::: ::::::::::::::::::::::::::::::::	A ::	679
luGlnAsnIleArgAlaLysIleCysGlyLeuAr 25	aArgIleGluGlr	243
<pre>irGlyLeuTyrargGlyMetLysAlaArgAsnLeu 242 ::::: ::::: !AAATTATCGTTGCGGAATCCAAGCAAGAAATAAC 678</pre>	leAspValProPheSerGlyL ::: ::::: TTGATCTTCCGGGCACAAATT	226 629
CAAGCTTGTTGTTGGGACTTTATCCGTTCCGA 62	CAA	7
luGluMetThrArqAsnLeuPheSerLeuProI 22	AlaPheGluGl	$\dot{\mathbf{L}}$
		ω
vAspGlvAspSerGluGlnGlnLeuValGlu 21	lnLeuAlaGlvAsr	9
PheArgIleAlaMetArgIle TTT	euMetPhe :: TGGCATTT	180 506
AATG	ATCAGTGG	465
ysGlyGluArgGlyLeuLeuValTyrPr	GluGlnTrpLeuSerCy	164
TGCCTAAAGTTGATCACTTC	<u>و</u> :	
DroVallleThrCl::ValCl::Corcorto 16	nG]nCveTvrVa] p	4
YSLYSVallleMetArgAlaPheSerArgGluAla 148 :: ::::: GAGGCTCGCTTCTGTCTCTCATAAGCTCGACCATG 414	erHisLysGlnArgLysLy: ::: GCCACCGGCTTATGAGAGAGG	132 365

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....GTGTTTCCG 1350
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alignment_block:
US-09-668-482-4 x AAC42516
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239 AlaArgAsnLeuIleHisAlaArgIleGluGlnAsnIleArgAlaLysIl 255
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893 GCAAGGAAAAACTTGTAGCTGCCTTT...CAGTCCATAGTGACTAACCG 939
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                                                                             GAGCAATGGGTATTAATCTTCCTGGGTTTGCTTATCATAGAGCTTTGAAG
                                                                                                heSerLeuProIleAspValProPheSerGlyLeuTyrArgGlyMetLys
                                                                                                                                                                                                                                                                     AlaMetArgIleLeuLeuGlyCysGluProGlnLeuAlaGlyAspGlyAs
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CTAGTAACAACACCAGAGACTTGTAGGCGAGTTCTAACAGATGATGATGC 516
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      yrGly......PheIleTyrLysThrHisLeuPheGlyArgProThrVal
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                                                                                                                                                         .....TCATTGGAACGGGAGTATACCAACCTTAACTATGGAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTCCTTTGTTGGTATCTCCTTTGAAGAACACAAGAGGCTCAGGCGTTTG
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990S 0147935 990S 0148171 990S 0148341 990S 0148341 990S 0149368 990S 01494684 990S 0149426 990S 0149426 990S 0149922 990S 0149922 990S 0150686 990S 0151080 990S 0151080 990S 0151080 990S 0151080 990S 0151080 990S 015133 990S 015133 990S 0151438 990S 0155438 990S 0155438 990S 0155486 990S 0156559 990S 0156559 990S 015696 990S 015933 990S 015933

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seq_documentation_block:
ID AAT85306 standard; cD
XX
AC AAT85306;
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DT 14-APR-1998 (first e.
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DE Arabidopsis thaliana (
XX
KW Cytochrome P450-type l
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                                                                                                                                                                                                                                                                                                                                                    488 AlaArgPheThr 491
       Cytochrome P450-type hydroxylase; identification; brassinosteroid;
                                                  Arabidopsis thaliana cytochrome P450-type hydroxylase cDNA
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alignment_scores:
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                                                                                                                                                                                                                                                           Align seg 1/1
                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes Arabidopsis thaliana cytochrome p450-type hydroxylase. The hydroxylase can be used to identify brassinosteroids or brassinosteroid inhibitors, useful to produce plants with modified physiological and/or phenotypic characteristics. The modified plants may show, e.g. stimulation of growth, increased cell elongation, increased wood production, accelerated seed germination at low temperatures, an increase in dry weight, repressed anthocyanin production during growth in light and/or inhibited de-etiolation which is induced, e.g. by cytokinin, in the dark or an increase in stress tolerance. The hydroxylase or its coding sequence can also be used for the recombinant production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated plant cytochrome P450-type hydroxylase gene - used to identify substances acting as brassino-steroid(s) or brassinosteroid inhibitors for the production of modified plants
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P-PSDB; AAW27153.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1608 BP; 382 A;
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                                                                                                                            114 CGTACACGTTACCGTCGGATGGGTCTGCCTCCGGGAAGCCTTGGTCTCC
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                                                                                                                                                 35 yArgAspArgSerCysAlaLeuProLeuProProGlyThrMetGlyPheP 52
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66 CTCCTCCTCTCTTCCATCGCCCGCCTTCCTCCTACTCCGC.. 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        compounds, e.g. teasterone.
                                                                           roPhePheGlyGluThrLeuGlnMetVal.....LeuGln 63
CCTGAGCCTTTCATCGACGAGAGAGTAGCCCGGTACGGTTCGGTTTTCAT
                           ArgArgLysPheLeuGlnMetLysArgArgLysTyrGlyPheIleTyrLy 80
                                                                CTCTGATAGGAGAGTTTTCAGCTGATCGGAGCTTACAAAACAGAGAAC
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/product= cytochrome_P450-type_hydroxylase
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Identity: 26.543
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eArgValAlaLeuLysThrPheGluLeuAsnGlyTyrGlnIleProLysG 391
                                                                                                  ATTCGTATAGTCTTGAATGGAGTGATTACAAGTCAATGCCATTCACACAA 1046
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                                  TGTGTGGTTAATGAGACGCTACGAGTGGCTAACATCATCGGCGGTGTTTT 1096
                                                                   CysValIleLysGluThrLeuArgLeuAsnProProValProGlyGlyPh 374
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AATCTTGATTCTTGGTCTTCT.......CGTGTTCTCCTCATGGA 550
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914	6 9	63
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491 1443	hrHisphe 493 CGATCTTC 1450	
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04-JUN 1999 07-JUN 1999 08-JUN 1999 10-JUN 1999 14-JUN 1999 14-JUN 1999 16-JUN 1999 17-JUN 1999 17-JUN 1999 18-JUN 1999 18-JUN 1999 18-JUN 1999 18-JUN 1999	07-MAY 199 11-MAY 199 14-MAY 199 14-MAY 199 14-MAY 199 14-MAY 199 14-MAY 199 18-MAY 199 20-MAY 199 20-MAY 199 21-MAY 199 22-MAY 199 23-MAY 199 26-MAY 199 27-MAY 199 28-MAY 199 20-MAY 199	PR 15-MAR-1999; 99US-0123548. PR 25-MAR-1999; 99US-0126264. PR 25-MAR-1999; 99US-0126264. PR 25-MAR-1999; 99US-0126785. PR 01-APR-1999; 99US-0128234. PR 06-APR-1999; 99US-0128714. PR 16-APR-1999; 99US-0128714. PR 16-APR-1999; 99US-0130047. PR 21-APR-1999; 99US-0130449. PR 23-APR-1999; 99US-0330510. PR 23-APR-1999; 99US-0330510. PR 23-APR-1999; 99US-033048. PR 30-APR-1999; 99US-033048. PR 30-APR-1999; 99US-033248. PR 05-MAY-1999; 99US-0132485. PR 06-MAY-1999; 99US-0132487.	Hybridisation protein identi metabolic path Arabidopsis th EP1033405-A2. 06-SEP-2000. 25-FEB-2000; 25-FEB-1999; 05-MAR-1999;	<pre>q_name: /SIDS1/gcgdata/geneseq/ q_documentation_block: AAC47986 standard; DNA; 1649 AAC47986; 18-OCT-2000 (first entry) Arabidopsis thallana DNA frac</pre>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 luAlaLeuGluCysTyrValProVal...IleThrGluGluValGlySer 162
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1009	TCAACTCAAGGAAGAGCATGAAAAGATTAGGGCAATGAAGAGTG	966

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Query length: 497
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-q-/cgn2_1/USPF0_spco1/US09668482/runat_05112001_13353_10897/app_query.fasta_1.1680
-q2-/cgn2_1/USPF0_spco1/US09668482/runat_05112001_13353_10897/app_query.fasta_1.1680
-DB-ISsued_Patents_NA -QFMT-fastap -SUFFIX=rni -GAPOP-12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPEXT=0.050 -VGAPEXT=0.050 -VGAPOP=10.000 -VGAPEXT=0.500
-FGAPOP-6.000 -FGAPEXT=7.000 -VGAPEXT=0.000 -VGAPEXT=0.500
-DELOP-6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-pct
-THR_MAX=100 -THR_MIN=0 -MAXLEN=200000000
-NORM-ext -MINLEN=0 -MAXLEN=2000000000
-USER-USO9668482_@CGN1_1_104 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:PCT-US95-05758-27 +
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-313-075A-29 + 23
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-948-564-9 + 238
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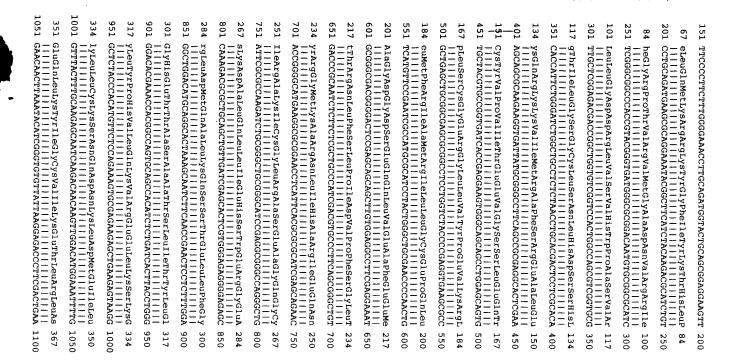
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seq_documentation_block:
; Sequence 5, Application US/08724466B
; Patent No. 6063606
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Ratio: 5.254
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,54
EILING DATE: June 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 5076
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Diskette,
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APPLICANT: Beckett, Barbara F
TITLE OF INVENTION: Retinoid
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                                               34 erGlyArgAspArgSerCysAlaLeuProLeuProProGlyThrMetGly 50
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PRIOR APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: OCTOB APPLICATION NUMBER: FILING DATE: OCTOB APPLICATION NUMBER: FILING DATE: OCTOB ATTORNEY/AGENT INFORM NAME: Hunt, John C REGISTRATION NUMBER REFERENCE/DOCKET NUM TELECOMMUNICATION INF TELEPHONE: (416) 863 FORMATION FOR SEQ ID SEQUENCE CHARACTERIST LENGTH: 1494 base	CORRESPONDENCE ADDRESSEE: STREET: Box CITY: Toron STATE: Onta COUNTRY: Ca ZIP: M5L 1A COMPUTER READA MEDIUM TYPE: COMPUTER: C COMPUTER: C COMPUTER: C COMPUTER: W SOFTWARE: W CURRENT APPLIC APPLICATION I APPLICATION APPLICA		uLeuA	rophe	ThrHis	nProPr TCCCCC snGlyT ATGGAT
APPLICATION APPLICATION NUMB LICATION NUMB ING DATE: JU LICATION NUMB LICATION NUMB LICATION NUMB LICATION NUMB LICATION NUMB ENENCE/DOCKET DAMUNICATION DAMUNICATION DAMUNICATION EPHONE: (416 EPHONE: (416) EPHONE: (416	DEENCE AD BEE: Bla BOX 25 TOIONTO ONTARIO CONTARIO CONTARIO TYPE: D RYPE: D RYPE: WORD E: WORD OFFICE WORD OFFI OFFI OFFI OFFI OFFI OFFI OFFI OFF	/cgn2_6/ptoda ntation_block 5, Applicati 5, Applicati 0, 6306624 INFORMATION: PETKOV CANT: PETKOV CANT: BECKET OF INVENTION R OF SEQUENCE	ASNGLY IIIIII AAATGGA SnLeuPr IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	GlyGl	ThrHisAspValal	YroVal
PLICATION DATA ATION NUMBER: DATE: June 2 ATION NUMBER: OCTOBE AGENT INFORMA HUNT, JOHN C. RATION NUMBER: NCE/DOCKET NUM UNICATION INFO ONE: (416) 86 X; (416) 863 X; (416) 86	I I O I I I I I I I I I I I I I I I I I	South Co. t	ProPr 	yGlyL 	APVALALAGI	/alProgly
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/667 1996 /724 /724 / 19 N: 19 6,42 6,42 6,42 15 17 10 10 13 14 3 15 15	sels rce pc pc pos r	a/6 888 Ma Ma ara	uLeuAsnGlyProProThrMetLysThrSerProThrValTyrP	ropheGlyGlyGlyLeuArgSerCysValGlyLysGluPheAlaLysIle	ePhe CTTC	nProProValProGlyGlyPheArgValAlaLeuLySThrPheGluLeuA
546 466 466 767	% Gra Court 1/2 in compat 5.1 5.1	B_COMB 2164D rtin, rrin,	ThrSerProThrVal	SValG	eThrAsni ACCAAC; uAspal; 	ValAlaLeuLys GTTGCTCTGAAG GTTGCTCTGAT PASnValIleTy
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; TYPE: nucleic acid
; STRANDEDNESS: singl
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US-08-882-164D-5
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Quality: 2611.00
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      spAsnLeuProAlaArgPheThrHisPheHisGlyGluIle 497
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seq_documentation_block:
; Sequence 31, Application US/08882164D
; Patent No. 6306624

GENERAL INFORMATION:

APPLICANT: Petkovich, P. Martin, White, Jay A.,

APPLICANT: Beckett, Barbara R., Jones, Glenville

TITLE OF INVENTION: Retinoid Metabolizing Protein

NUMBER OF SEQUENCES: 43

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-882-164D-31

```
COUNTRY: Canada
COUNTRY: Canada
ZIP: M51 1A9
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,164D
FILING DATE: June 25, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: June 21, 1996
APPLICATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
FELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEPHONE: (416) 863-4344
TELEPHONE: (416) 863-2653
INFORMATION FOR SED ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 1725 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
US-08-882-164D-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
Quality: 2437.00
Ratio: 5.035
Percent Similarity: 97.384
                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-668-482-4 x US-08-882-164D-31
                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-882-164D-31 from: 1 to: 1725
275
                                                                                                                    175
                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon STREET: Box 25, Commerce Court West
                                                        STREET: Box 25,
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 497
Gaps: 0
Percent Identity: 93.360
                                                                                                                                                                                                                                          174
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117 375	gThrIleLeuGlySerGlyCysLeuSerAsnLeuHisAspSerSerHisL l	34
134 425	ysGlnArgLysLysVallleMetArgAlaPheSerArgGluAlaLeuGlu 1 	50
151 475	CysTyrValProValIleThrGluGluValGlySerSerLeuGluGlnTr 1	67
167 525	pLeuSerCysGlyGluArgGlyLeuLeuValTyrProGluValLysArgL 1	84
184 575	euMetPheArgIleAlaMetArgIleLeuLeuGlyCysGluProGlnLeu 2 	00
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217 675	tThrArgAsnLeupheSerLeuProIleAspValPropheSerGlyLeuT 2 	34
234 725	yrargGlyMetLysalaargAsnLeuIleHisalaargIleGluGlnasn 2 :::	50 74
251 775	IleArgAlaLysIleCysGlyLeuArgAlaSerGluAlaGlyGlnGlyCy 2 	67 24
267 825	slysaspalaLeuGlnLeuIeuIleGluHisSerTrpGluArgGlyGluA 2 	84 74
284 875	rgLeuAspMetGlnAlaLeuLysGlnSerSerThrGluLeuLeuPheGly 3 	00
301 925	GlyHisGluThrThrAlaSerAlaAlaThrSerLeuIleThrTyrLeuGl 3 	17 74
317 975	YLeuTyrProHisValLeuGlnLysValArgGluGluLeuLysSerLysG 3 	34 024
334 1025	lyLeuLeuCysLysSerAsnGlnAspAsnLysLeuAspMetGluIleLeu 3 	50 074
351 1075	GluGlnLeuLysTyrIleGlyCysValIleLysGluThrLeuArgLeuAs 3	67 124
367 1125	nProProValProGlyGlyPheArgValAlaLeuLysThrPheGluLeuA 3 	84 174
384 1175	snGlyTyrGlnileProLysGlyTrpAsnValileTyrSerileCysAsp 4 	00 22 4
401 1225	ThrHisAspValAlaGluIlePheThrAsnLysGluGluPheAsnProAs 4 ACCCACGATGTGGCAGATAPCTTCACTAACAAGGAGGAATTTAATCCCGA 1	17 274

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SEQUENCE CHARACTERISTICS:

LENGTH: 1850 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-724-466B-3
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; Sequence 3, Application US/08724466B
; Patent No. 6063606
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                                                     alignment_scores:
Quality: 1738.00
Ratio: 4.080
Percent Similarity: 85.714
alignment_block:
US-09-668-482-4 x US-08-724-466B-3
                                                                                                                                                                                                                                                                                                                                          COUNTRY: Canada

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage

MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage

COMPUTER: COMPAQ, IBM PC compatible

OPERATING SYSTEM: MS-DOS 5.1

SOFTWARE: WORD PERFECT

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724,466B

FILING DATE: October 1, 1996

PRIOR APPLICATION NUMBER: 08/667,546

FILING DATE: June 21, 1996

APPLICATION NUMBER: 08/667,546

APPLICATION NUMBER: 36,6424

REPERENCE/DOCKET NUMBER: 50767/00004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 863-4344

TELEPHONE: (416) 863-364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1325 CATTTGGAGGAGGCCTTCGGAGCTGTGTAGGCAAAGAGTTTGCAAAAATT 1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             434 roPheGlyGlyGeuArgSerCysValGlyLysGluPheAlaLysIle 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCE: 30

CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon STREET: Box 25, Commerce Court West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: M5L 1A9
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toronto
                                                          Percent Identity:
                                                              68.008
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Align seg 1/1 to: US-08-724-466B-3

from: 1

to: 1850

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uargGlvGluargLeuAspMetGlnAlaLeuLysGlnSerSerThrGlu 29	œ (
aGlyGlnGlyCysLysAspAlaLeuGlnLeuLeuIleGluHisSerTrpG 280	263 864
SerGluAl 26 ::: AATGAAAA 86	247 817
AsnLeuIleHisAlaArg 24 ::: ::::: AATTTCATTCACTCCAAA 81	230 767
aPheGluGluMetThrArgAsnLeuPheSerLeuProIleAspValProP 230	213 717
AspSerGluGlnGlnLeuValGluAl 21	198 676
alLysargLeumetPheArgIleAlametArgIleLeuLeuGlyCysGlu 197:: :::	181 626
GluArg	167 588
CysTyrValProVallleThrGluGluValGlySerSerLeuGluGlnTr 167 ::: ::: ::::::::: CACTACATTCCCGTGATCCAGCAGGAGGTGAAGAGCGCCATACAGGAATG 587	151 538
ysGlnArgLysLysVallleMetArgAlaPheSerArgGluAlaLeuGlu 150 :::::: :::	134 488
9ThrIleLeuGlySerGlyCysLeuSerAsnLeuHisAspSerSerHisL 134 	117 438
LeuLeuGlyAspAspArgLeuValSerValHisTrpProAlaSerValAr 117	101 388
heGlyArgProThrValArgValMetGlyAlaAspAsnValArgArgIle 100 :::	84 338
eLeuGlnMetLysargArgLysTyrGlyPheIleTyrLysThrHisLeuP 84 ::: :::	67 288
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MetGlyLeuProAlaLeuLeuAlaSerAlaLeuCysThrPheValLeuPr 17 	1 88

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1464
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            SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: June 25, 1997
                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1
COMPUTER: COMPAQ, 1BM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
                                                                                                                                                                                                                                                                       APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
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                                                                                                                                                                     STATE: (
                                                                                                                                                                                                         STREET:
CITY: T
                                                                                                                                                                                                                      ADDRESSEE: Blake, Cassels & Graydon STREET: Box 25, Commerce Court West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTACCCAGTGGACAATCTCCCTACCAAATTCACTAGTTAT 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alTyrProValAspAsnLeuProAlaArgPheThrHisPhe 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              euLysSerLysGlyLeuLeuCysLysSerAsnGlnAspAsnLysLeuAsp 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAATTGGATTCTCTCAAACGGACCCCCGACAATGAAAACAGGCCCGACTA 1513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sAspTrpGlnLeuLeuAsnGlyProProThrMetLysThrSerProThrV 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTCCAGCCGGAGAGATTCATGAGCAAAGGTCTGGAGGACGGGTCCAGGT 1363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCAGGAGAAGGTTGAAATGGGCATGTATACACCTGGAAAGGGCTTGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hrPheGluLeuAsnGlyTyrGlnIleProLysGlyTrpAsnValIleTyr 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eThrTyrLeuGlyLeuTyrProHisValLeuGlnLysValArgGluGluL 330 ::::|||||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGGAGCTGTTGGACCAGCTGAAGTACACTGGATGTGTGATTAAAGAGAC
                                                                                                                                                           M5L 1A9
                                                                                                                                                                                                           Toronto
                                                                                                                                                                                      Ontario
                                                                                                                                                                                                                                                                                                                                                                               Application US/08882164D
                                                                                                                                                                       Canada
                                US/08/882,164D
                                                                                                                     1.4 Mb
                                                                                                                     storage
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alignment_scores:
Quality: 1738.00
Ratio: 4.080
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US-09-668-482-4 x US-08-882-164D-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1850 base pairs
588
                                                                                             151 CysTyrValProValI1eThrGluGluValGlySerSerLeuGluGlnTr
                                                                                                                                                488
                                                                                                                                                                                   134
                                                                                                                                                                                                                          438
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REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          338
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NAME: Hunt, John C.
                                                                                                                                                                                                                                                                                                                                                                                                             84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 erGlyArgAspArgSerCysAlaLeuProLeuProProGlyThrMetGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
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||||:::|||||||||
|TCTGCGCATGAAACGGCAGAATACGGGTGCATCTACAAGACGCACCTCT
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                                                                                                                                                                                                                        AACCATCCTGGGCTCTGACACCCTCTCCAATGTCCATGGAGTTCAACACA
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85.714
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. GTGCTGGTTTATCCAGAAA
625
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1364
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1464 CAATTGGATTCTCTCAAACGGACCCCCGACAATGAAAACAGGCCCGACTA 1513
                                                                                                                                                                                                                                                                                                                                                                     1314 GTTCCAGCCGGAGAGATTCATGAGCAAAGGTCTGGAGGACGGGTCCAGGT 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1264 AGCATCTGTGACACGCACGATGTGGCCGACGTCTTTCCAAACAAGAGGA 1313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1064 TTCAGGAGAAGGTTGAAATGGGCATGTATACACCTGGAAAGGGCTTGAGT 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 LeuLeuPheGlyGlyHisGluThrThrAlaSerAlaAlaThrSerLeuIl 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        914 GAAGTGACGAACCTTTTAGTTTGCAGGCGATGAAAGAAGCAGCTACAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 luArgGlyGluArgLeuAspMetGlnAlaLeuLysGlnSerSerThrGlu 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 864 CGAACAGAAATACAAAGACGCCCTTCAGCTGTTGATCGAGAACAGCAGAA 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 IleGluGlnAsnIleArgAlaLysIleCysGlyLeuArgAlaSerGluAl 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             717 TTTTGAGGAAATGATCAAAAACTTGTTCTCCTTGCCAATCGACGTTCCTT 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 aPheGluGluMetThrArgAsnLeuPheSerLeuProIleAspValProP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 Pro...GlnLeuAlaGlyAspGlyAspSerGluGlnGlnLeuValGluAl 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               626 TGAAGAAACTCATGTTTCGGATAGCTATGAGAATCCTGCTTGGTTTTGAA 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 alLysArgLeuMetPheArgIleAlaMetArgIleLeuLeuGlyCysGlu 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aGlyGlnGlyCysLysAspAlaLeuGlnLeuLeuIleGluHisSerTrpG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAGAGCAAATAAAGACGGAC......GAGCAAGAACTGGTGGAAGC
                                                                                                                                                          PheAlaLysIleLeuLeuLysIlePheThrValGluLeuAlaArgHisCy 463
                                                                                                                                                                                                                                                  heSerPheIleProPheGlyGlyGlyLeuArgSerCysValGlyLysGlu 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerIleCysAspThrHisAspValAlaGluIlePheThrAsnLysGluGl 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          euLysSerLysGlyLeuLeuCysLysSerAsnGlnAspAsnLysLeuAsp 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eThrTyrLeuGlyLeuTyrProHisValLeuGlnLysValArgGluGluL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTGAGGAAAACATCAGGAAGAAAATTCAAGAT...GACGACAATGAAAA 863
                                                           sAspTrpGlnLeuLeuAsnGlyProProThrMetLysThrSerProThrV 480
                                                                                                                            TTCGCCAAAGTGTTACTCAAGATCTTTTTAGTTGAGTTAACGCAGCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                             uPheAsnProAspArgPheSerAlaProHisProGluAspAlaSerArgP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rLeuArgLeuAsnProProValProGlyGlyPheArgValAlaLeuLysT 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1263
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-882-164D-38
                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-08-882-164D-38
                                                                                                                                                                                                                                                                                                                                                US-09-668-482-4 x US-08-882-164D-38
                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Petkovich, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1514 TITACCCAGTGGACAATCTCCCTACCAAATTCACTAGTTAT 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21,1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1,1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480 alTyrProValAspAsnLeuProAlaArgPheThrHisPhe 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 4164 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                           131 GGAAATACGGCTTCATCTACAAGACGCATCTGTTTGGGCGGCCCACGGTG 180
                                                                                                                                                   56 uThrLeuGlnMetValLeuGlnArgArgLysPheLeuGlnMetLysArgA 73
                                                                                                                                                                                                               40 CysAlaLeuProLeuProProGlyThrMetGlyPheProPhePheGlyGl 56
90 ArgValMetGlyAlaAspAsnValArgArgIleLeuLeuGlyAspAspAr 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/US/
FILING DATE: June 25, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hunt, John C. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                rgLysTyrGlyPheIleTyrLysThrHisLeuPheGlyArgProThrVal 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-882-164D-38
                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 1712.00
Ratio: 4.019
milarity: 40.727
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M5L 1A9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6306624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Blake, Cassels & Graydon Box 25, Commerce Court West
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                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50767/00010
                                                                                                                                                                                                                                                                                                     from: 1 to: 4164
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                                                                                                                                                                                                                                                                                                                                                                                                                 38.815
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288	274 euīleGluHisSerTrpGluArgGlyGluArgLeuAspMetGln	N
27 4 1080	257 yLeuArgAlaSerGluAlaGlyGlnGlyCysLysAspAlaLeuGlnLeuL ::: ::	10:
257 1030	241 AsnLeuileHisAlaArgIleGluGlnAsnIleArgAlaLysIleCysGl 	9 2 2
240 980	236Gly.MetLysAlaArg	9 2
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ũ	34 Tyrarq	
233	217 etThrArgAsnLeuPheSerLeuProIleAspValProPheSerGlyLeu 	80 N
217 830	200 uAlaGlyAspGlyAspSerGluGlnGlnLeuValGluAlaPheGluGluM 	7
200 780	184 LeuMetPheArgIleAlaMetArgIleLeuLeuGlyCysGluProGlnLe 	7:
183 730	167 rpLeuSerCysGlyGluArgGlyLeuLeuValTyrProGluValLysArg 	6
167 680	50 uCysTyrValp : 31 GTGCTACGTGC	6 11
150 630	39	5 1:
580	31 CGAAGGGGGGGGGCTGAGGGAAAGTAGAGGATTGTAACACTCTCT	Uī
138	38	н
530	81 TGGGTTAGTCCTGGGGGGGGACTGAAATTCTTGAAAGGGTACTCGGAAAG	4
138	38	11
480	31 GACCAGGACCCTCTCTATCTGAGATCCACTTTAGCTTTTCTGCTAGCAC	4
138	38	
430	81 TGGTTCAGGCAAAATAGAATGCGGGGGGGGGGGCTAGTCCTATGTGGTGG	ω
138	38	<u> </u>
380	31 AGGGTGAGCTGGCAACTCCTTGGCTGGCAGGGAGACCTCATCCTATGG	ω
138	38	1
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w	23 lvCvsLeuSerAsnLeuHisAspSerSerHisLvsGlnArgLvs.Lvs.	
123 280	106 gLeuValSerValHisTrpProAlaSerValArgThrIleLeuGlySerG	2:
230		18

3 2030	GGGGGAGAGACTCCACCTCGTGAATTTAAAAAGGCAGTTGTTTGT	1981
. 332		332
r 1980	GATACACCCAGTACTATGACAGTGAAGATCTGAGAGCTAGGTGGGACTGT	1931
. 332		332
1930	CATTCCTCTATTAACCACCACCACCACCCCCCCCTGTATATAAGTTTGCTC	1881
. 332		332
. 332 A 1880	LuLeuLysSer	329 1831
3 329 1 1830	ulleThrTyrLeuGlyLeuTyrProHisValLeuGlnLysValArgGluG 	312 1781
312 1 1 1780	GluLeuLeuPheGlyGlyHiSGluThrThrAlaSerAlaAlaThrSerLe 	296 1731
r 295 1 1730	AlaLeuLysGlnSerSerThr	289 1681
4 1680	CAATATTCTCAGGTCAGGTCTTTGTAACAGTGCTATAAACTGCACTCAGA	1631
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3 1630	TCTTTGACTTTCTATGAACAAAACGGATTTTACCCTTGAAGTCTTCCGTG	1581
. 288		288
3 1580	GGTTAAAGCGGAAGAGCAGGATTAAGGGAGTTTTGCGTTTTTGTTGTGG	1531
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N 1530	TGAGCAATGGGGAAGATCCCAAAGTTCAAAGGGCAAGGCTCATCTACAAA	1481
. 288		288
1480	AACCGTATTAAAGGGTGGCATTGGTCTAGAGAGCTGTGGAAGGGGGTGGC	1431
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3 1430	GAAGTAGCAACAAAGATAATTTTATCGTTGGGGGTCACCACAACACGAGG	1381
. 288		288
r 1380	ATATCCGATATTTACATCAAGAAACATAACAGTAGCAAAATTACCGTTAT	1331
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1330	CTTCACGGAGCCAAACAACCCTTTCAGAAGGGTCGCCTAAGAGCATCTGC	1281
. 288		288
1280	GTGGGCGGCGATGCTAGGTCTAGAGCTTTTCAACCTGTGGGTCGTGACCC	1231
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1180	AGCAATTTCAAAAAGGTGCCAAGGGCCGGGGAGTGCCTCTGACTTTCCAGA	1131
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N 1130	TGATTGAGCACTCGTGGGAGAGGGGGAGAGGGCTGGATATGCAGGTGAGA	1081

	2930	404 ValAlaGluTlePheThrAsnLysGluGluPheAsnProAspArgPheSe :::
	∞ o	yrSerTleCysAspThrHisA ACAGTATCTGTGACACCCACG
		2781 CCGGGATTGTCAATTCTTAGGATTTTTTTTTTTTTTAAACAGGGATACC
	2780	31 CTTAATGCCATCCATGCTAGTAATGACTTTTTGTTGTTGCAAGCTCAGG
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	2730	2681 TTGACAGTGTCCTGCCTCCTATGGTACTGGGAACCAATTTGCTCTCTCT
	382	382
	2680	2631 CTCTGCTATGCTGTTGAGCATCAGCTGCCCAGAGCAGTGGCTCACTGCCC
	382	382
	2630	2581 GAATGTGAGTGCACCTCTGTCCCCCACCCCAGCCCTCGTCCACGTCCA
	382	382
	2580	
	382	${\tt nProProValProGlyGlyPheArgValAlaLeuLysThrPheG}$
	366 2530	350 euGluGlnLeuLysTyrIleGlyCysVallleLysGluThrLeuArgLeu
	2480	GCTTACTTTGCAAGAGCAATCAAGACAACAAGTTAGACATGGAAACT
	350	LeuCysLysSerAsnGlnAspAsnLysLeuAspMetGluIl
	2430	2381 TTTTTGGAGTGCCCAGGGATCCATCACTCACTTTTTTATCTGTTTCCATA
	333	333Lys.
	2380	2331 CAGACGCCTTCAGGTTTAGTTAACAGGTGAGTCCTGCTGGGCTGACTTTT
	332	332
	2330	2281 AAAGGAAGGCCATCAGGCCATCAGCTCTTTCCCTTTTATCCTCTCCCATC
	332	332
	2280	2231 CCTGATAAGCAACATTGTCTGGATAATGGGTTTAGGCTGAGGAAGTGTGG
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	2230	2181 TGATCAGGGTCGCAGTGTTGGTGAGGGCTCAGGGTATGACCCTTTATATA
	332	332
	2180	2131 TTCTCCTTTCCCTGACCAAGAACATGAATAATGTGATTAGAGCCAATAGC
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•	2130	2081 CCTCTTCCTCCACCACCACCACCATCACCACCTTTTATAGAGCAAGG
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	2080	2031 GCTCTCTTGGGCAGAATTTGACCCTCTCCTCCTCCTCCTCCTCCT
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Patent No. 6306624
GENERAL INFORMATION:
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                                                                                                                                                                                                     APPLICATION NUMBER: US/08/882,164D
FILING DATE: June 25, 1997
PRIOR APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: OCTOBER: 08/724,466
FILING DATE: OCTOBER: 08/724,466
APPLICATION NUMBER: 08/724,466
FILING DATE: OCTOBER: 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: HUNT, JOHN C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEPHONE: (416) 863-2653
INFORMATION FOR SED ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 2677 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
alignment_block: US-09-668-482-4 \times US-08-882-164D-36
                                                                                                                             alignment_scores:
                                                                                                                                                                                          US-08-882-164D-36
                                                         Quality: 1365.00
Ratio: 4.320
Percent Similarity: 47.235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      470 yProProThrMetLysThrSerProThrValTyrProValAspAsnLeuP 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage COMPUTER: COMPAQ, IBM PC compatible OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: Canada ZIP: M5L 1A9 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Box 25
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Blake,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ontario
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Box 25, Commerce Court West
                                                               Percent Identity: 46.936
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157	141 MetArgAlaPheSerArgGluAlaLeuGluCysTyrValProValIleTh
1525	
140	Valile
1475	GTCTGGCAGGACTGGGGGTGTCTGGAAGGGGACGGCGGTAGACGAGAG
138	8
1425	CTTTCCCAGCTCGGAGAGTGCCAT
138	
1375	CGGGCTAGCAGCTTGAGGTGGGCT
138	
1325	3GGAGGGGGACCCCATTTATGAGCG
138	
138 1275	erSerHisLysGlnArgLysLys
122 1225	06 rgLeuValSerValHisTrpProAlaSerValArgThrIleLeuGlySer
106 1175	<pre>gArgIleLeuLeuGlyAspAspA ::: !CGCATCTTGCTCGGAGAGCACC</pre>
89 1125	yPheIleTyrLysThrHisLeuPheGlyArgProThrVa
72 1075	64ArgArgLysPheLeuGlnMetLysArg
1025	6 CAGGGCTG
63	ω
975	TGAAGTCGGGGTAGGCGCCCCCGGGAGGCATGCTATTGCGGCTAGGA
63	•
925	GGGCGGGACAGGCTGCTTCCCCGGAGCCCGGCGCGCGCTCTGGGCTTC
63	63
875	826 TICCCCTTCTTTGGGGAAACCTTGCAGATGNTACTNCAGGTAAGGGAGGG
63	- P
50 825	34 erGlyArgAspArgSerCysAlaLeuProLeuProProGlyThrMetGly
34 775	17 oLeuLeuPheLeuAlaAlaIleLysLeuTrpAspLeuTyrCysValS
17 725	1 MetGlyLeuProAlaLeuLeuAlaSerAlaLeuCysThrPheValLeuPr
	Align seg 1/1 to: US-08-882-164D-36 from: 1 to: 2677

2475	AAGATATTGCTTTCCTTGACTTTCTGTCAGCAAAACATTTAGCCCCTTCTA	2426	
288		288	
2425	TACTCGCCTTACTGCTCCAGCTGAACTAAAGGGACGTTGCATTTTTTTT	2376	
288		288	
2375	CTTTAACTCAGGAGTTTCCGGTAGRGCGGGGTCG	2326	
288		288	
2325	TCAAAGGGAAAGTTGGAATTTGCAAAAATGTTAATAAAGAACCTTGCGAT	2276	
288		288	
2275	GGAAGGGGCTGCGGMGGAAACTGGGAGCATCCCCTAGCCTTTAMCAGGTT	2226	
288		288	
2225	CAGCTATGGAATCCCGAAGGAAGGCTGAGACACCCGGTCAGGAGAGCTGC	2176	
288		288	
2175	AGCGCGCCTGGGGCCCAGCTTTCTGGAGTGGGCGGCCGGC	2126	
288		288	
2125	GCGGAGTTTGGTCCCCTGGCTTTCCAAGGCGCTGTTCCTGGGGCCCCCAA	2076	
288		288	
2075	GTAGCAGCTTCAGACCAGGCAC	2026	
288	rgGlyGluArgLeuAspMetGln	281	
281 2025	yGlnGlyCysLysAspAlaLeuGlnLeuLeuIleGluHisSerTrpGluA 	264 1976	
1975	GIUGINSNILEATGALALYSILECYSGIYLENATGALASETGINAIAGI 	1926	
		٠ .	
247 1925	CTCTCTGCGCTCAGGGCATGAAGGCGCGGAACCTCATTCACGCGCGCATC	236 1876	
1875	GGCTGCGGACTAGGGGCGCGGGACCTGGGCGTCTGCTCACCGCCGCGCG	1826	
235		235	
235 1825	euProIleAspValProPheSerGlyLeuTyrArg	224 1776	
224 1775	uGlnGlnLeuValGluAlaPheGluGluMetThrArgAsnLeuPheSerL 	207 1726	
207 1725	ArgIleLeuLeuGlyCysGluProGlnLeuAlaGlyAspGlyAspSerGl	191 1676	
190 1675	lyLeuLeuValTyrProGluValLysArgLeuMetPheArgIleAlaMet 	17 4 1626	
174 1625	rGluGluValGlySerSerLeuGluGlnTrpLeuSerCysGlyGluArgG 	157	
1575	ATGCGGGCCTTCAGCCGCGAGGCACTCGAATGCTACGTGCCGGTGATCAC	1526	

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seq_documentation_block:
                                     alignment_block: US-09-668-482-4 x US-08-724-466B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-724-466B-11
                                                                                                                                                                                                                US-08-724-466B-11
                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 08/667,541
APPLICATION NUMBER: 08/667,541
FILING DATE: June 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 50.76
REFERENCE/DOCKET NUMBER: 50.76
TELECOMMUNICATION INFORMATION:
TELEPAX: (416) 863-2633
INFORMATION FOR SEQ ID NO: 11:
                                                                                              Ratio:
Percent Similarity:
Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette, 3 1/2 inch; 1.4 Mb storage COMPUTER: COMPAQ, IBM PC compatible OPERATING SYSTEM: MS-POS 5.1 SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/724,466B FILING DATE: October 1, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Toronto
ZIP: M5L 1A9
COUNTRY: Canada
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 ln 324
                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 351 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: bun
STREET: bun
Timy: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rAlaAlaThrSerLeuIleThrTyrLeuGlyLeuTyrProHisValLeuG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysGlnSerSerThrGluLeuLeuPheGlyGlyHisGluThrThrAlaSe 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGCAGGCAGACTTGTGAGAATGTGGGTCTCACTCTATTCTTAGGCACTA 2575
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                                                                                                                                      Quality:
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Box 25, Commerce Court West
to: US-08-724-466B-11
                                                                                                                                                                                                                                      linear
                                                                                              : 614.00
: 5.248
: 100.000
                                                                                                                                                                                                                                                     single
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                                                                                            Length: 117
Gaps: 0
Percent Identity: 100.000
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  from: 1
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      351
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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-882-164D-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/08882164D Patent No. 6306624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: Peckovich, P. Martin, White, Jay A.,

APPLICANT: Beckett, Barbara R., Jones, Glenville

APPLICANT: Beckett, Barbara R., Jones, Glenville

TITLE OF INVENTION: Retinoid Metabolizing Protein

NUMBER OF SEQUENCES: 43
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396 TyrSerIleCysAspThrHisAspValAlaGluIlePheThrAsnLysGl 412
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                                                                        NAME: Hunt, John C.
REGISTAN NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
                                                                                                                                APPLICATION NUMBER: 08/667,546
FILLING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILLING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/
FILING DATE: June 25, 1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Blake, Cassers a commerce Court West
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGACTTTTGAATTAAATGGATACCAGATTCCCAAGGGCTGGAATGTTATC
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21, 1996
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                                                                                                   50767/00010
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US-08-882-164D-11
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US-09-668-482-4 x US-08-882-164D-11
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-882-164D-11 from: 1
                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08622166A Patent No. 5952545
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: KONCZ, CSABA
APPLICANT: MATHUR, JAIDEEP
APPLICANT: SZEKERES, MIKLOS
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                    APPLICANT: SZEKERES, MIKLOS
APPLICANT: ALTMANN, THOMAS
TITLE OF INVENTION: NUCLEIC MOLECULES ENCODING CYTOCHROME
TITLE OF INVENTION: P450-TYPE PROTEINS INVOLVED IN THE BRASSINOSTEROID SYNTHESIS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   379
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                                                                                      STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
                                                                                                                                          ADDRESSEE: Birch, St
STREET: P.O. Box 747
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAACTCCTCTTTGGAGGACACGAAACCACGGCCAGTGCAGCCACATCTCT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uThrLeuArgLeuAsnProProValProGlyGlyPheArgValAlaLeuL 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ysThrPheGluLeuAsnGlyTyrGlnIleProLysGlyTrpAsnValIle 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACCCTTCGACTGAATCCCCCAGTTCCAGGAGGGTTTCGGGTTGCTCTGA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACATGGAAATTTTGGAACAACTTAAATACATCGGGTGTGTTATTAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspMetGluIleLeuGluGlnLeuLysTyrIleGlyCysValIleLysG1 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGACTTTTGAATTAAATGGATACCAGATTCCCCAAGGGCTGGAATGTTATC
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PatentIn Release #1.0, Version
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5.248
100.000
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 #1.30
(EPO)
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; CLONE: C204
; FEATURE:
; NAME/KEY: CDS
LOCATION: 48
US-08-622-166A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-622-166A-1 from: 1 to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1608 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                           313 ACCGGTTTGTTCAGAACGAAGGGAAGCTTTTTGAGTGTTCTTATCCT 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
LIBRARY: lambd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT
NAME: SVENSS
                                                                                                                                                                                                                   263
                                                                                                                                                                                                                                                                                        213
                                                                                                                                                                                                                                                                                                                                                                163
                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 yArgAspArgSerCysAlaLeuProLeuProProGlyThrMetGlyPheP 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 CTCCTCCTCTCTTCCATCGCCGCCGCCTTCCTCCTCCTACTCCGC.. 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                      sThrHisLeuPheGlyArgProThrValArgValMetGlyAlaAspAsnV 97
                                                                                                                                                                                                                                                                                                         ArgArgLysPheLeuGlnMetLysArgArgLysTyrGlyPheIleTyrLy 80
::: |||:::::: ::: :::||||||
                                                                                                                                                                                                                                                                                                                                                                               roPhePheGlyGluThrLeuGlnMetVal.....LeuGln 63
||::::::||||||:::::::
TTCTTTGCATAAACGTATGCACTCTCTCACCATGAGCTTTGCTAATTCTT 462
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                                                                                                                                                                           alArgArgIleLeuLeuGlyAspAspArgLeuValSerValHisTrpPro 113
                                                                                                                                                                                                                                                                                        CCTGAGCCTTTCATCGACGAGAGAGTAGCCCGGTACGGTTCGGTTTTCAT 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuLeuPheLeuAlaAlaIleLysLeuTrpAspLeuTyrCysValSerGl 35
                                                                                                                                                                                                                                                                                                                                                                CTCTGATAGGAGAGACTTTTCAGCTGATCGGAGCTTACAAAACAGAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YAGENT INFORMATION:
SVENSSON, LEONARD R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lambda gt10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
48..1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    433.50
1.521
58.642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/622,166A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 486
Gaps: 13
Percent Identity: 26.543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1608
                                                                       412
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424 1246	PheThrAsnLysGluGluPheAsnProAspArgPheSerAlaProHisPr	408 1197
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374 1096	CysValIleLysGluThrLeuArgLeuAsnProProValProGlyGlyPh ::::: ::: 	358 1047
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341 996	nLysValArgGluGluLeuLysSerLysGlyLeuLeuCysLysSerAsnG ::::::::::::::::::::::::::::::::::::	32 4 953
32 4 952	aAla	308 903
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259 770	ი — დ	245 723
245 722	oPheSerGlyLeuTyrArgGlyMetLysAlaArgAsnLeuIleHisA 	229 684
229 683	rArgAsnLeuPheSerLeuProIleAspValPr ::::::::: :: ::::::	213 636
212 635	nLeuAlaGlyAspGlyAspSerGluGlnGlnLeuValGlu ::: :::::::::	196 601
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344	80 sThrHisLeuPheGlyArgProThrValArgValMetGlyALaAspAsnV	
80 294	IG::Yr	
63 244	47 lyThrMetGlyPheProPhePheGlyGluThrLeuGlnMetValLeuGln	
47 194	30 uTyrCysValSerGlyArgAspArgSerCysAlaLeuProLeuProProG :::	
30 169	14 PheValLeuProLeuLeuPheLeuAlaAlaIleLysLeuTrpAspLe ::::: ::: ::: 15 TTCATTATACCTTTGCTACTCTTATTGGGCCTAGTATCTCGGCTT	
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	1432 CGATCTTC 1439	
491 1431	tLysThrSerProThrValTyrProValAspAsnLeuProAlaArgPhef::::::::::::::::::::::::::::::::::::	
474 1381		
457 1346	441 erCysValGlyLysGluPheAlaLysIleLeuLeuLysIlePheThrVal (

373	yCysValIleLysGluThrLeuArgLeuAsnProProValProGlyGly	357
1154	CCGGCGAGTCGAAGAGAAAGACTTCGAGAAGCTCACCTACTTGA	1109
357	nAspAsnLysLeuAspMetGluIleLeuGluGlnLeuLysTyrIleG	340
1108	AGAACTCGCCGTGGTGGTGGGTCTT	1073
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324 1072	laAlaThrSerLeuIleThrTyrLeuGlyLeuTyrProHisValLeuGln	308 1023
1022	erThrGiuLeuLeuPheGlyGlyHisGluThrThrAlaSerA ::::::::: TCATGGACGTAATGTTTGGAGGGACCGAAACGGTGGCGTCCG	973
972	Η.	923
922	InGlyCyslysAspAlaLeuGlnLeuLleGluHisSerTrpGluArg	873
872	» c	
0 0	gAsnLeuIleHisAlaArgIleGluGlnAs 	234 773
233 772	roPheSerGly! ::: CTTGGCTCAAATGGGTTCCTCAGGGG	223 723
223 722	luMetThrargAsnLev :::::::::::::::::::::::::::::::::::	208 673
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151 520	rgAlaPheSerArgGluAlaLeuGluCys :: :: AATTATTTAGCCGGAAACGAGCCGAGTCG	135 471
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Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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Quality:
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TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1405 TCGTCGGTCTTGCCCCGGTATGCAACTCGGACTCTACGCGCTAGAGACG. 1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1493 CCGGACGGGATGAAACCGAGT 1513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1454 ..ACTGTGGCTCACCTCCTTCACTGTTCACGTGGGAGTTG...... 1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1255 GAAATCGCGGGTGATGATCAACGCGTGCGCCATCGGCCGGGACAAGAACT 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1205 CTCCACGAGACTGCCGAGGACGCCGAGGTCGGCGGCTACTACATTCCGGC 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438 yLeuArgSerCysValGlyLysGluPheAlaLysIleLeuLeuLysIleP 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424 ProGluAsp.....AlaSerArgPheSerPheIleProPheGlyGlyGl 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             471 ProProThrMetLysThrSer 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   455 heThrValGluLeuAlaArgHisCys...AspTrpGlnLeuLeuAsnGly 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     390 sGlyTrpAsnValIleTyrSerIleCysAspThrHisAspValAlaGluI 407
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1.376
56.054
                                                                                                                                                                                                             Length: 446
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Percent Identity: 25.112
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279 4120080	262 ualaGlyGlnGlyCysLysAspAlaLeuGlnLeuIleGluHisSerT
262 4120130	246 ArgIleGluGlnAsnIleArgAlaLysIleCysGlyLeuArgAlaSerGl::: :::::::::::::::::::::::::::::::
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4119		4119913
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μ ω	uThrLeuArgLeuAsnPro 	379 4119834
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. 3 4119	396 TyrSerIleCysAspThrHisAspValAlaGluIlePheThrAsnLysGl::::::::::::::::::::::::::::::::::::	412 4119734
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seq_d; Seq ; Path ; Gent ; Gent ; App ; App ; App ; TII ; TII ; TII ; CUU ; CUU ; SOO ; SEQ ; SE	seq_documentation_block: Sequence 1, Application US/09103840A Sequence 1, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION: APPLICANT: FILESCHMAN, Robert D. APPLICANT: FRASER, Claire M. APPLICANT: VENTER, John C. TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-20007.00 CURRENT APPLICATION UNMBER: US/09/103,840A CURRENT FILING DATE: 1998-06-24 NUMBER OF SEQ ID NOS: 2 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1 LENGTH: 4411529 TYPE: DNA ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37RV US-09-103-840A-1	MYCOBACTERIUM
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412	48 rMetGlyPheProPhePheGlyGluThrLeuGlnMetValLeuGln	63 4128543

4127718	GGC GGC
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329 4127735	312 uIleThrTyrLeuGlyLeuTyrProHisValLeuGlnLysValArgGluG::: ::::
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295 4127835	279 rpGluArgGlyGluArgLeuAspMetGlnAlaLeuLysGlnSerSerThr
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31 rCysValSerGlyArgAspArgSerCysAlaLeuProLeuProProGlyT 48	15 ValleuProLeuLeuPheLeuAlaAlaIleLysLeuTrpAspLeuTy 31 :::: ::::: 80 GTTGTCTCTTTTCATCTTCATCATCTTCATC	US-09-6 Align s	lignmen	LENGTH: TYPE: DA ORGANISA S-09-091-43	EARLIER APPLICATION EARLIER FILING DATE EARLIER FILING DATE EARLIER FILING DATE NUMBER OF SEQ ID NO SOFTWARE: Microsoft	CURRENT APPLICATION NUMBER: US/09 CURRENT FILING DATE: 1998-06-18 EARLIER APPLICATION NUMBER: PCT/U EARLIER FILING DATE: 1996-12-19	മ്ഷം	<pre>seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-09-091-432-1</pre>	446 GluPheAlaLysIleLeuLeuLysIlePheThrVal 457 ::: ::: :::::::: 4127447AACTTTTCGATGCGAGAGTTGATCACCGTA 4127418	429 rgPheSerPheIleProPheGlyGlyGlyLeuArgSerCysValGlyLys 445 :::::::::::	412 uGluPheAsnProAspArgPheSerAlaProHisProGluAspAlaSerA 429 : ::: ::: ::: ::: ::: :::	396 TyrSerIleCysAspThrHisAspValAlaGluIlePheThrAsnLysGl 412 :: ::: :: :: ::	379 ysThrPheGluLeuAsnGlyTyrGlnIleProLysGlyTrpAsnValIle 395 ::::::::::::::::::::::::::::::::::::	362 uThrLeuArgLeuAsnProProValProGlyGlyPheArgValAlaLeuL 379 :::::: :: 4127688GACGTTGCGGTCCGCCCGCCCGTTGACGGCTCGTGTCGCCGCGC 4127639	4127717GAAGCCTTCACGACGCGTGATCAACGA 4127689	362 uThrLeuArgLeuAsnProProValProGlyGlyPheArgValAlaLeuL 379
362 unthrieulargienAsspropovalProdlyGlyPheArgyalAlieui 379 412788BGACGTTGCGGGGGGGCGCGCGCGCGCGGGCGTTGACGGGCGGG	362 uffhrLeuArgLeuAsnProProValProGlyGlyPheArgVallAlaeuLi 379 4127688GACGTTGCGGGTGCGCCCGCCGCCGGTTGCGGGCCGCCCCCC	362 WithrleuArgieuAsplerproValProGlyGlyPheArgValAlLeLL 379	362 urhrLeuargLeuAsnProProValProGlyGlyPheArgValhileuL 379 4127688GACGTTGCCGCCCCCCCCCCCCCCCCCCCCCCTTGCCCCCCC	362 uThrLeuArgLeuAsnProProValProGlyGlyPheArgValAlaLeuL 379 4127688GACGTTGCGGGTGCGCCCCGCGCCCTTGACGGTTGACGGCTCGTGTGCCCCCC 4127639 379 ySThrPheGluLeuAsnGlyTyrGlnIleProLysGlyTrpAsnValIle 395 379 ySThrPheGluLeuAsnGlyTyrGlnIleProLysGlyTrpAsnValIle 395 3127638AACCACTAACCATCGGGGTTACCGTGTGAGGCTTGAGCACGAATCGTG 4127589 396 TyrSerIleCysAspThrHisAspValAlaGluIlePheThrAsnLysGl 412 412758BGTCCACATCATCGCGATCACCGCAGCAGCAGCAGCAACCAAC	362 uThrLeuArgLeuAsnProProValProGlyGlyPheArgValAlaLeuL 379	362 uThrLeuArgLeuAsnProProValProGlyGlyPheArgValAlaLeuL 379	362 uThrLeuArgLeuAsnProProValProGlyGlyPheArgValAlaLeuL 379	362 uThrLeuArgLeuAsnProProValProGlyGlyPheArgValAlaLeuL 379	362 uThrLeuArgLeuAsnProProValProGlyGlyPheArgValAlaLeuL 379 ::::: ::	362 uThrLeuArgLeuAsnProProValProGlyGlyPheArgValAlaLeuL 379 ::::: ::: 127688GACGTTGCGGGTGCGCCCCCCCCCCCCCCCCCCCCCCC	362 uThrLeuArgLeuAsnProProValProGlyGlyPheArgValAlaLeuL 379 ::::: ::: :::	362 uThrLeuArgLeuAsnProProValProGlyGlyPheArgValAlaLeuL 379	362 uThrLeuArgLeuAsnProProValProGlyGlyPheArgValAlaLeuL 379 ::::: ::: 27688GACGTTGCGGGTGCGTCCGCCCGCGCGTTGACGGCTCGTGTCGCCGCGC 412763			7717GAAGCCTTCACGACGCGGTGATCAACGA 4127

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237 736	alProPheSerGlyLeuTyr	228 687
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; Sequence 2, Application US/09103840A
; Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 2
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
-09-103-840a-2
                                                                                                                                                                                                                                                APPLICANT: FLEISCHIAN, Robert D.
APPLICANT: FLEISCHIAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WENTER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVERTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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                                                                                                 LENGTH: 4403765
TYPE: DNA
ORGANIAM: Mycobacterium tuberculosis
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alignment_scores: Quality: Ratio:

400.00 1.481

Length: Gaps:

ercent Similarity: 55.556 Percent Identity: 28.189	
.ignment_block: IS-09-668-482-4 x US-09-103-840A-2	
ulign seg 1/1 to: US-09-103-840A-2 from: 1 to: 4403765	
37 AspArgSerCysAlaLeuProLeuProProGlyThr	8 415334
49MetGlyPheproPhepheGlyGluThrLeuGlnMetValL 62	2 415384
62 euGlnArgArgLysPheLeuGlnMetLysArgArgLysTyrGlyPheIle 78 ::: ::: 3415385GCGGCGGACCGGACTATCTGATGTTCCTG 341	8 415413
79 TyrLysThrHisLeupheGlyArgProTh 88	8 415463
88 rValArgValMetGlyAlaAspAsnValArgArgIleLeuLeuGlyAspA 105	05 415513
105 spargLeuValSerValHisTrpProAlaSerValArgThrIleLeu 120 :::::	20 415563
121 GlySerGlyCysLeuSerAsnLeuHisAspSerSerHisLysGlnArgLy 137	37 415610
137 SLYSVALIILeMetArgAlaPheSerArgGluAlaLeuGluCySTyrValP 154 ::::::::::::::::::::::::::::::::::::	54 415660
154 roValIleThrGluGluValGlySerSerLeuGluGlnTrpLeuSer 169 ::: ::: ::::::: ::: 3415661aGCAGATGGACAGGGTCGTCTCGCGGGTGGTCGCCGACGACTGGGTC 341	.69 415707
170 CysGlyGluArgGlyLeuLeuValTyrProGluValLysArgLeuMetPh 186 ::::::::::::::::::::::::::::::::::::	.86 415757
ω κι	03 415801
ων	19 415851
220 AsnLeuPheSerLeuProIleAspValProPheSe 231	31 415892
231 rGlyLeuTyrAryGlyMetLysAlaArgAsnLeuIleHis	44 415939
245AlaArgIleGluGlnAsnIleArgAlaLysIleCysGlyLeuArgAla 260 ::::::::	60 415962
261 SerGluAlaGlyGlnGlyCysLysAspAlaLeuGlnLeuLeuIleGluHi 277 ::: ::: ::: ::: ::: 3415963GAAGCGTCGGGGCAACGACCTGCTGACGGTGTTGTGCCAGAC 341	77 416003
277 sSerTrpGluArgGlyGluArgLeuAspMetGlnAlaLeuLysGlnSerS 29	94

	485 snLeupro 487 ::::: 3416615GGATGCCG 3416622
485 3416614	468 uAsnGlyProProThrMetLysThrSerProThrValTyrProValAspA
468 3416574	452 LeuLysIlePheThrValGluLeuAlaArgHisCysAspTrpGlnLeuLe
451 3416532	443 alglytysglupheAlatysIleteu
443 3416482	426 pAlaSerArgPheSerPheIleProPheGlyGlyGlyLeuArgSerCysV :::::
426 3416432	411 LysGluGluPheAsnProAspArgPheSerAlaProHisProGluAs
410 3416382	394 alileTyrSerIleCysAspThrHisAspValAlaGluIlePheThrAsn
394 3416332	377 aLeuLysThrPheGluLeuAsnGlyTyrGlnIleProLysGlyTrPAsnV ::::::: ::: 3416283GGTGCGCGATACCGAACTGCTGGGCTACTACCTACCCAAGGGCACCAACG
377 3416282	361 LysGluThrLeuArgLeuAsnProProValProGlyGlyPheArgValAl:::: :::::
360 3416232	344 ysleuAspMetGluIleLeuGluGlnLeuLysTyrIleGlyCysValIle
344 3416182	327 gGluGluLeuLysSerLysGlyLeuLeuCysLysSerAsnGlnAspAsnL ::: ::: 3416154CGACGAATCGGACCGGCATGGCGATGGGC
327 3416153	311 SerLeuIleThrTyrLeuGlyLeuTyrProHisValLeuGlnLysValAr ::::::
310 3416103	294 erThrGluLeuLeupheGlyGlyHisGluThrThrAlaSerAlaAlaThr
3416053	3416004CGAAGACGACGACGGCAACCGGTTCTCCGACGCCGACATCGTCAACCACA 3416053

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Title:
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| SIDSI/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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Copyright (c) 1993 - 2000 Compugen Ltd
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            Cytochrome zP450RA
Zebrafish retinoid
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ALIGNMENTS

AAW37735 RESULT

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AAW37735 standard; Protein;

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AAW37735;

Identifying DNA encoding inducible or suppressible cytochrome P450 - by screening for drugs which reduce the catabolism of retinoic acid, useful in cancer chemotherapy and the treatment of acne and N-PSDB; AAV09252. 01-OCT-1996; 21-JUN-1996; 23-JUN-1997; 31-DEC-1997 W09749832-A2 Synthetic Retinoid regulated gene; cytochrome P450 gene; enzyme; oxidative metabolism; P450RAI; retinoic acid; RA; promoter; isoform. Cytochrome P450RAI isoform 07-JUL-1998 WPI; 1998-077193/07. Petkovich PM; (TOOH) UNIV QUEENS KINGSTON (first entry) 96US-0724466. 96US-0667546. 97WO-CA00488

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Best Local
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Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid; mouse; inhibitor; antibody; cancer; actinic keratosis; oral leukoplakia; head tumour; neck tumour;
                                                               Mouse retinoid metabolising protein mP450RAI.
                                                                                                                                                         AAW44161 standard; Protein; 497 AA
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                                                                                             (first entry)
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Matches 497
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21-JUN-1996;
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 301 GHETTASAATSLITYLGLYPHVLQKVREEIKSKGLLCKSNQDNKLDMETLEQLKYIGCVI 360
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                                                                                                                                                         121
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                                                                                                                                                                                                                                     61 VLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVHWPASVRTIL
                                                                                                                                                                                                                                                                             1 MGLPALLASALCTFVLPLLLFLAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETLQM
                                                                                         \verb|vkrlmfriam| rillgcepgpagggedeqqlveafeemtrnlfslpidvpfsglyrgvkar|
                                                                                                                                                                                        GAGCLSNLHDSSHKQRKKVIMQAFSREALQCYVLVIAEEVSSCLEQWLSCGERGLLVYPE
                               nliharieenirakirrlqatepdggckdalqlliehswergerldmqalkqsstellfg
                                                                                                                         VKRLMFRIAMRILLGCEPGPAGGGEDEQQLVEAFEEMTRNLFSLPIDVPFSGLYRGVKAR 240
                                                                                                                                                                                                                    vlqrrkflqmkrrkygfiykthlfgrptvrvmgadnvrrillgehrlvsvhwpasvrtil
                                                           NLIHARIEENIRAKIRRLQATEPDGGCKDALQLLIEHSWERGERLDMQALKQSSTELLFG
                                                                                                                                                       gagclsnlhdsshkqrkkvimqafsrealqcyvlviaeevsscleqwlscgergllvype
                                                                                                                                                                                                                                                                                                                                              497;
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100.0%; Score 2612; DB 19; 100.0%; Pred. No. 9e-244;

Length 497;

0; Mismatches

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Gaps

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240

300

180

120

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cells exposed to retinoic acid. Zebrafish, human and mouse P450RAIS (see AAW44159-61) are claimed. They can be expressed in host cells and used to metabolize retinoic acid in an organism or cell, in drug screening, and to raise antibodies useful for inhibiting retinoic acid hydroxylation for the treatment of cancer, actinic keratosis, oral leukoplakia, secondary tumours of the head and/or neck, non-small cell lung carcinomas, basal cell carcinomas, acute promyelocytic leukaemia, skin cancer, and premalignancy associated with actinic keratosis, acne, psoriasis and/or ichthyosis.
                                                                                                                                                                                              This protein comprises a novel mouse retinoid metabolising protein, designated mp450RAI. Its amino acid sequence was deduced from a cDNA clone (see AAV12205) isolated from a retinoic acid-treated P19 teratocarcinoma library. It includes a haem-binding motif characteristic of cytochrome P450 proteins. mp450RAI is a retinoid oxidase that has the ability to hydroxylate retinoic acid at the 4 position of the beta-ionone ring, and is inducible in epithelial cells exposed to retinoic acid. Pebrafish, human and mouse P450RAIs cells exposed to retinoic acid.
                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 65-66; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-small cell lung carcinoma; basal cell carcinoma;
acute promyelocytic leukaemia; skin cancer; acne; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Retinoid metabolising protein - useful to develop products to treat, e.g. cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TOOH ) UNIV QUEENS KINGSTON
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497 AA;
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96US-0667546
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Query Match
Best Local Similarity
Matches 464; Conserv
                                                                                                                                                                    This is the amino acid sequence of the human cytochrome P450RAI. Its expression is dependent on the presence of retinoic acid (RA). The retinoid-regulated genes such as the inducible cytochrome P450RAI gene specifically metabolises a derivative of the RA. The cytochrome P450 gene in general produces enzymes involved in the oxidative metabolism of endogenous and exogenous compounds. The cytochrome P450 nucleotide sequence can be used to induce or suppress the expression of its protein. P450RAI is highly induced by RA in cell lines and tissues. This allows for development of a drug screen using promoters and nucleotide sequences to identify drugs which are useful for reducing the catabolism of RA.
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21-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying DNA encoding inducible or suppressible cytochrome P450 by screening for drugs which reduce the catabolism of retinoic acid useful in cancer chemotherapy and the treatment of acne and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-077193/07.
N-PSDB; AAV09247.
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|ypvdnlparftyfqgdi 497
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96US-0667546.
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sm; P450RAI; retinoic acid; RA; promoter
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                                                                                                                                                         Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid; human; inhibitor; antibody; cancer; actinic keratosis; oral leukoplakia; head tumour; neck tumour; non-small cell lung carcinoma; basal cell carcinoma; acute promyelocytic leukaemia; skin cancer; acne; psoriasis; ichthyosis; therapy; diagnosis; screening.
                                                                                                                                                                                                                                                                AAW44160 standard;
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                                                                                                                                                                                                                Human retinoid metabolising protein hP450RAI.
                                                                                                                                                                                                                                 22-JUN-1998
                                                                     01-OCT-1996;
21-JUN-1996;
                                                                                             23-JUN-1997;
                                                                                                                            WO9749815-A1
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                         1998-077178/07.
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 metabolising
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                                        Jones G,
                                                       QUEENS KINGSTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This protein comprises a novel human retinoid metabolising protein, designated hp450RAI. Its amino acid sequence was deduced from a CDNA clone (see AAV12204) isolated from a retinoic acid-treated NT2 Ccell library. It includes a haem-binding motif characteristic of Cytochrome P450 proteins. hP450RAI is a retinoid oxidase that has the ability to hydroxylate retinoic acid at the 4 position of the beta-ionone ring, and is inducible in epithelial cells exposed to Cretinoic acid. Zebrafish, human and mouse P450RAIs (see AAW4159-61) Cretinoic acid. Zebrafish, human and mouse P450RAIs (see AAW4159-61) Cretinoic acid. They can be expressed in host cells and used to metabolize retinoic acid in an organism or cell, in drug screening, Creding and to raise antibodies useful for inhibiting retinoic acid hydroxylation for the treatment of cancer, actinic keratosis, oral cell lung carcinomas, basal cell carcinomas, acute promyelocytic cell lung carcinomas, basal cell carcinomas, acute promyelocytic cleukaemia, skin cancer, and premalignancy associated with actinic constants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 464;
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Best Local
  07-JUL-1998
                           AAW37733;
                                                AAW37733 standard;
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                                                                                                                                                                                                                                                                         GHETTASAATSLITYLGLYPHVLQKVREEIKSKGLLCKSNQDNKLDMETLEQLKYIGCVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              497 AA;
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  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               actinic keratosis, oral leukoplakia, acne, psoriasis
                                                 Protein;
entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                 492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2437; DB 19;
Pred. No. 7.3e-227;
4; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 497;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Pages 53-55; 113pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying DNA encoding inducible or suppressible cytochrome P450 - by screening for drugs which reduce the catabolism of retinoic acid, useful in cancer chemotherapy and the treatment of acne and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-077193/07.
N-PSDB; AAV09251.
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21-JUN-1996;
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                                                                                                                                             KARNLIHARIEENIRAKIRRLQATEPDGGCKDALQLLIEHSWERGERLDMQALKQSSTEL
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                                                                                                        rarnfihskie en irkkigd \hbox{-} ddnene qkykdalqlliensr rsdepfslgamke aatel
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336; Conserv
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96US-0667546.
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sm; P450RAI; retinoic acid; l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.4%; Score 1734; DB 19; 67.7%; Pred. No. 6e-159; 67.7% 61: Mismatches 89;
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                                    This protein comprises a novel zebrafish retinoid metabolising CC protein, designated zP450RAI. Its amino acid sequence was deduced CC from a cDNA clone (see AAV12203) isolated from a 6-18 hr embryo CC library. It includes a haem-binding motif characteristic of the cytochrome P450 proteins. zP450RAI is a retinoid oxidase that has CC the ability to hydroxylate retinoic acid at the 4 position of the Octavione ring, and is inducible in epithelial cells exposed to CC retinoic acid. Zebrafish, human and mouse P450RAIs (see AAW44159-61) CC are claimed. They can be expressed in host cells and used to CC metabolize retinoic acid in an organism or cell, in drug screening, CC and to raise antibodies useful for inhibiting retinoic acid hydroxylation for the treatment of cancer, actinic keratosis, oral C leukoplakia, secondary tumours of the head and/or neck, non-small C cell lung carcinomas, basal cell carcinomas, acute promyelocytic C leukaemia, skin cancer, and premalignancy associated with actinic recompositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid; zebrafish; inhibitor; antibody; cancer; actinic keratosis; oral leukoplakia; head tumour; neck tumour; non-small cell lung carcinoma; basal cell carcinoma; acute promyelocytic leukaemia; skin cancer; acne; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW44159 standard; Protein; 492 AA.
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21-JUN-1996;
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                                                                                                                                                                                                                                                                                  Claim 1; Page 50-51; 110pp; English
                                                                                                                                                                                                                                                                                                                           Retinoid metabolising e.g. cancer, actinic)
                                                                                                                                                                                                                                                                                                                                                                                                                   Beckett
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                             acne, psoriasis and/or ichthyosis
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                                                                                                                                                                                                                                                                                                                                                                                                                   Jones
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96US-0667546
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ف
                                                                                                                                                                                                                                                                                                                             protein - useful to develop products to treat, keratosis, oral leukoplakia, acne, psoriasis or
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Best Local Sim
Matches 336;
                                                                                                                                                                                                                                                                                                                                                                                                                      Human; PSEC64;
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                       protein
                                         A protein related to
                                                                                     WPI; 2000-468126/41.
N-PSDB; AAA60752.
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                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 23102.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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29-OCT-1999
                                                                                                                                                                                                                                                                                                                                 AAB07921 standard; Protein;
                                                                                                                                                                                      A cytochrome P450 enzyme designated DWF4
                                                                                                                                                                                                                                                                                     AAB07921;
                                                                                                                  DWF4; cytochrome
plant phenotype;
                                                                                                                                                                                                                                       14-NOV-2000
                             WO200047715-A2
                                                                      Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             338 veslrmasiisftfreavvdveykgylipkgwkvmplfrnihhnpkyfsnpevfdpsrfe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 KETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADIFTNKEEFNPDRFI 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480 VYPVDNLPARF 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTASAATSLITYLGLYPHVLQKVREEIKS--KGLLCKSNQDNK-LDMETLEQLKYIGCVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ivseiicerrekralqt------dflghllnfknekgrvltqeqiadniigvlfaaqd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGCEPGPAGGGEDEQQLVEAFEEMTRNLF-----SLPIDVPFSGLYRGVKARNLIHA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shirklvqssfypetirklipdiehialsslqswanmpi--vstyqemkkfafdvgilai 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KORKKVIMOAFSREALOCYVLVIAEEVSSCLEOWLSCGERGLLVYPEVKRLMFRIAMRIL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vvpililclllv---rvivskkkknsrgklppgsmgwpylgetlqlysqnpnvfftskqk
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ilarity 27.3%;
Conservative 9:
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99US-0161359.
99US-0161360.
99US-0161361.
99US-0161920.
99US-0161920.
99US-0161993.
99US-0161993.
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99US-0160980.
99US-0160981.
99US-0160989.
                                                                                                                       \texttt{P450} enzyme; brassinosteroid; 22alpha-hydroxylation; cell elongation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93;
                                                                                                                                                                                                                                                                                                                                      513
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Pred. No. 3e-37;
3; Mismatches 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 468;
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22-JUL-1999 23-JUL-1999 23-JUL-1999 23-JUL-1999 26-JUL-1999 27-JUL-1999 27-JUL-1999 27-JUL-1999 27-JUL-1999 27-JUL-1999 27-JUL-1999 27-JUL-1999 27-JUL-1999 27-JUL-1999 28-JUL-1999 29-AUG-1999 20-AUG-1999 20-AUG-1999 21-AUG-1999 21-AUG

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990S-015106.

-0160814

PD X P P P X

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Matches 148;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated dwf4 polynucleotide useful for altering the phenotype of plants, for diagnostic assays and in the production of antibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ARIZ-) ARIZONA BOARD OF REGENTS
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                           467 laklemavfihhlvlkfnwelae----ddqpfafpfvdfp 502
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                                                                                                             \tt pvisavhldnsrydqpnlfnpwrwqqqnngasssgsfstwgnnympfgggprlcagse
                                                                       FAKILLKIFTVELARHCDWQLLNGPPTMKTSPTVYPVDNLP 487
                                                                                                                                                         YSICDTHDVADIFTNKEEFNPDRFIVPHPEDASRFS------FIPFGGGLRSCVGKE 446
                                                                                                                                                                                                LCKSNQDNKLDMETLEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVI
                                                                                                                                                                                                                                                                                                                                                                                                                             VKARNLIHARIEENIRAKIRRLQATEPDGGCKDALQLLIEHSWE-----RGERLDMQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aqdeakkftfnlmakhimsmdpge----eeteqlkkeyvtfmkgvvsaplnlpgtayhka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gilgkwsmlvlvgdmhrdmrsislnflsharlrtillkdverhtlfvldswqq--nsifs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TILGAGCLSNLHDSSHKQRKKVIMQAFSREALQCYVLV-IAEEVSSCLEQWLSCGERGLL 176
                                                                                                                                                                                                                                                                                             lgwvlkhsnlsteqildlilsllfaghetssvaialaifflqacpkaveelreehleiar
                                                                                                                                                                                                                                                                                                                                       ---ALKQS--STE-----LLFGGHETTASAATSLITYLGLYPHVLQKVREEIKSKGL
                                                                                                                                                                                                                                                                                                                                                                                lqsratilkfierkmee--rkldikeed---qeeeevktedeaemsksdhvrkqrtdddl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pytattlgdfmqqhvskygkiyrsnlfgeptivsadaglnrfilqnegrlfecsyprsig 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -QMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVHWPASVR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ipllilpsi----islilfillik-----rrnrktrfnlppgksgwpflgetigylk 57
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DB; AAA59599.
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99US-0119658.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 461; DB 21;
Pred. No. 6.2e-36;
8; Mismatches 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 513;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64;
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05-MAR-1999;
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16-APR-1999;
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06-APR-1999;
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RESULT 11
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RESULT 12
AAG46491
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                                                          EP1033405-A2
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           25-FEB-2000; 2000EP-0301439.
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137; Conservative
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99US-0161993.
99US-0161993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is Arabidopsis thaliana cytochrome P450-type hydroxylase. The hydroxylase can be used to identify brassinosteroids or brassinosteroid inhibitors, useful to produce plants with modified physiological and/or phenotypic characteristics. The modified plants may show, e.g. stimulation of growth, increased cell elongation, increased wood production,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytochrome P450-type hydroxylase; identification; brassinosteroid; brassinosteroid inhibitor; modified plant; recombinant production;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    accelerated seed germination at low temperatures, an increase in dry weight, repressed anthocyanin production during growth in light and/or inhibited de-etiolation which is induced, e.g. by cytokinin, in the dark or an increase in stress tolerance. The hydroxylase or its coding sequence can also be used for the recombinant production
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated plant cytochrome P450-type hydroxylase gene - used to identify substances acting as brassino-steroid(s) or brassinosteroid inhibitors for the production of modified plants
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N-PSDB; AAT85306, AAT85307.
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   180 EVKRLMFRIAMRILLGCEPGPAGGGEDEQQLVEAFEEMTRNLFSLPIDVPFSGLYR-GVK
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                                                                                                                                                                                                                                                                                                                                                                   6 LLASALCTFYLPLLLFLAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETLQMV----
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                                                                                                                             GAGCLSNLHDSSHKQRKKVIMQAFSREALQCYVLV-IAEEVSSCLEQWLSCGERGLLVYP
                                                                                                                                                                                                                                             -LQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVHWPASVRTIL 120
                                                                gkhslllmkgslhkrmhsltmsfanssiikdhlmldidrlvrfnldswss----rvllme
                                                                                                                                                                                                                                                                                                      llssiaagfllll-----rrtryrrmglppgslglpligetfqligayk 52
                                                                                                                                                                                   tenpepfidervarygsvfmthlfgeptifsadpetnrfvlqnegklfecsypasicnll 112
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RESULT 14
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    99US-0125788.
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99US-0135124.
99US-0135353.
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RESULT 1
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Best Local Similarity 26.6%;
Matches 134; Conservative 9
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26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
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29-OCT-1999;
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Search completed: November 6, 2001, 13:25:27 Job time: 12655 sec

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AL532444 AL532444 LTI_NFL001_I
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Ratio: 4.853
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223

Percent Identity:

96.667

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AL539668 LTI_FL013_FBrn1
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Li,W.B., Gruber,C., Jessee,
Full-length cDNA libraries
Unpublished (2001)
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1 (bases 1 to 974)
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AL539668
AL539668.1 GI:12869097
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Genoscope
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Homo sapiens cDNA clone CSODF036YG04
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593 | BG486108 dad60f10.xl Wellcome
1054 | AL348447 Tetraodon nigrovir
367 | BG348623 dad18c02.yl Wellcom
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AL532445
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           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 893)
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  Gruber, C.,
  Jessee,J.
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Polayes,D.
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                       Hominidae;
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Contact: Genoscope
Genoscope - Centre National
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/note-*Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com*
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Percent Length: Gaps: Identity: 4 93.485

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150

139 alIleMetArgAlaPheSerArgGluAlaLeuGluCysTyrValProValAGCCGCGAGGCACTCGAATGCTACGTGCCGGTG 155

172 279

172 uArgGlyLeuLeuValTyrProGluValLysArgLeuMetPheArgIleA 189

189 laMetArgIleLeuLeuGlyCysGluProGlnLeuAlaGlyAspGlyAsp CCATGCGCATCCTACTGGGCTGCGAACCCCAACTGGCGGGGGGACGGGGAC 205

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                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1028)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                    AL532444 1028 bp mRNA
AL532444 LTI_NFL001_NBC4 Homo
prime, mRNA sequence.
                                                                                                                                                                                              Contact: Genoscope
Genoscope - Centre National de Sequencage
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                                                                                                                                                               91006 EVRY cedex - France segref@genoscope.cns.fr, W
                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH10B"
'note="Organ: brain; Vector: pCMVSPORT 6;
                                                  /sex="male"
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CDNA clone CS0DM014YL13
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OASPATGPheSerAlaProHisProGluAspAlaSerArgPheSerPheI
                                                                                                                                      TAAATGGATACCAGATTCCCAAGGGCTGGAATGTTATCTACAGTATCTGT
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                                                                               AspThrHisAspValAlaGluIlePheThrAsnLysGluGluPheAsnPr
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                                                           GATACTCATGATGTGGCAGAGATCTTCACCAACAAGGAAGAATTTAATCC
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                 Quality: 1045.00
Ratio: 5.148
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                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 440.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW513600 618 bp mRNA xo47b06.x1 NCI_CGAP_Ut1 Homo similar to SW:CP26_HUMAN 0431
                                                                                                                                                                                                                                                                                                                                                                                                              Possible reversed clone: similarity Seq primer: -400P from Gibco
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National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW513600.1
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                                                                                                                                  Ω
                                                                                                                                                                 /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.75 kb. Life Technologies catalog #
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/clone="IMAGE:2707091"
/clone_lib="NCI_CGAP_Ut1"
/tissue_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"
/lab_host="UH10B"
 5.148
98.544
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98.058
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SOURCE
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    TITLE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 847)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
                                                                                                                                                                        AL539667 LTI_FL013_FBrn1 Homo sapiens cDNA clone CS0DF036YG04
                                                                                                               EST.
                                                                             Homo sapiens
                                                                                               human
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Organ: Fetal brain; Vector: PCMVSPORT 6; 1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and Cloned into the Not I and Eco RV sites of the
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/clone=lib="LTI_FL013_FBrn1"
/clone_lib="LTI_FL013_FBrn1"
/dev_stage="pooled tissue from
week, 24 week and 26 week)"
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
Mammalia; E
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BE236243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST discovery in swine Unpublished (2000) Contact: Smith TPL
                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACKWARD: GTTTTCCCAGTCACGACG
Plate: 85 row: B column: 21
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 537)
Fahrenkrug, S.C., Fr
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Sus scrofa
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                                                                                                                                                                                                                                                     96
                                                                                                                                                                                                                                          /tissue_type="pooled"
/lab_host="PDH10B"
/note="Vector: pCMV SPORT6; Site_1: X
/nota="Vector: pcmv SPORT6; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC lPIG"
881.00
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98.305
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com pooled tissue from day 11, 13, 15, 20,
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Percent Similarity:

Percent Identity:

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Ratio:

alignment_block:

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LOCUS BF385034
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                                                                                                                                                                                                                                                                                                                                                                            gb_est87:BF385034
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Tecopies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution informat
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602045632F1 NCI_CGAP_L19
                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                            mRNA sequence.
                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                 Unpublished (1999)
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pLeuSerCysGly
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                               TGCTACGTGCCCGTGATCGCTGAGGAAGTCAGCAGTTGTCTGGAGCAGTG
                                                                                                                                                       TTGCTGGGAGAGCACCGGTTGGTGTCGGTGCACTGGCCCGCGTCGGTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM9530 row: o column: 07 High quality sequence stop: 539.
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Gaps: 0
Percent Identity: 94.152
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LOCUS BF533769
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US-09-668-482-4 x BF533769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9779 row: c column: 22
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BF533769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone=lib="NGI_CGAP_Li9"
/clone_lib="NGI_CGAP_Li9"
/lab_host="DH10B_(T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
a 172 c 189 g 114 t
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/strain="FVB/N"
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Identity: 94.152
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REFERENCE
AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db61c05.y1 Wellcome CRC pSK egg Xenopus laevis cDNA clone IMAGE:3377480 5' similar to gb:gb|AF057566.1|AF057566 Xenopus laevis retinoic acid converting enzyme (XENOPUS);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopodinae: Xenopus.
1 (bases 1 to 696)
Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D.
Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D.,
Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person
Materston, R., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
on Jun 22, 2000 this sequence version replaced other ESTE: db6Lo5.xl
Contact: Sandy Clifton, Ph.D.
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                 Library constructed by N. Garrett, P. LeMaire, A.M. Zo Gurdon (Wellcome/CRC Institute). DNA Sequencing by: Wa University Genome Sequencing Center Clone distribution: Xenopus clones from this library through the I.M.A.G.E. Consortium/LLNL at: info@image. Seq.primer: -40RP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WashU Xenopus EST project, 1999
                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
                                                                                                                                                                                              quality sequence stop: 483.
                                                                                                       /organism="Xenopus laevis"
/db_xref="taxon:8355"
/note="Vector:
                  /tissue_type="egg"
/lab_host="DH10B_(|
                                                               /clone="IMAGE:3377480"
/clone_lib="Wellcome CRC pSK egg"
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pBluescript SK-;
                     (phage-resistant)"
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||TGATGTGCCATGTAGCGGCCTCTACCGGGGTCTGCGGGCTAGAGACCTT
    GCTGCTCGAAGCCTTCGAGGAAATGACCCGAAATCTCTTCTCTGTGCCTA
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                                gAlaSerGluAlaGlyGlnGlyCysLysAspAlaLeuGlnLeuIleG
                                                                                    IleHisAlaArgIleGluGlnAsnIleArgAlaLysIleCysGlyLeuAr 259
                                                                                                                                                                                                                                          CTGCTCGGCTGCGATCCCCAGCGCATG...GACAGCCAACATGAGGAGAC
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Gaps: 4
Percent Identity: 71.064
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CAGAAAGTTCGAGAAGAGATAAAGAGCAAGGGCTTACTTTGCAAGAGCAA
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alignment_block:
US-09-668-482-4 x AA239785
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AUTHORS
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                                                              Align seg 1/1 to: AA239785
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324 GlnLysValArgGluGluLeuLysSerLysGlyLeuLeuCysLysSerAs
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                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 474)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T. Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellnberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Marian, D., Band, M., Steptoe, M., Tan, F., Gearea B. Wilson B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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Contact: Marra M/Mouse EST Project
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/clone_lib="Soares mouse NML"
/tissue_type="Liver"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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Bento Soares and
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LOCUS BF236872
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF236872 545 bp mRNA
602027980F1 NCI_CGAP_Li9 Mus
                                                                                                                                                                                                                                                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 545)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LLAM9446 row: p column: 19
High quality sequence start: 2
High quality sequence stop: 545.
Location/Qualifiers
                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                              house mouse.
                                                                                                                                                                                                   DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4163202"
/clone_lib="NCI_CGAP_Li9"
                                                                   /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus cDNA clone IMAGE:4163202
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474 401 457 351 440 301 424 251 407 201 390

451

FEATURES

26

REFERENCE

KEYWORDS

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alignment_block:
US-09-668-482-4 x BF236872
                                                                                                  seq_documentation_block:
LOCUS BF055367
                                                                                                                                               seq_name: gb_est82:BF055367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 TTCCCATTCTTGGGGA...AACATGCAGATGGTGCTTCAGCGGAGGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 TCTTGCTGGGAGAGCACCGGTTGGTGTCGGTGCACTGGCCCGCGTCGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 TIGGCCGCC...ACGGTGCGGGTGATGGGCGCGGATAATGTGCGGCGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAGCCGCGATCGCAGCTGCGCCCTTCCCCTTGCCCCCGGTACCATGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leLeuLeuGlyAspAspArgLeuValSerValHisTrpProAlaSerVal
                                                                                                                                                                                                                   TrpLeuSerCysGly 171
                                                                                                                                                                                                                                                       CAAGCAGCGAAAGAAGGTGATTATGCAGGCCTTCAGCCGCGAGGCACTCC
                                                                                                                                                                                                                                                                                                                                                                                              CGCACCATCCTGGGCGCTGCCTGCCTCCCAACCTGCACGATTCCTCGCA
                                                                                                                                                                                       TGGCTAAGCTGCGGC
BF055367
BF055367.1
EST.
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                                                                BF055367 646 bp mRNA EST 16-OCT-2000 7j78f12.xl Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone TMAGE:3392591 3' similar to SW:CP26_HUMAN 043174 CYTOCHROME P450
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                                                  mRNA sequence.
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4.633
95.954
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                 GI:10809263
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TITLE
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                                                                                                                                                                                                                                                                       382 luLeuAsnGlyTyrGlnIleProLysGlyTrpAsnValIleTyrSerIle 398
                                                                                                                                                                                                                                                                                                                                           432 heIleProPheGlyGlyGlyLeuArgSerCysValGlyLysGluPheAla
                                                                                                                                                        496
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                                                                                                                                                                                                                                                                                                                                                                                                                                             646 ATTTTGGCCCACCTTAAATACTTCGGGTGTGTTATAAAGGAGACCCTTNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 IleLeuGluGlnLeuLysTyrIleGlyCysValIleLysGluThrLeuAr 365
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                                                                             nProAspArgPheSerAlaProHisProGluAspAlaSerArgPheSerP 432
                                                                                                                                                                          CysAspThrHisAspValAlaGluIlePheThrAsnLysGluGluPheAs
                                                                                                                                                                                                                                                ATTAAAATGGATACCAGATTCCCAAGGGCTGGAATGTTATCTACAGTATC
                                                                                                                                                TGTGATACTCATGATGTGGCAGAGATCTTCACCAACAAGGAAGAATTTAA
                                                 TCCTGACCGATTCATGCTGCCTCACCCAGAGGATGCATCCAGGTTCAGCT
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Ratio:
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quality sequence stop: 450.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecc RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSP pool 1: 309384-310919, 323208-325895 Soares NbHSP pool 1: 150407, 151176-152327 Soares NbHSP8-9W pool 1: 758280-760583, 772104-774407 Soares NbHSP8-pool 1: 758280-760583, 772104-774407 Soares NbHSPA pool 1: 30476-306311, 320136-322823, 326280-326663 Soares NbHOT pool 1: 723720-7264407, 739080-740999 Subtraction by Bento Scares and M Fartima Annalog "
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5.336
95.973
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:3392591"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity:
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120 g 194 t
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BASE COUNT
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LOCUS AW174347
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sugano,S., Kawakami,K., Johnson,S., Li,F., Marra,M., Eddy,S., Hiller,L., Clifton,S., Allen,M., Gibbons,M., Jost,S., Kucaba,T., Martin,J., Pape,D., Steptoe,M., Underwood,K., Theising,B., Ritter, E., Bowers,Y., Wylie,T., Waterston,R. and Wilson,R. WashU Zebrafish EST Project 1999 Unpublished (1999) Other_ESTs: fi42a06.x1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Library constructed by Dr. Sumio Suga
Sequencing by: Washington University
Seq primer: T3 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinide; Rasborinae; Danio.
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AW174347
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2640274 5' similar to SW:CP26_BRARE P79739 CYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
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              172
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Location/Qualifiers
/dev_stage="adult"
/lab_host="pH10B (phage resistant)"
/lab_host="pH10B (phage resistant)"
/note="vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CACCATGTG); lst strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor [TGTTGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science) and kindly donated by Dr. Koichi Kawakami. Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
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                                                                                                                                                                                                                                                                                                                                                                                                                                         unfertilized eggs)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Sugano Kawakami zebrafish
/sex="mixed (one male and one female,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Danio rerio"
/strain="AB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="2640274"
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Jniversity Genome Sequencing Center
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704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACGAGTCGATCCGAACTGCAGAAGTCCTCTACCGCCAGGTACCATGGGC
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                                                                                                                                                                                                                                                                                                                             CACTACATTCCCGTGATCCATCAGGAGGTGAAGAGCGCCCATACAGGAATG
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                                                                                                                                                                                                                                                                                                                                                                                                            ysGlnArgLysLysVallleMetArgAlaPheSerArgGluAlaLeuGlu 150
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                 heSerGlyLeuTyrArg 235
                                                                                             aPheGluGluMetThrArgAsnLeuPheSerLeuProIleAspValProP 230
                                                                                                                               CCACAGCAAATAATGACTGAC.....
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                                                              TTTGGAGCGAATGATCAGCGACGTGGTCTGCTTGCCAATCCACGTTCCTT
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US-09-668-482-4 x AW765767
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WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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Unpublished (1999)
Other_ESTs: da77a02.x1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berkeley)
DNA Sequencing by: Washington University Genome Sequencing Center DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml
Seq primer: -40Rp from GibCo
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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African clawed frog.
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1 (bases 1 to 669)
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                                                                                                                                                                  Ratio:
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                                                                                                                       731.50
4.228
86.935
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Percent Identity:
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Align seg 1/1

to:

AW765767

from:

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REFERENCE
AUTHORS
                          COMMENT
                                                                                                                                                                                                                                                                                                                      KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS AI667038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_est23:AI667038
                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CysTyrValProValIleThrGluGluValGlySerSerLeuGluGlnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pLeuSerCysGlyGluArgGlyLeuLeuValTyrProGluValLysArgL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ysGlnArgLysLysVallleMetArgAlaPheSerArgGluAlaLeuGlu 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuLeuGlyAspAspArgLeuValSerValHisTrpProAlaSerValAr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eLeuGlnMetLysArgArgLysTyrGlyPheIleTyrLysThrHisLeuP
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                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Meopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasborinae; Danio.

1 (bases 1 to 640)

1 (clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwoo, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Watterston, R.
                  WashU Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
                                                                                                                                                                                                                                                                                                                                                                   AI667038 640 bp mrNA EST 18-MAY-1999 fC24h03:y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to SW:CP26_BRARE P79739 CYTOCHROME P450 26 ;, mRNA sequence.
Washington University School of Medicine
                                                                                and Wilson, R.
                                                                                                                                                                                                                                                                                 Danio rerio
                                                                                                                                                                                                                                                                                                   zebrafish
                                                                                                                                                                                                                                                                                                                                           AI667038.1 GI:4805394
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AI667038
                                                                                                                                                                                                               162. GACGAGTCGATCCGAACTGCAGAAGTCCTCTACCGCCAGGTACCATGGGC
                                                                                                                                                                                                                                                                                                                                      62
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                                                                                                                                                                                                                                                                                                                                                                                1 MetGlyLeuProAlaLeuLeuAlaSerAlaLeuCysThrPheValLeuPr 17
erGlyArgAspArgSerCysAlaLeuProLeuProProGlyThrMetGly 50
                                  PheProPhePheGlyGluThrLeuGlnMetValLeuGlnArgArgLysPh 67
                                                                                                                                                                                                                                                                                                                             ATGGGGCTGTACACCCTTATGGTCACCTTTCTCTGCACCATCGTGCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
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cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Possible reversed clone: similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               www.rzpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=""Vector: pSPORTI; Site_1: Not1; Site_2: Sal1; lst strand cDNA was primed with a Not I - oligo(dT)15 primer [5 pcAraGTTCAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTT]3 ; double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORTI vector (BRL), Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max planck Institut fuer Molekulare Genetik, Berlin). cDNAs for EST analysis were selected following oligonuclotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
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86.802
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/lab_host="XL1-blue MRF"
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/clone_lib="Zebrafish WashU MPING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="26 somite embryos,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167
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                                                                                                           211
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eLeuGlnMetLysArgArgLysTyrGlyPheIleTyrLysThrHisLeuP

262	::: :::	1
84	heGlyArgProThrValArgValMetGlyAlaAspAsnValArgArgIle 100	0
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101	LeuLeuGlyAspAspArgLeuValSerValHisTrpProAlaSerValAr 117	7
362	CTGCTGGGCGAACACAAGCTGGTGTCTGTTCAGTGGCCAGCATCAGTGAG 411	1
117		4
412	AACCATCCTGGGCTCTGACACCCTCTCCAATGTCCATGGAGTTCAACACA 461	1
134	ysGlnArgLysLysVallleMetArgAlaPheSerArgGluAlaLeuGlu 150	0
462	AAAACAAGAAAAAGGCCATTATGAGGGCGTTCTCTCGAGATGCTCTGGAG 511	<u> </u>
151		7
512	CACTACATTCCCGTGATCCAGCAGGAGGTGAAGAGCGCCCATACAGGAATG 561	ĭ
167	pLeu	Ë
562	GCTGCAAAAAGACTCCTGC	9
181		
600	TGAAGAAACTCATGTTTCGGATAGCTATGAGAATCCTGCTT 640	

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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maximum
    Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB seq length: 0
DB seq length: 2000000000
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2437
1734
1734
450
358.5
358.5
261.5
261.5
261.5
251.5
255.5
255.5
255.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/
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3: /cgn2_6/ptodata/2/
4: /cgn2_6/ptodata/2/
5: /cgn2_6/ptodata/2/
6: /cgn2_6/ptodata/2/
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Gapop 10.0 , Gapext 0.5
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2612
1 MGLPALLASALCTFYLPLLL......PTYYPYDNLPARFTYFQGDI 497
  212252 seqs, 22503292 residues
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-882-164D-4
US-08-724-466B-2
US-08-882-164D-2
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126.891 Million cell updates/sec
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           Sequence 32, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
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Sequence 6, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 6, Appli
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Sequence 25, Appli
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Sequence 27, Appli
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Sequence
Sequence
Sequence
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QΥ

Query Match 100.0%; Score 2612; DB 4; Best Local Similarity 100.0%; Pred. No. 5.5e-276; Matches 497; Conservative 0; Mismatches 0;

Length 497; Indels 0

0; Gaps

0;

1 MGLPALLASALCTFYLPLLLFLAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETLQM 60

; STRANDEDNESS: ; TOPOLOGY: lin US-08-882-164D-32

linear

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US-08-882-11 Sequence Patent NC Pate	22 20 20 20 20 20 20 20 20 20 20 20 20 2
JILT 1 198-882-164D-32 squence 32, Application US/ squence 32, Application US/ squence 32, Application US/ squence 32, Application US/ squence 32, Application US/ ApplicaNT: Petkovich, P. ApplicaNT: Beckett, Barb TITLE OF INVENTION: Retil NUMBER OF SEQUENCES: 43 CORRESPONDENCE ADDRESS: ADDRESSEE: Blake, Casss STREET: Box 25, Commer CITY: Toronto STATE: Ontario COUNTRY: Canada ZIP: M51 1A9 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, COMPUTER: COMPAO, IBM OPERATING SYSTEM: M55 SOFTWARE: WORD PERFECT CURRENT APPLICATION NUMBER: 08 FILING DATE: JUNE 25, PRIOR APPLICATION NUMBER: 08 FILING DATE: JUNE 21, APPLICATION NUMBER: 08 FILING DATE: JUNE 21, APPLICATION NUMBER: 08 FILING DATE: JUNE 21, APPLICATION NUMBER: 08 FILING DATE: JOHN C. REGISTRATION NUMBER: 08 FILING DATE: JOHN	237.5 237.5 237.5 237.5 237.5 237.5 237.5 237.5 231.5 231.5 231.5 231.5 231.5 231.5 231.5
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ich, P. Martin, White, Jay A., t, Barbara R., Jones, Glenville t, Barbara R., Jones, Glenville : Retinoid Metabolizing Protein S: 43 e, Cassels & Graydon commerce Court West Commerce Court West Commerce Court West MS-DOS 5.1 PERFECT MD DATA: MS-DOS 5.1 PERFECT MD DATA: BER: 08/667,546 nne 21, 1996 nne 21, 1996 tober 1, 1996 tober 1, 1996 tober 36,424 f NUMBER: 50767/00010 INFORMATION: 1 B63-4344 863-2653 ID NO: 32: LISTICS: L	1 US-08-201-118-3 US-08-238-821B-9 2 US-08-238-821B-9 2 US-08-238-821B-9 2 US-08-28-821B-9 3 US-08-948-564-10 3 US-08-948-564-10 3 US-08-948-566-2 4 US-09-292-768-66 4 US-09-292-768-66 4 US-09-172-339-6 1 US-08-238-821B-1 2 US-08-238-821B-1 3 US-08-238-821B-1 5 PCT-US95-05744-1 1 US-08-238-821B-1 3 US-08-201-118-13 1 US-08-238-821B-13 1 US-08-2744-13 1 US-08-2744-13 1 US-08-457-274A-2
	Sequence 3, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 10, Appli Sequence 10, Appli Sequence 12, Appli Sequence 66, Appli Sequence 11, Appli Sequence 11, Appli Sequence 12, Appli Sequence 13, Appli

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                                              TELEFAX: (416) 863-26
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 30
            SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acid
                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00004
                                                                                                                                                             APPLICATION NUMBER: US/08/724,466B
FILING DATE: October 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
                                                                                                                                                                                                                                          COMPUTER: COMPAQ, IBM
OPERATING SYSTEM: MS-D
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           CITY: TOLO...
ZIP: M5L 1A9
ConnTRY: Canada
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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TOPOLOGY: lin
US-08-724-466B-4
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/88
FILING DATE: JUNE 25, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,5
FILING DATE: June 21, 1996
                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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Best Local
                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch,
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
                                                                                                                                                                                                                                                    APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Proteir NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
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CITY: Toronto
STATE: Ontario
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ZIP: M5L 1A9
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1, 1996
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; Pred. No. 6.7e-257;
14; Mismatches 19;
                                                                                                         compatible 5.1
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EILING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
REFERENCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEPAN: (416) 863-2653
INFORMATION FOR SEQ ID NO: 4:
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US-08-724-466B-2
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Best Local
                                                                                                                               Sequence 2, Application US/08724466B Patent No. 6063606 GENERAL INFORMATION:
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LENGTH: 497 amino acids
TYPE: amino acid
STRANDEDNESS: single
                       APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
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                                                                                                                                                                                                                                           YPVDNLPARFTHFHGEI 497
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93.4%;
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Best Local S
Matches 336
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FILING DATE: June 21, 19
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WORD PERFECT
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MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
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LENGTH: 492 amino acids
TYPE: amino acid
STRANDENESS: single
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478 PTVYPVDNLPARETYF 493
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474 PTIYPVDNLPTKETSY 489
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                                                                        RFIVPHPEDASRFSFIPFGGGLRSCVGKEFAKILLKIFTVELARHCDWQLLNGPPTMKTS
                                                                                                                 LFGGHETTASTATSLVMFLGLNTEVVQKVREEVQEKVEMGMYTPGKGLSMELLDQLKYTG
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                                                        REMSKGLEDGSRENYIPEGGGSRMCVGKEFAKVLLKIFLVELTQHCNWILSNGPPTMKTG
                                                                                                                                           CVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADIFTNKEEFNPD 417
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336; Conserv
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US-08-882-164D-2

Sequence 2, Application Patent No. 6306624

US/08882164D

SENERAL INFORMATION:

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Best Local Similarity
Matches 336; Conserv
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APPLICATION NUMBER: US/08/882,164D FILING DATE: June 25, 1997 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,546 FILING DATE: June 21, 1996
FILING DATE: June 21, 1996
FILING DATE: June 21, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
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FILING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
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ZIP: M5L 1A9
COMPUTER READABLE FORM:
MEDIUM TYPE: Disketto
                                                                                                                                                                              238 KARNLIHARIEENIRAKIRRLQATEPDGGCKDALQLLIEHSWERGERLDMQALKQSSTEL
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                                                                                                                                                                                                                                                                                                              121 GSDTLSNVHGVQHKNKKKAIMRAFSRDALEHYIPVIQQEVKSAIQEWLQKDSC----VLV
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                                                                                                                                                                                                                                                                                                                                                                                                                 61 VLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGBHRLVSVHWPASVRTIL 120
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hunt, John C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Toronto
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CVIKETLRINPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADVFPNKEEFQPE 413
                      CVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIVSICDTHDVADIFTNKBEFNPD
                                                                                                    LFGGHETTASAATSLITYLGLYPHVLQKVREEIKSKGLLCKSNQDNKLDMETLEQLKYIG
                                                                                                                                                                                                                                    YPEMKKLMFRIAMRILLGFEPEQI--KTDEQELVEAFEEMIKNLFSLPIDVPFSGLYRGL
                                                                              LFGGHETTASTATSLVMFLGLNTEVVQKVREEVQEKVEMGMYTPGKGLSMELLDQLKYTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.4%; Score 1734; DB 4; 67.7%; Pred. No. 2.9e-180; tive 61; Mismatches 89;
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Matches 134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 205-805
TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 22040 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC PC-DOS/MS-DOS
PC-DOS/MS-DOS
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SZEKERES, APPLICANT: ALIMANN, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 0147-0153P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
REGISTRATION NUMBER: 30,330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Birch, Stev
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
                             180 EVKRLMFRIAMRILLGCEPGPAGGGEDEQQLVEAFEEMTRNLFSLPIDVPFSGLYR-GVK 238
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     169
                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 472 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 27-MAR CLASSIFICATION: 800
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                                                                                                                                                                                                                                      6 LLASALCTFVLPLLLFLAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETLQMV----
   EAKKITFELTVKQLMSFDP---
                                                                   GKHSLLLMKGSLHKRMHSLTMSFANSSIIKDHLMLDIDRLVRFNLDSWSS----RVLLME
                                                                                              GAGCLSNLHDSSHKQRKKVIMQAFSREALQCYVLV-IAEEVSSCLEQWLSCGERGLLVYP 179
                                                                                                                                    TENPEPFIDERVARYGSVFMTHLEGEPTIFSADPETNREVLQNEGKLFECSYPASICNLL
                                                                                                                                                           -LQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVHWPASVRTIL 120
                                                                                                                                                                                                         LLSSIAAGFLLLL-------RTRYRRMGLPPGSLGLPLIGETFQLIGAYK 52
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5. 5952545
                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                              Conservative
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: 27-MAR-1996
ON: 800
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26.6%;
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                                                                                                                                                                                                                                                                          Score 450; DB 2;
Pred. No. 2.8e-40;
90; Mismatches 217
-GEWSESLRKEYLLVIEGFFSLPLPL-FSTTYRKAIQ
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                                                                                                                                                                                                                                                                                                           Length 472;
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US-08-622-166A-4
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                                             Matches
                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: KONCZ,
                                                                                                                                                                                                                 TELEFAX: (703) 205-80
TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING CYTOCHROME
TITLE OF INVENTION: P450-TYPE PROTEINS INVOLVED IN THE BRASSINOSTEROID SYNTHESIS
                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 0147-0153P TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                355
                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      442 VPAEQDKLVFFPTTRTQKRYPIF
                                                                                                                                                                                LENGTH: 472 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP STREET: P.O. Box 747 CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 27-MAR CLASSIFICATION: 800
                                                                                                                                                      TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
6 LLASALCTFVLPLLLFLAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETLQMV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SZEKERES, MIKLOS ALTMANN, THOMAS
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                                             Conservative
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                                             90;
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                                            Score 450; DB 2; Length 472;
Pred. No. 2.8e-40;
90; Mismatches 217; Indels 62;
                                                                         Length 472;
                                             Gaps
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CURRENT APPLICATION NUMBER: US/08/991,677A
CURRENT FILING DATE: 1997-12-16
EARLIER APPLICATION NUMBER: US 60/033,381
EARLIER FILING DATE: 1996-12-16
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 511
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Liquidambar styraciflua US-08-991-677-4
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US-08-991-677-4
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 26.7
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08991677A Patent No. 6252135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Carraway, Daniel T
APPLICANT: Smeltzer, Richard H
TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
FILE REFERENCE: 50617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 442
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120 DMAFAHYGPFWRQMRKLCVMKLFSRKRAESWESVRDEVDSAVRVVASNIGST----
                                                                                           89
                                                                                                                                         74
                                                                                                                                                                                                              14 FVLPLLLFLAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETIQMVLQRRKFLQMKRR 73
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                                                                                         QYGGLFHLKMGFLHMVAVSTPDMARQVLQVQDNIFS-NRPATI-----AISYLTYDRA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NPDRF----IVPHPEDASRFSFIPFGGGLRSCVGKEFAKILLKIFTVELARHCDWQLLNG
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                                                                                                                                      KYGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVHWPASVRTILGAGCLSNL-HDSS 132
                                                                                                                                                                                    FIIPLLLLEGLV------SRLRQ-RLPYPPGPKGLPVIGNMLMMDQLTHRGLAKLAK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPAEQDKLVFFPTTRTQKRYPIF 464
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                                             -HKQRKKVIMQAFSREALQCY------VLVIAEEVSSCLEQWLSCG 171
                                                                                                                                                                                                                                                                                                   13.7%; Score 358.5; DB 26.7%; Pred. No. 3e-30;
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                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                  200;
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                           Length 511;
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         -VNIG
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Best Local Similarity
Matches 133; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Sequence is deduced from DNA sequence of SEQ Patent No. 5981837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 2
LENGTH: 520
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Patent No. 5981837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: US 60/009,119
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: US 60/013,388
EARLIER FILING DATE: 1996-03-14
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Microsoft Word 2.0C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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CURRENT FILING DATE: 1998-06-18
EARLIER APPLICATION NUMBER: PCT/US96/20094
EARLIER FILING DATE: 1996-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chapple, Clint TITLE OF INVENTION: A Method For Regulation FILE REFERENCE: 7024-325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                     133
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                                                                                                                                                                    71 YGGL--CHLRMGFLHMYAVSSPEVARQVLQVQDSVFSNRPATI-----AISYLTYDRA
                                                                                                                                                                                                                     75
                                                                                                                                                                                                                                                       15 VLPILLFLAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETLQMVLQRRKFLQMKRRK 74
                                     LVYPEVKRLMFRIAMRILLGCEPGPAGGGEDEQQLVEAFEEMTR--NLFSLPIDVPFSGL 233
                                                                                  DMAFAHYGPFWRQMRKVCVMKVFSRKRAESWASVRDEVDKMVRSVSCNVGKPINVGEQ--
                                                                                                                                                                                                            YGFIYKTHL-FGRPTVRVMGADNVRRILLGEHRLVSVHWPASVRTILGAGCLSNL-HDSS 132
    -IFALTRNITYRAAFG--SACEKG
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                                                                                                                            ------HKQRKKVIMQAFSREALQCYVLV-----IAEEVSSCLEQWLSCGERGL 175
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                    12.9%; Score 337; DB 2; 25.8%; Pred. No. 6.8e-28;
                                                                                                                                                                                                                                                                                                                                                Mismatches
-QDEFIRILQEFSKLFGAFNVADFIPYFGW
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DP QA

41 ALPLPPGT----MGFPFFGETLQMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADN 96

Mismatches

Indels 138;

Gaps

21;

78

SMPIAEGAVSDLLGRPLFFSLYDWFLE----

---HGAVYKL-AFGPKAFVVVSDPI 125

Matches

Conservative

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; MOLECULE TYPE: US-08-948-564-16
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                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 576 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 5051-409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: PO Box 37428
CITY: Raleigh
STATE: No. 6121512th Carolina
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TELEFAX: 919-854-1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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VENTION: No. 6121512el Cytochrome P-450 Constructs and
VENTION: Methods of Producing Herbicide-Resistant Transgenic Plants
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Dewey, Ralph E.
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Score 300; DB 3; Pred. No. 8.7e-24;
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                                   Length 576;
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US-08-948-564-4
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                                                                                           TELEFAX: 919-854-1401
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Corbin, Frederick T.
TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and
TITLE OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic Plants
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 510 amino acid
                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 919-854-1400
                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia
                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: PO Box 37428
CITY: Raleigh
STATE: No. 6121512th Carolina
                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                    NAME: Bennett, Virginia C. REGISTRATION NUMBER: 37,09 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                 TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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PO Box 37428
                                                     510 amino acids
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Best Local Similarity 24.4
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 50,
Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                  FILING DATE: 27-MAR-PRIOR APPLICATION DATA:
                                                                                       CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 LLLFLAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETLQMV--LQRRKFLQMKRRKY 75
                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City
                                                     APPLICATION NUMBER: AU PL 1538/92 FILING DATE: 27-MAR-1992
                                                                                                                            APPLICATION NUMBER: FILING DATE: 30-NO
                                                                                                                                                                                                                                                                               ZIP:
                                                                                                                                                                                                                                                                                            STATE: New York COUNTRY: U.S.A.
                     APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPL--MHLKLGEVSNIIVTSPEMAQEIMKTHDLNFSDRPDFVLSRIVSYNGSGIVFSQHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLFGGHETTASAATSLITYLGLYPHVLQKVREEIK----SKGLLCKSNQDNKLDMETLEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEFNPDRFIVPHPE-DASRFSFIPFGGGLRSCVGKEFAKILLKIFTVELARHCDWQLLN 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKYIGCVIKETLRLNPPVPGGF-RVALKTFELNGYQIPKGWNVIYSICDTHDVADIFTNK 411
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                                                                                                                              30-NOV-1994
   07-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                   GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES AND USES THEREFOR
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                                                                                                                                                 US/08/313,075
                   AU PL 6698/93
                                                                                                                                                                                         #1.25
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; Sequence 68, Application US/09292768
; Patent NO. 6194185
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Lupien, Shari L
; APPLICANT: Karp, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AN
; TITLE OF INVENTION: LIMONENE HYDROXYLASES
; FILE REFERENCE: wsur13463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
   CURRENT APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-456
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 50
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REFERENCE/DOCKET NUMBER: 9433
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                   443 PLAMRMIPVALGSLLNSFNWKLYGG 467
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TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                     QIPKGWNVIYSICDTHDVADIFTNKEEFNDDRFIVPHPEDASR-FSFIPFGGGLRSCVGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGKPNLVDYFPFLEKIDPQGIKRRMTNNFTKFLGLISGLIDD--RLKERNLR----DNAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDVLDALLNISQENPEEIDRNQIEQLCLDLFAAGTDTTSNTLEWAMAELLQNPHTLQKAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSSRDRSCALPLPPGTMGFPFFGETLQMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVM 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.4%; Score 270.5; DB 1; nilarity 23.2%; Pred. No. 1.1e-20; Conservative 66; Mismatches 197;
NUMBER: US/09/292,768
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                                                       AND
                                                     METHODS
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                                                   FOR THE PRODUCTION OF
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CURRENT FILING DATE: 1999-04-14

EARLIER APPLICATION NUMBER: 08/881,784

EEARLIER FILING DATE: 1997-06-24

NUMBER OF SEQ ID NOS: 70

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 68

LENGTH: 500

TYPE: PRT
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SEQ ID NO 4
LENGTH: 500
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09292768 Patent No. 6194185
                                                                                 CURRENT APPLICATION NUMBER: US/09/292,768
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: 08/881,784
EARLIER FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 70
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Best Local Similarity
Matches 115; Conserv
                                                                                                                                                                                                                                                        APPLICANT: Croteau, Rodney
APPLICANT: Lupien, Shari L
APPLICANT: Karp, Frank
                                                                                                                                                                                         TITLE OF INVENTION: RECOMBINANT MATERIALS
TITLE OF INVENTION: LIMONENE HYDROXYLASES
FILE REFERENCE: WSUI 13463
                                                                 SOFTWARE: PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       433 GAGRRICPGLNFGLANVEVPLAQLLYHFDWKLAEGMNPSDMDMS 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELVKDALSMASGFELADMFPSSKLLNLLCWNKSKLWRMRRRVDAILEAIVEEHKLKKSGE 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMTRNLFSLPIDVPFSGLYRGVKARNLI------HARIEENIRAKI--RRLQATEP 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QDEVSRLLGHLRSSAAAG-----EAVDLTERIATLTCSIICRAAFGSVIRDHEELV----
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                                                                                                                                                                                                                                                                                                           Rodney B
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                                                                                                                                                                                                                                        AND METHODS FOR THE PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGRPTVRVMGADN 96
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GENERAL INFORMATION:

APPLICANT: Croteau, Rodney B

APPLICANT: Lupien, Shari L

APPLICANT: Lupien, Shari L

APPLICANT: Karp, Frank

IIILE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF

IIILE OF INVENTION: LIMONENE HYDROXYLASES

FILE REFERENCE: WSU13463

CURRENT APPLICATION NUMBER: US/09/292,768

CURRENT FILING DATE: 1999-04-14

EARLIER APPLICATION NUMBER: 08/881,784

EARLIER APPLICATION NUMBER: 08/881,784

EARLIER FILING DATE: 1997-06-24

NUMBER OF SEQ ID NOS: 70

SOFTWARE: Patentin Ver. 2.0

INORTH: SOO

TYPE: PRT

OPERITAN: Artificial Sequence
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US-09-292-768-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-09-292-768-70
                                                                                                   ; ORGANISM: Artificial Sequence US-09-292-768-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 115; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 70, Application US/09292768 Patent No. 6194185
Query Match 10.0%; Score 261.5; DB 4; Best Local Similarity 21.9%; Pred. No. 1.1e-19; Matches 115; Conservative 88; Mismatches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 -DDIIFSPY---SVHW-------RQMRKICVSELLSARNVRSFGFIR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323 VMAKAQAEVRA---ALKGKTD--WDVDDVQELKYMKSVVKETMRMHPPIPLIPRSCREEC 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 FGG-EDIIDVLFRMQKDSQIKVPITTNAIKAFIFDTFSAGTETSSTTTLWVMAELMRNPE 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 DGGCKDALQLLIEHSWERGERLDM--QALKQSSTELLFGGHETTASAATSLITYLGLYPH 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 QDEVSRLLGHLRSSAAAG-----EAVDLTERIATLTCSIICRAAFGSVIRDHEELV---- 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          433 GAGRRICPGLNFGLANVEVPLAQLLYHFDWKLAEGMNPSDMDMS 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 VRRILLGEHRLVSVHWPASVRTILGAGCLSNLHDSSHKQRKKVIMQAFSREALQCYVLVI 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 LASALCTFVLPLLLFLAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETLQMVLQR-- 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QHALASVAKQYGPVAHVQLGEVFSVVLSSREATKEAMKLVDPACADRFESIGTKIMWYDN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEEVSSCLEQWLSCGERGLLVYPEVKRLMFRIA-MRILLGCEPGPAGGGEDEQQLVEAFE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGLRSCVGKEFAKILLKIFTVELARHCDWQLLNG--PPTMKTS 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMTRNLFSLPIDVPFSGLYRGVKARNLI------HARIEENIRAKI--RRLQATEP 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVNGYTIPNKARIMINVWSMGRNPLYWEKPETFWPERF----DQVSRDFMGNDFEFIPF 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELNGYOIPKGWNVIYSICDTHDVADIFTNKEEFNPDRFIVPHPEDASR-----FSFIPF 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.0%; Score 261.5; DB 4; Length 500; nilarity 21.9%; Pred. No. 1.1e-19; Conservative 88; Mismatches 216; Indels 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 105;
                                          Length 500;
      Indels 105;
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        Gaps
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D 24	рь	Qy	DЪ	Qy	ф	Qy	Db	Qy	Db	Qy	DЪ	Qy	Db	Qy	DЬ	Qy
436	378	382	323	322	264	264	204	216	153	157	117	97	57	65	5	7
GGGLRSCYGKEEAKILLKIFTYELAKHCUWQULNG ** FF FRA 15 **// ::: : !	EVNGYTIPNKARIMINVWSMGRNPLYWEKPETFWPERFDQVSRDFWGNDFEEIPF 452	VPHPEDASRFSFIPF	VMAKAQAEVRAALKGKTDWDVDDVQELKYMKSVVKETMRMHPPIPLIPRSCREEC 377	VLQKVREEIKSKGLLCKSNQDNKLDMETLEQLKXIGCVIKETLRLNPPVPGGFRVALKTF 381	FGG-EDIIDVLFRMQKDSQIKVPITTNAIKAFIFDTFSAGTETSSTTTLWVMAELMRNPE 322	DGGCKDALQLLIEHSWERGERLDMQALKQSSTELLFGGHETTASAATSLITYLGLYPH 321	ELVKDALSMASGFELADMFPSSKLLNLLCWNKSKLWRMRRRVDAILEAIVDEHKLKKSGE 263	EMTRNLFSLPIDVPFSGLYRGVKARNLIHARIEENIRAKIRRLQATED 263	QDEVSRLLGHLRSSAAAGEAVDLTERIATLTCSIICRAAFGSVIRDHEELV 203	AEEVSSCLEOWLSCGERGLLVYPEVKRLMFRIA-MRILLGCEPGPAGGGEDEQQLVEAFE 215	-DDIIFSPYSVHWRQMRKICVSELLSARNVRSEGFIR 152	VRRILLGEHRLVSVHWPASVRTILGAGCLSNLHDSSHKQRKKVIMQAFSREALQCYVLVI 156	QHALASVAKQYGPVAHVQLGEVFSVVLSSREATKEAMKLVDPACADRFESIGTKIMWYDN 116	RKFLQMKRRKYGFIYKTHL	ISSAIIILVVTYTTISLLIIKQWRKPKPQENLPPGPPKLPLIGH-LHLLWGKLP 56	LASALCTEVLPLLLFLAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETLQMVLQR 64

Search completed: November 6, 2001, 13:27:06 Job time: 9919 sec

Scoring table:	Title: Perfect score: Sequence:	OM protein - pro Run on:	
BLOSUM62 Gapop 10.0 , Gapext 0.5	US-09-668-482-32 2612 1 MGLPALLASALCTFVLPLLLPTVYPVDNLPARFTYFQGDI 497	OM protein - protein search, using sw model Run on: November 6, 2001, 13:35:30; Search time 71.14 Seconds (without alignments) 532.173 Million cell updates/sec	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Total number of hits satisfying chosen parameters:
Minimum DB seg length: 0

Searched:

219241 seqs, 76174552 residues

219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database: PIR_68:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	ω.	7	o	U	4	ω	2	ш	Result	
310	312.5	314.5	315.5	317	322.5	323	323	323.5	323.5	325	326	329.5	332	337	339	339	359	406	410	418	442	442	450	461	494.5	501.5	511.5	668.5	Score	
11.9	12.0	12.0	12.1	12.1		12.4	12.4	12.4	12.4	12.4	•	12.6	12.7		13.0	13.0	13.7	15.5		٠	σ.	16.9	17.2	•			19.6	25.6	Match	de
509	520	512	495	441	476	509	472	511	496	511	503	512	503	520	503	486	519	489	492	457	490	464	472	513	457	482	485	444	Length	
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84/553	H84663	T13611	T06288	C70616	F70791	S68855	G70932	A34260	S41192	A39381	JC4759	н96759	JC7243	T04591	JC4758	JC4240	T02263	B84733	D70649	D85429	H86185	T07859	S55379	T46143	T0444	T02739	A84859	S75761	ID	
CY COULT OHIE E430 CY		hypothetical prote	probable cytochrom	cytochrome P450 Rv	cytochrome P450 Rv	lanosterol 14alpha	probable monoxygen	laurate omega-hydr	cytochrome P450 4D	cytochrome P450 4	sterol 14-demethyl	\vdash	sterol 14alpha-dem	ferulate-5-hydroxy	lanosterol 14alpha			probable cytochrom	cytochrome P450 Rv	cytochrome P450 li	Ω	cytochrome P450 ho	cytochrome P450 CY	w	cytochrome P450 -	probable cytochrom	probable cytochrom	cytochrome P450 -	Description	

ALIGNMENTS

Q 288	235 NNOPLSLPELKDQILLLLFAGHETLTSALSSFCLLLGQHSDIRERVRQEQNKLQ	Дb
3N 340	281 RGERLDMQALKQSSTELLFGGHETTASAATSLITYLGLYPHYLQKVREEIKSKGLLCKSN	Qγ
7E 280 : DD 234	221 LFSLPIDVPFSGLYRGVKARNLIHARIEENIRAKIRRLQATEPDGGCKDALQLLIEHSWE	Qy Db
N 220 N 180	161 SSCLEQWLSCGERGLLVYPEVKRLMFRIAMRILLGCEPGPAGGGEDEOQLVEAFEEMTRN	Qу Дъ
V 160 128	101 LLGEHRLYSVHWPASVRTILGAGCLSNLHDSSHKORKKVIMQAFSREALOCYVLVIAEEV	Qy
T 68	41 ALPLPPGTMGFPFFGETLOMVLORRKFLOMKRRKYGFIYKTHLFGRPTVRVMGADNVRRI 100	Qy Db
Gaps 8;	/ Match 25.6%; Score 668.5; DB 1; Length 444; Local Similarity 34.1%; Pred. No. 1.7e-44; nes 154; Conservative 87; Mismatches 181; Indels 29;	Query Best Matcl
homology	F;391/Binding site: heme iron (Cys) (axial ligand) #status predicted F;31/Binding site: heme iron (axial ligand) #status predicted F;391/Binding site: heme iron (Cys) (axial ligand)	C; Super C; Super C; Keywo F; 251-4 F; 391/B
0496.1; PID:g100 y, June 1996	A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Rosidues: 1-444 < KANN A;Cross-references: EMBL:D64003; GB:AB001339; NID:g1001200; PIDN:BAA10496.1; A;Cross-references: EMBL:D64003; GB:AB001339; NID:g1001200; PIDN:BAA10496.1; A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June	A; Sta A; Mol A; Res A; Cro A; Not
		A; Ref
ange 21-Jul-2000 ; Nakamura, Y.; Miyajima, anabe, A.; Yamada, M.; Yas cyanobacterium Synechocys	pCC 6803	A; Variet C; Date: C; Access R; Kaneko o, K.; C DNA Res. A; Title:
	RESULT 1 S75761 cytochrome P450 - Synechocystis sp. (strain PCC 6803) N;Alternate names: protein slr0574 N;Contains: oxidoreductase (EC 1) C;Species: Synechocystis sp.	RESULT \$75761 cytoch N;Alte N;Cont

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C:Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 C:Keywords: heme; iron; metalloprotein
F:432/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                 Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE002093; NID:g4512670; PIDN:AAD21724.1; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-485 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487
A;Accession: A84859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: A84859 R; Lin, X.; Kaul, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable cytochrome P450 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
mes 132; Conserv
             EFAKILLKIFTVELARHCDWQLLNGPPTMKTSPTVYPVDNLPARFT 491: | : | : | : ;
                                                                        YTIPKGWKILWTTYGTHYNPEIFQDPMSFDPTRFDKP----IQAYTYLPFGGGPRLCAGH
                                                                                                                                                                                                     EEIKSKGLLCKSN--QDNKLDMETLEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNG
                                                                                                                 YQIPKGWNVIYSICDTHDVADIFTNKEEFNPDRFIVPHPEDASRFSFIPFGGGLRSCVGK
                                                                                                                                                            DTLLQEHAQIKANKGEGEYLTVEDVKKMKYSWQVVRETMRLSPPIFGSFRKAVADIDYGG
                                                                                                                                                                                                                                                                         HSWERGERLDMOALKOSSTE-----LLFGGHETTASAATSLTTYLGLYPHVLQKVR
                                                                                                                                                                                                                                                                                                                                    VLEGVFALPVEFPCSKFARAKKARLEIETFLVGKVREKRREM---EKEGAEKPNTTLF--
                                                                                                                                                                                                                                                                                                                                                                  -----SRLVEELIKGVITEEEVVDNMVLLVFAAHDTTSYAMSMTFKMLAQHP----TCR 319
                                                                                                                                                                                                                                                                                                                                                                                                                        DTVKFHHETEWR--GKEEISLYRSAKVLTFTVVFECLYGIKV-----EIGMLEVFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEVSSCLE-QWLSCGERGLLVYPEVKRLMFRIAMRILLGCEPGPAGGGEDEQQLVEAFEE 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIILSNEFSLVVSSWPSSSVQLMGMNCIMAKQGEKHRVLRGIVANSLSVIGLESLIPKLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRILLGEHRLVSVHWPASVRTILGAGCLSNLHDSSHKQRKKVIMQAFSREALQCYVLVIA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLPGEMGLPWIGETMDFYKAQKSNRVFEDFVNPRIIKHGNIFKTRIMGSPTIVVNGAEAN 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPPGTMGFPFFGETLQMVLQRRK-----FLQMKRRKYGFIYKTHLFGRPTVRVMGADNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRLIQQEDWTLLPGQNLELVVTPSPRPKDNL 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSQELTAETLKKMPYLDQVLQEVLRLIPPVGGGFRELIQDCQFQGFHFPKGWLVSYQISQ 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 511.5; DB 2
Pred. No. 3.6e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 201; Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 485
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                           Qy
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A;Reference number: A84420; MUID:20083487
A;Reference number: A84420; MUID:20083487
A;Reference number: A84420; MUID:20083487
A;Residues: preliminary
A;Rolecule type: DNA
A;Residues: 1-482 <GFO>
A;Cross-references: GB:AE002093; NID:g3461849; PIDN:AAC33235.1; GSPDB:GN00139
C;Genetics: A;Gene At2g2090; T9I4.17
A;Map position: 2
A;Introns: 80/2; 187/3; 238/3; 321/3; 351/3; 413/3; 453/2
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology
F; 291-453/Domain: cytochrome P450 homology <P45>
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Best Local Similarity
                                                                                                                                                                                                                                                239
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                                                                                                                                                                                                                                                                                                                                    187
                                                                                                                                                                                                                                                                                                                                                                  183 RIMFRIAMRILLGCEPGPAGGGEDEQQLVEA----FEEMTRNLFSLPIDVPFSGLYRGVK 238
                                                                                                                                                                                                                                                                                                                                                                                                                        129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      436 QLAKISILVFMHFVVTGFDWSLVYPDETISMDPLPFPSLGMPIKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 PALLASALCTFVLPLLLFLAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETLQMVLQ
      DRF-IVPHPEDASRFSFIPFGGGLRSCVGKEFAKILLKIFTVELARHCDWQLLNGPPTMK
                                                               TRVIQETLRAASVLSFTFREAVQDVEYDGYLIPKGWKVLPLFRRIHHSSEFFPDPEKFDP
                                                                                                                                                                                                                                                                                                                                                                                                                  EALFFHQGPYHSTLKRLVQSSFMPSALRPTVSHIELLVLQTLSSWTSQKSINTLEY--MK
                                                                                                      GCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADIFTNKEEFNP 416
                                                                                                                                                                                            LFGGHETTASAATSLITYLGLYPHVLQKV-REEIKSKGLLCKSNQDNKLDMETLEQLKYI 356
                                                                                                                                                   IFAATDTTASVLTWLLKYLHDHPNLLQEVSREQFSIRQKIKKENR--RISWEDTRKMPLT 349
                                                                                                                                                                                                                                                                                  ARNLIHARIEENIRAKI-RRLQATEPDGGCKDALQLLIEHSWERGERLDMQALKQSSTEL
                                                                                                                                                                                                                                                                                                                         RYAFDVAIM-----SAFGDKEEPTTIDVIKLLYQRLERGYNSMPLDLPGTLFHKSMK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NPNSFFATRQNKYGDIFKTHILGCPCVMISSPEAARMVLVSKAHLFKPTYPPSKERMIGP
                                                                                                                                                                                                                                       AR----IELSEELRKVIEKRRENGREEGG----LLGVLLGAKDQKRNGLSDSQIADNIIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCLSNLHDSSHKQRKKVIMQAFSREALQCYVLVIAEEVSSCLEQWLSCGERGLLVYPEVK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R-RKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVHWPASVRTILGA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PALITLTIVVVVVVLLE-----KWWLHWKEQR-----LRLPPGSMGLPYIGETLRLYTE
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28.2%;
94;
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Pred. No. 2.1e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 219;
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43;

Gaps

13;

89 63

186

51

475

481

A;Cross-references: EMBL:AC005315; NID:g3461834; PID:g3461849
A;Experimental source: cultivar Columbia
R;Lin, X:; Kaul, S:; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter nature 402, 761-768, 1999 C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001 C;Accession: T02739; D84692 R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, submitted to the EMBL Data Library, August 1998 A;Description: Arabidopsis thaliana chromosome II BAC T9I4 genomic sequence. A;Reference number: Z14710 A;Accession: T02739 probable cytochrome P450 At2g29090 [imported] - Arabidopsis thaliana N;Alternate names: cytochrome P450 homolog T9I4.17 C;Species: Arabidopsis thaliana (mouse-ear cress) the plant Arabidopsis thaliana

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cytochrome P450 - Arabidopsis thaliana cytochrome P450 - Arabidopsis thaliana N;Alternate names: protein T18B16.200; protein T5K18.10 N;Alternate names: protein T18B16.200; protein T5K18.10 N;Contains: oxidoreductase (EC 1.-.-) R;Contains: oxidoreductase (EC 1.-.-) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 28-Jul-200 C;Accession: T04444; T05806 C;Accession: T04444; T05806 C;Accession: T04444; T05806 Squence Database, April 1998 A;Reference number: Z15359 A;Accession: T04444
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A;Introns: 67/2; 173/3; 302/3; 358/1; 393/3
A;Introns: 67/2; 173/3; 302/3; 358/1; 393/3
A;Note: T18B16.200; T5K18.10
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology C;Keywords: chromoprotein; electron transfer; heme; iron; monooxygenase; oxido: F;272-433/Domain: cytochrome P450 homology <P45>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: cultivar Columbia; BAC clone T18B16 R; Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; submitted to the Protein Sequence Database, April 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-457 <BEV>
A; Cross-references: EMBL: AL021687
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A; Residues: 131-457 <BEW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTLFAGSLFLYFLRCLISQRRFGSSKLPLPPGTMGWPYVGETFQLYSQDPNVFFQSKQKR
                                                                                                                                                                                                                                                                                                                                                                                            QRKKVIMQAFSREALQCYVLVIAEEVSSCLEQWLSCGERGLLV--YPEVKRLMFRIAMRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLLFLAALKLWDLYCVSSRDR--SCALPLPPGTMGFPFFGETLQMVLQ-RRKFLQMKRRK
                                                                                                                                                                                                                                   ENIRAKIRRLOATEPDGGCKDALQLLIEHSWERGERLDMQALKQSSTELLFGGHETTASA 308
                                                                                                                                                                                                                                                                                                               LLGCEPGPAGGGEDE----QQLVEAFEEMTRNLFSLPIDVPFSGLYRGVKARNLIHARIE 248
                                                                                                                                                                                                                                                                                                                                                       KLRKLVLRAFMPESIRNMVPDIESIAQDSLRSW-----EGTMINTYQEMKTYTFNVALLS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                     YGSVFKTHVLGCPCVMISSPEAAKFVLVTKSHLFKPTFPASKERMLGKQAIFFHQGDYHA
                                                                            PVPGGERVALKTFELNGYQIPKGWNVIYSICDTHDVADIFTNKEEFNPDRF-IVPHPEDA 427
                                                                                                                 MSWILKYLAENPNVLEAVTEE--QMAIRKDKEEGESLTWGDTKKMPLTSRVIQETLRVAS 341
                                                                                                                                                      ATSLITYLGLYPHYLQKYREEIKSKGLLCKSNQDNKLDMETLEQLKYIGCVIKETLRLNP 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVHWPASVRTILGAGCLSNLHDSSHK 134
    SRFSFIPFGGGLRSCVGKEFAKILLKI----FTVELARHCDWQLL 468
                                         ILSFTFREAVEDVEYEGYLIPKGWKVLPLFRNIHHSADIFSNPGKFDPSRFEVAPKPN--
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Pred. No. 7e-31;
""smatches 191;
                                                                                                                                                                                                  -LLGSFMGDKEELTDEQ-IADNIIGVIFAARDTTASV 283
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A; Accession: T46143
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Matches 148
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A;Map position: 3
A;Introns: 74/2; 182/3; 233/3; 338/3; 369/3; 396/1; 432/3
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology
C;Superfamily: Synechocystis cytochrome P450 homology
C;Superfamily: Synechocystis cytochrome P450 homology
C;Superfamily: Synechocystis cytochrome P450 homology
C;Superfamily: Synechocystis cytochrome P450 homology
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C;Accession: T46143
C;Accession: T46143
R;Bloecker, H; Mewes, H.W.; Mayer, K.F.X.; Lemcke, K.; Ssubmitted to the Protein Sequence Database, December 1999
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N;Alternate names: protein T3A5.40
C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-513 <BLO>
A; Cross references: EMBL: AL132979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LPALLASALCTFVLPLLLFLAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---ALKQS--STE------LLFGGHETTASAATSLITYLGLYPHVLQKVREEIKSKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LQSRATILKFIERKMEE--RKLDIKEED---QEEEEVKTEDEAEMSKSDHVRKQRTDDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQDEAKKFTFNLMAKHIMSMDPGE----EETEQLKKEYVTFMKGVVSAPLNLPGTAYHKA
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FAKILLKIFTVELARHCDWQLLNGPPTMKTSPTVYPVDNLP
                                                                                                                                                                                   YSICDTHDVADIFTNKEEENPDRFIVPHPEDASRFS-----FIPFGGGLRSCVGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VKARNLIHARIEENIRAKIRRLQATEPDGGCKDALQLLIEHSWE-----RGERLDMQ-
                                                                                                  PVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSE
                                                                                                                                                                                                                                                                                                                        AKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64;
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cytochrome P450 CYP90 - Arabidopsis thaliana R; Contains: oxidoreductase (EC 1.-.-) R; Contains: oxidoreductase (EC 1.-.-) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000 C; Accession: S5379 R; Szekeres, M.; Nemeth, K.; Koncz, Z.; Nagy, F.; Koncz, C. submitted to the EMBL Data Library, May 1995
                   C;Accession: T07859

R;Bishop, G.J.; Harrison, K.; Jones, J.D.

Plant Cell 8, 959-969, 1996

A;Title: The tomato Dwarf gene isolated by heterologous transposon tagging encodes the A;Accession: T07859

A;Accession: T07859
                                                                                                                                                                           cytochrome P450 homolog - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 c;Keywords: chromoprotein; electron transfer; heme; iron; metalloprof F;275-440,Domain: cytochrome P450 homology <P45> F;418/Binding site: heme iron (Cys) (axial ligand) #status predicted
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A; Molecule type: mRNA
A; Residues: 1-472 <SZE>
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preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                 VPAEQDKLVFFPTTRTQKRYPIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKHSLLLMKGSLHKRMHSLTMSFANSSIIKDHLMLDIDRLVRFNLDSWSS-----RVLLME 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGCLSNLHDSSHKQRKKVIMQAFSREALQCYVLV-IAEEVSSCLEQWLSCGERGLLVYP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TENPEPFIDERVARYGSVFMTHLFGEPTIFSADPETNRFVLQNEGKLFECSYPASICNLL 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPWRWQSNSVTTGPSNV----FTPFGGGPRLCPGYELARVALSVFLHRLVTGFSW-----
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26.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----RRTRYRRMGLPPGSLGLPLIGETFQLIGAYK 52
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heme; iron; metalloprotein; mono
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R!Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Wh Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay, C.A.; Li, J.R.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A, Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A, Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: H86185
A; Accession: H86181
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A; Residues: 1-464 <BISS /
A; Cross-references: EMBL:U54770; NID:91421740; PIDN:AAB17070.1; PID:91421741
A; Experimental source: strain GCR758
C; Genetics:
C; Genetics: dwarf
C; Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homolog
F; 273-436/Domain: cytochrome P450 homology <P45>
A;Cross-references: GB:AE0051
C;Genefics:
A;Map position: 1
C;Superfamily: Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #te
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A; Residues: 1-490 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LCIFCTALLRWNQVKYNQKN------LPPGTMGWPLFGETTEFLKLGPSFMKNQRARYGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLLFLAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETLQMVLQRRKFLQMKRRKYGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVFGGGTRQCPGKELGVAEISTFLHYFVTKYRWEEIGGDKLMK 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLRKTTQDMEINGYIIPKGWRIYVYTRELNYDPRLYPDPYSFNPWRWMDKSLEHQN--SF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFRVALKTFELNGYQIPKGWNVIYSICDTHDVADIFTNKEEFNPDRFIVPHPEDASRFSF 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKYLHDHPKVLEELRKE--HMAIREKKKPEDPIDYNDYRSMRFTRAVILETSRLATIVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITYLGLYPHVLQKVREEIKSKGLLCKSNQDNKLDMETLEQLKYIGCVIKETLRLNPPVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKIRRLQATEPDGGCKDALQLLIEHSWERGERLDMQALKQSSTELLFGGHETTASAATSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESTSLA-----QEFMSEFFNLVLGTLSLPINLPNTNYHRGFQARKIIVNLLRTLIEE--R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPGPAGGGEDEQQLVEAFEEMTRNLFSLPIDVPFSGLYRGVKAR----NLIHARIEENIR 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GALLSLISPIMIRDQLLPKIDEFMRSHLINW---DNKVIDIQEKINKMAFLSSLKQIAGI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVIMQAFSREALQCYVL-VIAEEVSSCLEQWLSCGERGLLVYPEVKRLMFRIAMRILLGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                 GB:AE005172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----HDMLGYLMNEEATRFKLTDDEMIDLIIT-ILYSGYETVSTTSMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;; Score 442; DB 2;
;; Pred. No. 9e-27;
94; Mismatches 210
                                                                                 NID:g2388581;
                                                                                    PIDN: AAB71462.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210;
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                                                                                                                                                                                                                                                                                          Southwick, A.M.; Sun,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Maiti, R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346
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cytochrome P450 slr0574; cytochrome P450 homology

Tallo

Kim,

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A; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A; Reference number: A85001; MUID:20083488
A; Accession: D85429
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-457 <STO>
A; Cross-references: GB:NC_001268; NID:97270586; PIDN:CAB80304.1; GSPDB:GN00140
C; Genetics:
A; Gene: A74936380
A; Map Cstiton: 4
C; Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology
C; Keywords: heme; iron; metalloprotein
C; Seywords: heme; iron; metalloprotein
F; 396/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytochrome P450 like protein [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Apr-200 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Apr-200 C;Accession: D85429 R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, Nature 402, 769-777, 1999
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D85429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 CRRVLTDDDAF-KPGWPTSTMELIGRKSFVGISFEEHKRLRRLTAAPVNGHEALSTYIPY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97
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      61
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                                                         99
                                                                                                                                               44 LPPGTMGFPFFGETLQMV---LQRRKFLQMKRRK--YGFIYKTHLFGRPTVRVMGADNVR 98
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   KVVLQNHGNTFVPAYPKSITELLGENSILSI-NGPHQKRLHTLIGAFLRSPHLKDRITRD 119
                                                      RILLGEHRLVSV-HWPASVRTILGAGCLSNLHDSSHKQRKKVIMQAF-----SRE 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAKILLKIFTVELARHCDWQLLNGPPTMKTSPTVYPVDNLPARFTY 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -QEMILKSRPEGQKGLSLKETRKMEFLSQVVDETLRVITFSLTAFREAKTDVEMNGYLIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E----MTRNLFSLPIDVPFSGLYRGVKARNLIHARIEENIRAKIRRLQATEPDGGCKDAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPPGDLGWPFIGNMLSFLRAFKTSDPDSFTRTLIKRYGPKGIYKAHMFGNPSIIVTTSDT 104
                                                                                                                IPNGSLGWPVIGETLNFIACGYSSRPVTFMDKRKSLYGKVFKTNIIGTPIIISTDAE-VN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGWKVLTWFRDVHIDPEVFPDPRKFDPARWDNGFVP-----KAGAFLPFGAGSHLCPGND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKGLLCKSNQDNK--LDMETLEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIP 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REYTALNYGVRAMAVNIPGFAYHRALKARKTLVAAF-QSIVTERRNQRKQNILSNKKDML
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                                                                                                                                                                                                                                                            Similarity
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27.7%;
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                                                                                                                                                                                                                              80;
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                                                                                                                                                                                                                                                      Score 418; DB 2;
Pred. No. 6.6e-25;
                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                              206; Indels
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                                                                                                                                                                                                                                                                                    Length 457;
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                                                                                                                                                                                                                              54;
                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                              14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: Rv3059
C;Superfamily: Mycobacterium cytochrome P450 Rv3059; cytochrome P450 homology C;Superfamily: Mycobacterium cytochrome P450 Rv3059; cytochrome P450 homology C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase F;300-461/Domain: cytochrome P450 homology <P45>
F;439/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987

A;Accession: D70649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:283866; GB:AL123456; NID:g3261691; PIDN:CAB06263.1; PID:g17811 A;Experimental source: strain H37Rv C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D70649
cytochrome P450 Rv3059 - Mycobacterium tuberculosis (strain H37RV)
N;Contains: oxidoreductase (EC 1.-.-)
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: D70649
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A; Residues: 1-492 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148
                                                                                                                                                                    141 MQAFSREALQCYVLVIAEEVSSCL-EQWLSCGERGLLVYPEVKRLMFRIAMRILLGCEPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394 RLCPGLELSKLEISIFLHHLVTRYSWTA--EEDEIVSFPTVKMKRRLPIR 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             440 RSCVGKEFAKILLKIFTVELARHCDWQLLNGPPTMKTSPTVYPVDNLPAR 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 DVEIKGYLIPKGWCVLASFISVHMDEDIYDNPYQFDPWRWDRINGSANSSICFTPFGGGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              380 TFELNGYQIPKGWNVIYSICDTHDVADIFTNKEEFNPDRFIVPHPEDASRFSFIPFGGGL 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 HVLQK-VREEIKSKGLLCKSNQDNKLDMETLEQLKYIGCVIKETLRLNPPVPGGFRVALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 NILKLEFEEFIKGLICIPIKFPGTRLYKSLKAKERLIKMVKKVVEERQVAMTTTSP---A
                                                                                                                                                                                                                                                                                                                                              42
                                                                                                                                                                                                                              94 DSAVLPGVAALGPDAAQVIYSNRNKDYSQQGWVPVIGPFFHRG-LMLLDFEEHMFHRRIM
                                                                                                                                                                                                                                                                                                                                                                                                  37 DRSCALPLPPGT-----MGFPFFGETLQMVLQRRKFLQMKRRKYGFIYKTH---LFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VALAKLVEENMEMKRRKLELGEEYK--WTDYMSLSFTQNVINETLRMANIINGVWRKALK
-----TDHELVTKVNKAFTITTRAGNAVIRTSVP---PFT-WWRGLRARELL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQLVEAFEEMTRNLFSLPIDVPFSGLYRGVKARNLIHARIEENIRAKIRRLQATEPDGGC
                                                      PAGGGEDEQQLV----EAFEEMTRN-----LFSLPIDVPFSGLYRGVKARNLIHARIEEN 250
                                                                                                                                                                                                                                                                                    ----RPTVRVMGADNVRRILLGEHRLVSVH-WPASVRTILGAGCLSNLHDSSHKQRKKVI 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NDVVDVLLRDGG-----DSEKQSQPSDFVSGKIVEMMIPGEETMPTAMTLAVKFLSDNP
                                                                                                                QEAFVRSRLAGYLEQMDRVVSRVVADDWV-VNDARFLVYPAMKALTLDIASMVFMGHEPG
                                                                                                                                                                                                                                                                                                                                              EKKLAEP-PPGSGLKPVVGDAGLPILGHMIEMLRGGPDYLM----FLYKTKGPVVFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.7%; Score 410; DB 1; Length 492 29.2%; Pred. No. 3.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            78; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            186; Indels
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Holroyd,

geno

82;

Gaps

23;

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93

152

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Unature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable cytochrome p450 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: B84733
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C; Superfamily: Synechocystis cytochrome P450 slr0574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-489 <STO>
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B84733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE002093; NID:g3831452; PIDN:AAC69934.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                   163
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                                                      329 QERIVKKRAPGQKLTLKETREMVYLSQVIDETLRVITFSLTAFREAKSDVQMDGYIIPKG
                                                                                                                                                                                                                                                                        212 REYTNLNYGVRAMGINLPGFAYHRALKARKKLVAAF-QSIVTNRRNQRKQNISSNRKDML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 15.5%; Score 406; DB 2; Local Similarity 27.8%; Pred. No. 6.3e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 LPPGDLGWPVIGNMWSFLRAFKTSDPESFIQSYITRYGRTGIYKAHMFGYPCVLVTTPET 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 LPPGTMGFPFFGETLQMV-----LQRRKFLQMKRRKYG--FIYKTHLFGRPTVRVMGADN 96
WNVIYSICDTHDVADIFTNKEEFNPDRFIVPHPEDASRFSFIPFGGGLRSCVGKEFAKIL 451
                                                                                                       SKGLLCKSNQDNKLDMETLEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKG
                                                                                                                                                                                                                  QLLIEHSWERGERLDMQALKQSSTELLFGGHETTASAATSLITYLGLYPHVLQKVREEIK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRRVLTDDDAF-HIGWPKSTMKLIGRKSFVGISFEEHKRLRKLTSAPVNGPEALSVYIQF 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVYPVDNLP 487
                                                                                                                                                              DNLIDVKDENGRVLDDEEIIDLLLMYLNAGHESSGHLTMWATILMQEHPMILQKAKEE--
                                                                                                                                                                                                                                                                                                                                                                                                                                    IAEEVSSCLEQWLSCGERGLLVYPEVKRLMFRIAMRILLGCEPGPAGGGEDEQQLVEAFE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRRILLGEHRLVSVHWPASVRTILGAGCLSNLHDSSHKQRKKVIMQAFS-REALQCYVLV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RHRYAFTPFGGGVHKCIGMVFDQLEIKTILHRLLRRYRLELSRP-DYQ-----PRWDYSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPVQWAMRQTVRDTELLGYYLPKGTNVIAYPGMNHRLPEIWTDPLTFDPERFTEPRNEHK 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YFTARVKERR----EASG--NDLLTVLCQTEDDDGNRFSDADIVNHMIFLMMAAHDTSTS
                                                                                                                                                                                                                                                                                                                         EMTRNL----FSLPIDVPFSGLYRGVKARNLIHARIEENIRAKIRRLQATEPDGGCKDAL
                                                                                                                                                                                                                                                                                                                                                                                   IEETVNTDLEKWSKMGEIEFLSH--LRKLTFKVIMYIFLSSE-----SEHVMDSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 489;
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                                                                                                                                                                                                                                                                                                                            271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Description: involved in an early step in gibberellin biosynthesis A;Pathway: gibberellin biosynthesis C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology C;Keywords: oxidoreductase F;325-488/Domain: cytochrome P450 homology <P45>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The maize dwarf3 gene encodes a cytochrome A;Reference number: Z14648; MUID:96004534 A;Accession: T02263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Winkler, R.G.; Helentjaris, T. Plant Cell 7, 1307-1317, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytochrome P450 DWARF3 - maize
N;Contains: oxidoreductase (EC 1.-.-.)
C;Species: Zea mays (maize)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
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  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-519 <WIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    452 LKIFTVELARHCDWQLLN-GPPTMKTSPTVYPVDNLPARFT 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 CKQVLMDDDAFVT-GWPKATVALVGPRSFVAMPYDEHRRIRKLTAAPINGFDALTGYLPF 190
                                                                                475 EISVFLHHFLLGYKLAR-----TNPRCRVRYLPHPRPVDNCLAKIT 515
                                                                                                                                       451 LLKIFT-----VELARHCDWQLLNGPPTMKTSPTVYPVDNLPARFT 491
                                                                                                                                                                                           418 GWKVQLWYRSVHMDPQVYPDPTKFDPSRWEGHSPRAG---TFLAFGLGARLCPGNDLAKL
                                                                                                                                                                                                                                            391 GWNVIYSICDTHDVADIFTNKEEFNPDRFIVPHPEDASRFSFIPFGGGLRSCVGKEFAKI 450
                                                                                                                                                                                                                                                                                                                                                   331 KSKGLLCKSNODNKLDMETLEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPK 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 LQLLIEHSWERGERLDMQALKQSSTELLFGGHETTASAATSLITYLGLYPHVLQKVREEI 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 RSYTELNYGMRAMAINLP-GFAYRGALRARRRLVA-VLQGVLDERRAARAKGVSGGGVDM 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 EAFEEMTRNLFSLPIDVPFSGLYRG-VKARNLIHARIEENIRAKIRRLQATEPDGGCKDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             446 ISIFLHHFLLKYRVERSNPGCPVM-FLPHNRPKDNCLARIT 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 LPPGTMGFPFFGETLQMVLQRRK-----FLQMKRRKYG--FIYKTHLFGRPTVRVMGADN 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 VRRILLGEHRLVSVHWPASVRTILGAGCLSNLHDSSHKQRKKVIMQAFSR-EALQCYVLV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 LPPGEMGWPLVGGMWAFLRAFKSGKPDAFIASFVRRFGRTGVYRSFMFSSPTVLVTTAEG 131
  13
                                                                                                                                                                                                                                                                                                  EAIMRSIPSSQ-RGLTLRDFRKMEYLSQVIDETLRLVNISFVSFRQATRDVFVNGYLIPK 417
                                                                                                                                                                                                                                                                                                                                                                                                          MDRLIEAQDERGRHLDDDEIIDVLVMYLNAGHESSGHITMWATVFLQENPDMFARAKAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IAEEVSSCLEQWLSCGERGLLVY-PEVKRLMFRIAMRILLGCEPGPAGGGEDE----QQLV 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDRTVTSSLRAWADHG--GSVEFLTELRRMTFKIIVQIFL-----GGADQATTRALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123;
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Gaps

15;

240

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C;Superfamily: human C;Keywords: chromopro F;291-454/Domain: cyt F;432/Binding site: P
lanosterol 14alpha-demethylase (EC 1.14.14.-) cytochrome P450 51 - rat N;Alternate names: pRT-9 protein C;Species: Rattus norvegicus (Norway rat) C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2000 C;Accession: JC4758; PC4170; JC5888; JC2334 R;Aoyama, Y.; Noshiro, M.; Gotoh, O.; Imaoka, S.; Funae, Y.; Kurosawa, N.; 1
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A;Residues: 43-60;206-213;254-267;369-387;420-428;433-443
A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Cloning and functional expression of the cDNA encoding rat lanosterol 14-alpha A;Reference number: JC4240; MUID:95394364
A;Accession: JC4240
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                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lanosterol 14alpha-demethylase (EC 1.14.14.-) cytochrome P450 51 - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Comment: This enzyme is a cytochrome P-450 enzyme which catalyzes one of the essential;Superfamily: human cytochrome P450 Cy551; cytochrome P450 homology cytochrome cytochrome p450 homology cytochrome p450 homology cytochrome p450 homology cy45>;291-454/Domain: cytochrome P450 homology cy45>;432/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Species: Rattus norvegicus (Norway rat);Date: 21-Nov-1995 #sequence_revision 08-Feb-1995 #text_change 28-Jul-2000;Accession: JC4240; PC4069
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276 GRPLTDDEIAGMLIGLLLAGQHTSSTTSAWMGFFLARDKPLQDKCYLEQKT---VCGEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114
                                                                                                                                                                                                                                                        452 LYEFDLINGYFPSVNYTTMIHTPENPVIRY
                                                                                                                                                                                                                                                                                                      462 HCDWQLLNGP-PTMKTSPTVYPVDNLPARF 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 P-PLTYEQLKDLNLLDRCIKETLRLRPPIMTMMRMAKTPQTVAGYTIPPGHQVCVSPTVN 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342 DNKLDMETLEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDT 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282 GERLDMQALKQSSTELLFGGHETTASAATSLITYLGLYPHVLQKVREEIKSKGLLCKSNQ 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 GWLPLPSFRRDRAHREIKNIFYKAIQK-----RRL-SKEP---AEDILQTLLDSTYKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 N--VFEALSELIILTASHCL-----HGKEIRSQLNEKVAQLYADLDGGFSHAAWLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 GLLVYPEVKRLMFRIAMRILLGCEPGPAGGGEDEQQLVEAFEEMTRNL---FS-----LP 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 HAIAFGKSPIEFLENAYEKYGPVFSFTMVGKTFTYLLGSDAAALLFNSKNEDLNAEEVYG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLASAL--CTFVLPLL-LFLAALKLWDLYCVSSRDRSCALPLPPGTMG------FPFFG 55
                                                                                                                                                                                                                                                                                                                                                         QRLKDSWVERLDFNPDRYLQDNPASGEKFAYVPFGAGRHRCIGENFAYVQIKTIWSTMLR 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDVPFSGLYRGVKA----RNLIHARIEENIRAKIRRLQATEPDGGCKDALQLLIEHSWER 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLTTPVFGKGVAYDVPNAVFLEQKKILKSGLNIAHFKQYVSIIEKEAKKYFKSWGESGER 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETLOMVLORRKFLOMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVH--WP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLSTLLIACAFTLSLVYLFRLAV-------GHMVQLPAGAKSPPYIYSPIPFLG
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                                                                                                                                                                                                                                                        481
  S.; Funae, Y.; Kurosawa, N.; Horiuchi,
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A;Description: catalyzes the removal of the 14-methyl group of 14-methylsterols C;Superfamily: human cytochrome P450 (CY551; cytochrome P450 homology C;Keywords: chromoprotein; heme; liron; liver; metalloprotein; monooxygenase; oxidored F;308-471/Domain: cytochrome P450 homology <P45>
F;449/Binding site: heme iron (Cys) (axial ligand) #status predicted
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A;Residues: 74-503 <AOY>
A;Cross-references: DDBJ:D29962
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R;Aoyama, Y.; Funae, Y.; Noshiro, M.; Horiuchi, T.;
Biochem. Biophys. Res. Commun. 201, 1320-1326, 1994
A;Title: Occurrence of a P450 showing high homology
A;Reference number: JC2334; MUID:94296405
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A;Accession: JC5888
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A;Accession: PC4170
A;Molecule type: protein
A;Residues: 52-109;305-319;324-334;467-482;488-499 <AOY2>
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A;TitLte: Sterol 14-demethylase P450 (P45014DM) is
A;Reference number: JC4758; MUID:96389999
A;Accession: JC4758
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A; Residues: 1-503 < NOS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-503 <AOY1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: JC2334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Introns: 59/3; 91/3; 150/3; 193/1; 251/2; 291/2; 356/3; 388/3; 445/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 ASVRTILGAGCLSNLHDSSHKQRKKVIMQAFSREALQCYVLVIAEEVSSCLEQWLSCGER 173
402 HDVADIFTNKEEFNPDRFIVPHPEDASRFSFIPFGGGLRSCVGKEFAKILLKIFTVELAR 461
                                                                     350 P-PLTYEQLKDLNLLDRCIKETLRLRPPIMTMMRMAKTPQTVAGYTIPPGHQVCVSPTVN 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 N--VFEALSELIILTASHCL-----HGKEIRSQLNEKVAQLYADLDGGFSHAAWLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 GLLVYPEVKRIMFRIAMRILLGCEPGPAGGGEDEQQLVEAFEEMTRNL---FS-----LP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 LLSTLLIACAFTLSLVYLFRLAV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 LLASAL--CTFVLPLL-LFLAALKLWDLYCVSSRDRSCALPLPPGTMG-----FPFFG
                                                                                                                                                                                                                                                                       GERLDMQALKQSSTELLFGGHETTASAATSLITYLGLYPHVLQKVREEIKSKGLLCKSNQ
                                                                                                                                                                                                                                                                                                                                             GWLPLPSFRRRDRAHREIKNIFYKAIQK-----RRL-SKEP---AEDILQTLLDSTYKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RLTTPVFGKGVAYDVPNAVFLEQKKILKSGLNIAHFKQYVSIIEKEAKEYFKSWGESGER
                                                                                                                                                                                                         GRPLTDDEIAGMLIGLLLAGQHTSSTTSAWMGFFLARDKPLQDKCYLEQKT----VCGEDL
                                                                                                                                                                                                                                                                                                                                                                                                           IDVPFSGLYRGVKA----RNLIHARIEENIRAKIRRLQATEPDGGCKDALQLLIEHSWER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HATAFGKSPIEFLENAYEKYGPVFSFTMVGKTFTYLLGSDAAALLFNSKNEDLNAEEVYG
                                                                                                                                   DNKLDMETLEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETLQMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVH--WP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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23.7%;
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Pred. No. 1.1e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T.; Gotoh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GHMVQLPAGAKSPPYIYSPIPFLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 one of the most ancient and
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A;Residues: 1-520 <BEV>
A;Cross-references: EMBL:AL022141
A;Experimental source: cultivar Columbia; BAC clone F23E13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: T04591
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; submitted to the Protein Sequence Database, March 1998
A;Reference number: Z15378
A;Accession: T04591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ferulate-5-hydroxylase (EC 1.-.-) Arabidopsis thaliana
N;Alternate names: cytochrome P450-dependent monooxygenase; protein F23E13.110
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 28-Jul-2000
C;Accession: T04591
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                       AKILLKIFTVELA----RHC-DWQLLNGPPTMKTS 477
                                                                                                                                                                                                                                               WERGERLDMQ------ALKQSSTELLFGGHETTASAATSLITYLGLYPHVLQKVREEI 330
----LGLYALDLAVAHILHCFTWKL---PDGMKPS 490
                                                                                                           KGWNVIYSICDTHDVADIFTNKEEFNPDRFIVPHPED--ASRFSFIPFGGGLRSCVGKEF
                                                                                                                                               AEVVGL-----DRRVEESDIEKLTYLKCTLKETLRMHPPIPLLLHETAEDTSIDGFFIP 403
                                                                                                                                                                                                                         KLVSETADLQNSIKLTRDNIKAIIMDVMFGGTETVASAIEWALTELLRSPEDLKRVQQEL
                                                                                                                                                                                                                                                                                                 IDPQGINKRLVKARNDLDGFIDDIIDEHMKKKENQNAVDDGDVVDTDMVDDLLAFYSEEA
                                                                                                                                                                                                                                                                                                                                   Y-----RGVKARNLIHARIEENI--RAKIRRLQATEPDGG-----CKDALQLLIEHS
                                                                                                                                                                                                                                                                                                                                                                      -IFALTRNITYRAAFG--SACEKG-----QDEFIRILQEFSKLFGAFNVADFIPYFGW 229
                                                                                                                                                                                                                                                                                                                                                                                                        LVYPEVKRLMFRIAMRILLGCEPGPAGGGEDEQQLVEAFEEMTR--NLFSLPIDVPFSGL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                              DMAFAHYGPFWRQMRKVCVMKVFSRKRAESWASVRDEVDKMVRSVSCNVGKPINVGEQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGFIYKTHL-FGRPTVRVMGADNVRRILLGEHRLVSVHWPASVRTILGAGCLSNL-HDSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVSLFIFIS-----FITRRRRP---PYPPGPRGWPIIGNMLMMDQLTHRGLANLAKK 70
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                                                                       KKSRVMINAFAIGRDPTSWTDPDTFRPSRFLEPGVPDFKGSNFEFIPFGSGRRSCPGMQ-
                                                                                                                                                                                   -KSKGLLCKSNQDNKLDMETLEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIP 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YGGL--CHLRMGFLHMYAVSSPEVARQVLQVQDSVFSNRPATI-----AISYLTYDRA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 194; Indels
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Search completed: November Job time: 599 sec 6, 2001, 13:35:31

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Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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 SPTREMBL_16:*
1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_invertebr:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelie
9: sp_phage:*
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11: sp_rodent:*
11: sp_vertebr:
13: sp_vertebr:
14: sp_virus:**
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Gapop 10.0 , Gapext 0.5
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2612
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                                                                                                               sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_bacteria:*
sp_fungi:*
sp_rodent:*
sp_unclassified:*
sp_vertebrate:*
sp_virus:*
                                                                                sp_organelle:*
sp_phage:*
                                                                  sp_plant:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	8	7	6	ر ن	4	ω	ν	_	Result
418	418	418.5	432	455.5	461	461	494.5	501.5	511.5	517.5	538	569	668.5	1036	1048.5	1758.5	2057.5	2609	Score
16.0	16.0	16.0	16.5	17.4	17.6	17.6	18.9	19.2	19.6	19.8	20.6	21.8	25.6	39.7	40.1	67.3	78.8	99.9	Query Match
474	457	465	443	465	513	513	457	482	485	463	107	477	444	525	512	492	492	497	Length
10	10	10	10	10	10	10	10	10	10	10	13	10	N	4	4	13	13	11	DB
Q9LKH7	Q9M066	Q9LH81	Q9LJK2	Q9FMA5	Q9SCQ9	064989	065624	081077	Q9SJH2	Q9FH76	Q9PUG2	Q9LVY7	Q59990	Q9NP41	Q9NR63	093323	Q9PUB4	Q9R1F4	ij
Q91kh7 phaseolus a	Q9m066 arabidopsis	Q91h81 arabidopsis		Q9fma5 arabidopsis	_	064989 arabidopsis	065624 arabidopsis	081077 arabidopsis	~	Q9fh76 arabidopsis		Q9lvy7 arabidopsis	Q59990 synechocyst	Q9np41 homo sapien	Q9nr63 homo sapien	093323 xenopus lae	Q9pub4 gallus gall		Description

4	44	43	42	41	40	39	3 8	37	36	35 5	34	ဒ္	32	31	30	29	28	27	26	25	24	23	22	21	20
314	315.5	317.5	318	318.5	318.5	318.5	327	329.5	333	336	336.5	340	341	342	350.5	351	351	358.5	374	380	400.5	404	406	407.5	418
12.0	12.1	12.2	12.2	12.2	12.2	12.2	12.5	12.6	12.7	12.9	12.9	13.0	13.1			13.4	13.4	13.7	14.3	14.5	15.3	15.5	15.5	15.6	16.0
464	495	459	497	513	491	474	498	512	518	521	735	318	520	520	513	503	486	511	504	475	496	478	489	464	524
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004949	Q9T0K2	Q59163	076478	Q9SBP8	Q9NGK3	Q9SHY7	016806	Q9FX29	Q9FI38	Q9XFM2	Q9LG17	Q9LVY3	Q9FVB9	Q9FVC0	Q9FVB8	Q9JIP8	Q9JIY3	Q9SWR1	Q9SNG3	Q9x7G9	Q9FQY4	Q9LN73	Q9ZV72	Q9LIC5	023242
004949 arabidopsis				Q9sbp8 populus tri	Q9ngk3 tribolium c	Q9shy7 arabidopsis	016806 drosophila	Q9fx29 arabidopsis			_	Q9Lvy3 arabidopsis		Q9fvc0 brassica na		Q9jip8 mus musculu			_		Q9fqy4 cucurpica m				

ALIGNMENTS

QY 1 MGLPALLASALCTEVLPLLLELAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETLQM 	Query Match 99.9%; Score 2609; DB 11; Length Best Local Similarity 99.8%; Pred. No. 1.3e-205; Matches 496; Conservative 1; Mismatches 0; Indels	SQ SEQUENCE 497 AA; 56191 MW; 67CB167A997842C1 CRC64;	PROSITE; PS00086; CYTOCHKOME_P430; ONANGWN_1. Electron transport; Endoplasmic reticulum; Heme;	DR InterPro; IPR001128;		-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOFLASMIC SIMILARITY).	OXIDIZED FLAVOPROTEIN + H(2)0 (BY SIMILARITY).	RL Connect. Tissue wes. 38:237-207(1990).	genin-interacting	RX PubMed=11063033;	TISSUE-TOOTH;	RP SEQUENCE FROM N.A.	Rodentia;	Mus musculus (Mouse). Fukarvota: Metazoa: Chordata: Craniata; Vertebrata;	CYTOCHROME F	DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)	(TrEMBLrel. 13, Creat	
LPPGTMGFPFFGETLQM 60	Length 497; Indels 0; Gaps	CRC64;	Membrane; Microsome;		AMILY.	ASMIC RETICOTOM (BI	ALL THE	N + O(2) = ROH +	racting proteins using				dae; Murinae; Mus.	ta; Euteleostomi;	E P45URA.	te)		
	0;																	

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 Query Match
Best Local
                                                                                       Dev. Bidd. 0:00(2000).

-i- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) =

OXIDIZED FLAVOPROTEIN + H(2)O (BY SIMILARITY).

-i- SUBCELULAR IOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETIC

SIMILARITY).

I- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

EMBL; AF199462; AAF09250.1; -.

InterPro; IPR001128; -.

Ffam; PF00067; P450. 1.

PRINTS; PR00385; P450. 1.
                                                                                                                                                                                                                                                                                                                                                   Q9PUB4 PRELIMINARY; PRT; 492 AA.
Q9PUB4;
Q9PUB4;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 16, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CYTOCHROME P450 26 (EC 1.14...) (RETINOIC ACID METABOLIZING CYTOCHROME) (P450RAI) (RETINOIC ACID 4-HYDROXYLASE).
                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
Archosauria; Aves; Neogn
                                             PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Electron transport; Endoplasmic reticulum; He
Monooxygenase; Oxidoreductase.
SEQUENCE 492 AA; 55264 MW; 7F28B72E75C232
                                                                                                                                                                                                               "Complementary Domains of Retinoic Acid Production the Early Chick Embryo.";
                                                                                                                                                                                                                                           Swindell E. 
Eichele G.;
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
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 Similarity
                                                                                                                                                                                                                                                     E.C., Thaller C., Sockanathan
                                                                                                                                                                                                                                                                                                           ; Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
 78
 .18;
 Score
Pred.
                                             7F28B72E75C232FB
2057.5; DB 1
No. 2.1e-160;
                                                                                                                                                                                                                                                  s.,
                                                                     Heme;
                                                                                                                                                                                                                                                  Petkovich M.,
        DB 13;
                                              CRC64;
                                                                    Membrane;
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          Length
                                                                                                                                                                 RETICULUM
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                                                                    Microsome;
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Best Local
     Matches
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O93323;
O1-NOV-1998 (TrEMBLrel. 08, Created)
O1-NOV-1998 (TrEMBLrel. 08, Last sequence update)
O1-NAR-2001 (TrEMBLrel. 16, Last annotation update)
CYTOCHROME P450 26 (EC 1.14...) (RETINOIC ACID-METABOLIZING
CYTOCHROME) (P450RAI) (RETINOIC ACID 4-HDROXYLASE).
CYTOCHROME) (P450RAI) (RETINOIC ACID 4-HDROXYLASE).
Xenopus laevis (African clawed frog).
Xenopus laevis (African Clawed frog).
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae;
                                                            InterPro; IPR001128; -...,
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450; 1.
PRINTS; PR00385; P450; UNKNOWN_1.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 492 AA; 55459 MW; D1D4BB7651BF2D
                                                                                                                                 Chen J.L., Grunz H., Panitz F., Pieler T., Hollemann T., Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases -i- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY. EMBL; AF057566; AAC25138.1; -.
                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                           Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt MGFSALVASALCTFLLPLLLFLAAVRLWDLYCASGRDPSCPLPLPPGTMGLPFFGETLQM}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               398;
               Similarity
  Conservative
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              67.3%;
68.1%;
                                                                                                                                                                                                                                                                                                                                                                                                               492
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 63;
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Score 1758.5; DB 1: Pred. No. 6.9e-136; 3; Mismatches 89;
                                                              D1D4BB7651BF2D3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                       DB 13; Length
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 Indels
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7;
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 Gaps
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MGLPALLASALCTFVLPLLLELAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETLQM

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61 61

VLQRRRFLQVKRSQYGRIYKTHLFGSPTVRVTGAENVRQILMGEHKLVSVHWPASVRTIL VLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVHWPASVRTIL MDLYTLLTSALCTLALPLLLLLTAAKLWEVYCLRRKDAACANPLPPGTMGLPFFGETLQM

60

Matches

220;

Conservative

44.48;

88;

Pred. No. 1.2e-77; 8; Mismatches 164

164;

Indels

23;

Gaps

9;

Best Local Similarity

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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CYTOCHROME P450 RETINOID METABOLIZING PROTEIN P450RAI-2.
CYP26B1.
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01-OCT-2000
01-OCT-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDIINE=20300913; PubMed=10823918;

White J.A., Ramshaw H., Taimi M., Stangle W., Zhang A., E
White J.A., Ramshaw H., Taimi M., Stangle W., Zhang A., E
Creighton S., Tam S.-P., Jones G., Petkovich M.;

Creighton S., Tam S.-P., Jones G., Petkovich M.;

"Identification of the human cytochrome P450, P450RAI-2,
predominantly expressed in the adult cerebellum and is re
predominantly expressed in the adult cerebellum and is re
all-trans-retinoic acid metabolism.";

Proc. Natl. Acad. Sci. U.S.A. 97:6408(2000).

--- CATALYTIC ACTUVITY: RH + REDUCED FLAVOPROTEIN + O(2)

OXIDIZED FLAVOPROTEIN + H(2)0 (BY SIMILARITY).
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                                                                                                 :- SIMILARITY: BELONGS TO THE CYTO EMBL; AF252297; AAP76003.1; -. InterPro; IPR001128; -. Pfam; PF00067; p450; 2. PRINTS; PR00385; P450. PRINTS; PR00385; CYTOCHROME_P450; PROSITE; PS00086; CYTOCHROME_P450; PROSITE; PS00086; CYTOCHROME_P450; PS00086; CYTOCHROME_P450; PROSITE; PS00086; CYTOCHROME_P450; CY
   Electron transport; Endoplasmic reticulum; Monooxygenase; Oxidoreductase. SEQUENCE 512 AA; 57512 MW; A06D1D9944E
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Primates;
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Query Match

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Q9NP41;
01-OCT-2000 (
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01-MAR-2001 (
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Sulston J.E., Waterston R.;
"Toward a complete human genome sequence.
Genome Res. 8:1097-1108(1998).
                                                                                                                                                                                                                                                                                                                  WUGSC:n_wan).
Homo sapiens (Human).
Metazoa; Chordata;
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                                                                 Waterston R.;
Submitted (APR-2000) to
-i- CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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"The sequence of Hom
Submitted (MAR-1999)
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OXIDIZED FLAVOPROTEIN + H(2)0 (BY SIM SUBCELLULAR LOCATION: MEMBRANE-BOUND. SIMILARITY).
SIMILARITY: BELONGS TO THE CYTOCHROME IL; AC007002; AAF65576.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                       C., Pape K., Jones T.;
Homo sapiens BAC clone RP11-493L16.";
999) to the EMBL/GenBank/DDBJ database
                                                                                                                                                                                                                                                                                                         Primates;
                                                      the EMBL/GenBank/DDBJ databases.
RH + REDUCED FLAVOPROTEIN + O(2)
IN + H(2)O (BY SIMILARITY).
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Q59990;
O1-NOV-1996 (TrEMBLrel. 01, Created)
O1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
O1-NOV-1996 (TrEMBLrel. 16, Last annotation update)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
O1-MAR-2001 (TrEMBLREL. 16, Last annotation update)
O1-MAR-2001 (TrEMBLREL. 16, Last annotation update)
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Kaneko T., Tanaka A., Sato
Sugiura M., Tabata S.;
"Sequence analysis of the (
                                                                    SEQUENCE FROM N.A. MEDLINE=96127529;
                                                                                                                                                                                 STRAIN-PCC6803;
                                                                                                                                                             Tabata
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                        Submitted
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Pfam; PP00067; p450; 1.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Electron transport; Endoplasmic reticulum; Heme; Membrane;
MONOOXYGENASE; Oxidoreductase.
SEQUENCE 525 AA; 59124 MW; 71D47B6752A60315 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TEWPRSTRMLLGPNTVSNSIGDIHRNKRKVFSKIFSHEALESYLPKIQLVIQDTLRAWSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFSGYRRGIQARQILQKGLEKAIREKLQCTQGKD----YLDALDLLIESSKEHGKEMTMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPE-AINVYQEAQKLTFRMAIRVLLGFSIP-----EEDLGHLFEVYQQFVDNVFSLPVDL
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                                    PubMed=8590279;
A., Sato S., Kotani H.,
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                                                                                                                                    EMBL/GenBank/DDBJ databases
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Pred. No. 1
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  unicellular
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1.3e-76;
                                             Sazuka
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                                    T., Miyajima
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A Q9LVY7

A Q9LVY7

A Q9LVY7;

C Q9LVY7;

C Q9LVY7;

T 01-OCT-2000 (TrEMBLrel. 15, Created)

JT 01-OCT-2000 (TrEMBLrel. 16, Last sequence v

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation

DE CYTOCHROME P450-LIKE.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Embryophyta; Tr:

""""" (Signal of the control o
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Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00067; p450; 1.

PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.

Hypothetical protein; Heme; Monooxygenase; Oxidoreductase SEQUENCE 444 AA; 50578 MW; 8F6ZA9EED3B54BDC CRC64;
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-1- SIMILARITY: BELONGS TO THE EMBL; D64003; BAA10496.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."
                                                                                                                                                                                                                                                                                                                                                                                          406
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                                                                                                                                                                                                                                                                                                                                                                                     TRLIQQFDWTLLPGQNLELVVTPSPRPKDNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGYLEQWGKANE--VIWYPQLRRMTFDVAATLEMGEKV-----SQNPQLFPWFETYIQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSCLEQWLSCGERGLLVYPEVKRLMFRIAMRILLGCEPGPAGGGEDEQQLVEAFEEMTRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTKEQETFQATWPLSTRILLGPNALATQMGEIHRSRRKILYQAFLPRTLDSYLPKMDGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLPIPPGDFGLPWLGETLNF-LNDGDFGKKRQQQFGPIFKTRLFGKNVIFISGALANRFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87;
                                                                                                                                                 Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 668.5; DB 2
Pred. No. 1.3e-46;
7; Mismatches 181
                                                  core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOCHROME
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                                                                       Tracheophyta;
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                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181;
                                                  Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
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                                                                       Spermatophyta;
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EMBL; AB018112; BAA96885.1; -.
Interpro; IPR001128; -.
Pfam; PF000867; P450; 1.
PRINTS; PR00385; P450.
PROSITE; P800086; CYTOCHROME_P450; UNKNOWN_1.
Electron transport; Endoplasmic reticulum; Heme; Membly Monooxygenase; Oxidoreductase.
SEQUENCE 477 AA; 54850 MW; 304B4B2C4970E405 CRC64.
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Q9PUG2;
01-MAY-2000
01-MAY-2000
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[1]
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                        VRRESSSSCVFKTHLFGSPTAVVTGASGNKFLFTNENKLVVSWWPDSVNKIFP----SS
                                                                                                                                                                                                                                                                                                                                                                                                                           RRKY----GFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVHWPASVRTILGAGCLSN
                                                                                                             VDNLPAR 489
                                                                                                                                                                                                                                      TTASAATSLITYLGLYPHYLQKVREEIKSKGLLCKSNQDNKLDMETLEQLKYIGCVIKET
                                                                                                                                                                                                                                                                                     HARIEENIRAKIRRLQATEPDGGCKDALQLLIEHSWERGERLDMQALKQSSTELLFGGHE
                                                                                                                                                                                                                                                                                                                 FTFSIACRSFLSME-DPA----RVRQLEEQFNTVAVGIFSIPIDLPGTRFNRAIKASRLL
                                                                                                                                                                                                                                                                                                                             LMFRIAMRILLGCEPGPAGGGEDEQQLVEAFEEMTRNLFSLPIDVPFSGLYRGVKARNLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154;
                                                                                                                                                                                                                         TASIVCTFVVNYLAEFPHVYQRVLQE--QKEILKEKKEKEGLRWEDIEKMRYSWNVACEV
                                                                                                                                                                                                                                                                    RKEVSAIVRORKEELKA---
                                                                                                                                   MRIVPPLSGTFREAIDHFSFKGFYIPKGWKLYWSATATHMNPDYFPEPERFEPNRFEGSG
                                                                                                                                                                                          LRLNDPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADIFTNKEEFNPDRFIVPH
                                                                                        DKGLPIR
                                                                                                                                                        PEDASRESFIPFGGGLRSCVGKEFAKILLKIFTVELARHCDWQ-LLNGPPTMKTSPTVYP
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 (TrEMBLrel.
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                                   PRELIMINARY;
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  13,
13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 569; DB
Pred. No. 2.1e-
82; Mismatches
   Last sequence update)
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                                    PRT;
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. No. 2.1e-38;
ismatches 215;
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                                    AA
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Matches 97
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Q9FH76;
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasianinae;
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InterPro; IPR001128; -.
Pfam; PF00067; P450; 1.
PRNINTS; PR00385; P450;
PROSITE; PS00086; CYTOCHROME_P450;
Electron transport; Endoplasmic ret
                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Embryophyta; Trachec Magnollophyta; eudicotyledons; core eudicots; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF185266; AAD56546.1; HSSP; P14779; 1BU7.
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                                                                                                SECULINGE STRAIN-COLLMBIA; STRAIN-COLLMBIA; PubMed-10718197; MEDLINE-20181125; PubMed-10718197; Nakamura Y., Kaneko T., K
                                                                                                                                                                                                                                                                                                                                                                                                                                                Monooxygenase; Oxidoreductase.
                                     EMBL; ABO
SEQUENCE
                                                clones.";
clones.";
nas. 7:31-63(2000)
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                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        433
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                                                                                              Tabata
                                                                           features
                                                                                     "Structural
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
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                                               AB020744;
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107 AA;
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                                                                           analysis of
the regions
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                                               BAB10255.1;
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                                                                                                                                                                                                                                                                                                                                                                                 Score 538; DB 13;
Pred. No. 8.6e-37;
6; Mismatches 4
Score 517.5; DB 10;
Pred. No. 3.4e-34;
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                                       CCD17293F553F812 CRC64;
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                                                                                                        Katoh T., Asamizu E.,
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                                                                                                                                                                                     Tracheophyta;
                                                                             covered
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            Length 463;
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                                                                                                           Kotani
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Query Match
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).4e-34; nes 212;

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                                                                   SIMILARITY: BELONGS TO ; AC006931; AAD21724.1;
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                                                                                                                                      SIMILARITY).
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Best Local
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081077;
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PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.

Electron transport; Endoplasmic reticulum; Heme; Membrane; Microsome; Monoxygenase; Oxidoreductase.

MONOXYGENASE; D45 AA; 55405 MW; 08B0B16474620F82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaeae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (Tremblrel. 08, 01-NOV-1998 (Tremblrel. 08, 01-mar-2001 (Tremblrel. 16, PUTATIVE CYTOCHROME P450.
                                                                                                                                           Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J. "Arabidopsis thaliana chromosome II BAC T914 genomic sequence. Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AC005315; AAC33235.1; --
                                                                                                                                                                                                                                                                                                                        STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
         Heme; Monooxygenase; SEQUENCE 482 AA;
                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436
                                                                                                                   nterPro; IPR001128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     446
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132; Conser
                                                            PF00067; p450; 1.
TE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                  COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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      ; Oxidoreductase
55175 MW; AB6A
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Pred. No. 1.1e
36; Mismatches
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         AB6A07AB2778DD3B CRC64;
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                                                                                                                                                                                                           CYTOCHROME P450.

T18B16.200 OR AT4G19230.

T18D16.200 OR AT4G19230.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Si

Eukaryota; eudicotyledons; core eudicots; Rosidae;

Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                              065624 PRELIMINARY;
065624;
01-AUG-1998 (TrEMBLrel. 07,
01-AUG-1998 (TrEMBLrel. 07,
01-MAR-2001 (TrEMBLrel. 16,
                                                                                          Benes V.,
Mayer K.F.
                                                                                                                                      Bevan M., Benes V., Rechmann S., Borkova D., Mewes H.W., Mayer K., Schueller C.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                 NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129
  SEQUENCE FROM
                        Submitted
                                                                                                                                                                                                                                                                                                                                                                                                             476
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                                   Volckaert
                                                          SEQUENCE OF 131-457 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      465
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                                                                                                                                                                                                                                                                                                                                                     12
                     Der Schueren J., Chuang Y.J.,
ckaert G., Mewes H.W., Lemcke
mitted (MAR-2000) to the EMBL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R-RKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVHWPASVRTILGA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PALLASALCTFYLPLLLFLAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETLQMYLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EALFFHQGPYHSTLKRLVQSSFMPSALRPTVSHIELLVLQTLSSWTSQKSINTLEY--MK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCLSNLHDSSHKQRKKVIMQAFSREALQCYVLVIAEEVSSCLEQWLSCGERGLLVYPEVK 182
                                                                                                                                                                                                                                                                                                                                                                                                             TSPTVYPVDNLPARFT 491
                                                                                                                                                                                                                                                                                                                                                                                                                                   SRFEVAPKP----YTYMPFGNGVHSCPGSELAKLEMLILLHHLTTSFRWEVIGDEEGIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRVIQETLRAASVLSFTFREAVQDVEYDGYLIPKGWKVLPLFRRIHHSSEFFPDPEKFDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADIFTNKEEFNP
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                                                                                             Rechmann
.X.;
                                                                                 (MAR-2000)
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  N.A.
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28.2%;
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                                                                                                                                                                                                                                                                                 Created)
Last sequence up
                        Y.J., Aert R., Delemcke K., Mayer K.I
EMBL/GenBank/DDBJ
                                                                                  EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 501.5; DB 10; Pred. No. 7.4e-33;
                                                                                                                                                                                                                                                                                                                               PRT;
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                                     Defoor E., K.F.X.;
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                                                                                                                                                               Ansorge W.,
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                                                                                  databases
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e; eurosids II;
                                                                                                        H.W.,
                                                 Robben
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                                                                                                                                                                   Bancroft
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                                                                                                          Lemcke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Best Local S
Matches 137
                                                                                                                                               064989
064989;
07. Created)
08-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 17, Last sequence up
01-AUG-1998 (TrEMBLrel. 16, Last annotation
STEROID 22-ALPHA-HYDROXYLASE.
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Pfam; PF00067; p450; 1.
PRINTS; PR00385; p450.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heme; Monooxygenase; Oxidoreductase SEQUENCE 457 AA; 52436 MW; 61051
                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
  Plant Cell 10:0-0(1998).
-!- SIMILARITY: BELONGS '
EMBL; AF044216; AAC05093
                                       Choe S., Dilkes Feldmann K.A.;
                                                                                                  NCBI_TaxID=3702;
                                                                                                               Brassicales; Brassicaceae;
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                                                              STRAIN-WS-2
                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                           PVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADIFTNKEEFNPDRF-IVPHPEDA
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29.5%;
                                                     Fujioka
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                                                                                                                 Arabidopsis
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Pred. No. 2.
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                CYTOCHROME
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                                                     Takatsuto
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                   FAMILY
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Best Local S
Matches 148
SEQUENCE FROM N.A.

EU Arabidopsis sequencing project;
EU Arabidopsis sequencing project;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

-i- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AL132979; CAB62435.1;
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                                                                                                                                                                                                                                                                                                                                                                                      Q9SCQ9;

Q1-MAY-2000 (TrEMBLrel. 13, Created)

Q1-MAY-2000 (TrEMBLrel. 13, Last sequence of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the 
                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                    SEQUENCE FROM N.A. Bloecker H., Mewes Salanoubat M.;
                                                                                                                                                                                                                                                              Brassicales; Bra
NCBI_TaxID=3702;
                                                                                                                                                Submitted
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Pfam; PF00067; p450; 1.
PROSITE; PS00008; CYTOCHROME_P450; UNKNOWN_1.
Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 513 AA; 58867 MW; B1639BDD9A4DA6
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Similarity 28.4%;
48; Conservative
                                                                                                                                              (NOV-1999)
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                                                                                                                                           EMBL/GenBank/DDBJ
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8; Mismatches
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Pred. No. 1
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                                                                                                                                                                                        Mayer
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1.7e-29;
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Best Local Similarity 28.4%;
Matches 148; Conservative 7
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MEDLINE-98290546; PubMed=9628582;
Sato S., Kaneko T., Kotani H., Nakamura
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                     "Structural analysis of Arabidopsis thaliana (Sequence features of the regions of 1,456,315 physically assigned pl and TAC clones."; DNA Res. 5:41-54(1998).
                                                                                                                                                                                                                                                                                                      Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; endicotyledons; core endicots; Rosidae
Brassicales; Brassicaceae; Arabidopsis.
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PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
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8; Mismatches 231;
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Best Local Similarity
Matches 497; Conser
                                                         White J.A., Beckett-vull
Jones G., Petkovich M.;
Jones G., Petkovich M.;
"CDNA cloning of human retinoic acid-metabolizing
identifies a novel family of cytochromes P450.";
J. Biol. Chem. 272:18538-18541(1997):
                                                                                                                                                                                                                                                                                                                                         CP26_HUMAN STANDARD; PRT; 497 AA.
043174;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CYTOCHROME P450 26 (EC 1.14.--) (RETINOIC ACID-METABOLIZING
CYTOCHROME) (P450RAI) (RETINOIC ACID 4-HYDROXYLASE).
CYP26A1 OR CYP26.
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MEDLINE-97373542; PubMed-9228017;
White J.A., Beckett-Jones B., Guo
Jones G., Petkovich M.;
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MEDLINE=98380037; PubMed=9716180;
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; 33B07D7C29134471 CRC64;
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Pred. No. 5.7e-175;
; Mismatches 0;
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                                                                                                                                            enzyme
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                     Schulkes
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                                                                                                                                        (hP450RAI)
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A Trofimova-Griffin M.E., Juchau M.R.;

Trofimova-Griffin M.E., Juchau M.R.;

Trofimova-Griffin M.E., Juchau M.R.;

TEXPRESSION of Cytochrome P450RAI (CYP26) in human fetal hepatic and all charms of cytochrome P450RAI (CYP26) in human fetal hepatic and all charms of cytochrome P450RAI (CYP26) in human fetal hepatic and all cephalic tissues.*;

Texpression of cytochrome P450RAI (CYP26) in human fetal hepatic and all cephalic tissues.*;

Texpression of cytochrome P450RAI (CYP26) in human fetal hepatic and all cephalic tissues.*;

Texpression of cytochrome P450RAI (CYP26) in human fetal hepatic and all cephalic tissues.*;

Texpression of cytochrome P450RAI (CRA) AND ITS (CYP26) in HIGHEST LEVELS IN ADULT LIVER, HEART, CYP10UTARY CLAND, ADREMAL GLAND, PLACENTA AND REGIONS OF THE BRAIN.

THE TISSUE SPECIFICITY: HIGHEST LEVELS IN ADULT LIVER, HEART, CYP10UTARY CLAND, ADREMAL GLAND, PLACENTA AND REGIONS OF THE BRAIN.

THE TISSUE SPECIFICITY: HIGHEST LEVELS IN ADULT LIVER, HEART, CYP10UTARY CLAND, ADREMAL GLAND, PLACENTA AND REGIONS OF THE BRAIN.

THE TISSUE SPECIFICITY: HIGHEST LEVELS IN ADULT LIVER, HEART, CYP10UTARY CLAND, ADREMAL GLAND, PLACENTA AND REGIONS OF THE BRAIN.

THE TISSUE SPECIFICITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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Best Local Similarity
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Ffam; pF00067; p450; 1.

PRINTS; PR00385; p450;

PROSITE; pS00086; CYTOCHROME_P450; 1.

Oxidoreductase; Monooxygenase; Membrane; Heme; Endoplasmic reticulum.

BINDING 42 42 HEME (POTENTIAL).

SEQUENCE 497 AA; 56162 MW; EAB6B84B24B2EAB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF005418; AAB88881.1; MIM; 602239; -.
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Cell Growth Differ. 9:629-637(1998).
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                                      KETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADIFTNKEEFNPDRFI
                                                                                                                                                                          NLIHARIEENIRAKIRRLQATEPDGGCKDALQLLIEHSWERGERLDMQALKQSSTELLFG
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                                                                                                                                                      NLTHARTEQNIRAKICGLRASEAGQGCKDALQLLTEHSWERGERLDMQALKQSSTELLFG
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93.4%;
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Pred. No. 4.7e-163;
6; Mismatches 17;
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; EAB6B84B24B2EAB3
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P79739;
15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wnite J.A., Guo Y.-D., Baetz K., Beckett-Jones B., Hsu K.E., Dilworth F.J., Jones G., Petkovich M., "Identification of the retinoic acid-inducible allacid 4-hydroxylase.";
J. Biol Characterists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brachydanio rerio (Zebrafish) (Zebra danio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Actinopteryqii, Neopteryqii; Teleostei; Buteleostei;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Last annotation update)
CYTOCHROME P450 26 (EC 1.14.-.-) (RETINOIC ACID-METABOLIZING
CYTOCHROME) (P450RAI) (RETINOIC ACID 4-HYDROXYLASE).
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
CYTOCHROME P450 26 (EC 1.14.-.-) (RETINOIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U68234; AAC60045.1;
ZFIN; ZDB-GENE-990415-44;
InterPro; IPR001128; -.
Pfam; PF00067; p450; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endoplasmic reticulum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; 1.
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SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INDUCTION: BY RETINOIC ACIDS (RA).
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3101. Chem. 271:29927-29927(1996).
FUNCTION: PLAYS A KEY ROLE IN SETINOIC ACID METABOLISM. AC RETINOIDS, INCLUDING ALL-TRANS-RETINOIC ACID (RA) AND ITS STEREOISOMER 9-CIS-RA. CAPABLE OF 4-HYDROXYLATION; HYDROXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VPHPEDASRESFIPFGGGLRSCYGKEFAKILLKIFTVELARHCDWQLLNGPPTMKTSPTV
                                                                                                                                                 MGLPALLASALCTFVLPLLLFLAALKLMDLYCVSSRDRSCALPLPPGTMGFPFFGETLQM 60
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ILQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVRTIL 120
                                                       VLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVHWPASVRTIL 120
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                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             56281 MW;
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Pred. No. 8.6e-114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
CYTOCHHOME P450 90A1 (EC 1.14.-.-).
CYP90Al OR CYP90 OR CPD.
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Q42569;
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                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                Oxidoreductase; Monooxygenase; BINDING 418 418 HI
                                                                                          InterPro; IPR001128; -.
Pfam; PF00067; p450; 2.
PROSITE; PS00086; CYTOCHROME_P450;
                                                                                                                                                                                 EMBL; X87367; CAA60793.1; -. EMBL; X87368; CAA60794.1; -.
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Query Match Best Local

Local Similarity

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Q43147;

15-DEC-1998 (Rel. 37, Created)

15-DEC-1998 (Rel. 37, Last sequence update)

15-DEC-1998 (Rel. 37, Last annotation updat

CYTOCHROME P450 85 (EC 1.14.-.-) (DWARF PRO
       or send
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                                                                                                                                                                                   Bishop G.J., Harrison K., Jones J.J.G.D.;
"The tomato Dwarf gene isolated by heterologous transposon tagging encodes the first member of a new cytochrome P450 family.";
                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=CV. GCR758; MEDLINE=96266705; PubMed=8672892;
                                                                                                                                                                                                                                                                                                                              Magnoliophyta; eudicotyledons; core Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                         Lycopersicon esculentum (Tomato).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
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                                                                                                                                                                       Cell 8:959-969(1996)
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Pred. No. 2.5e-24;
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Best Local
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
CYTOCHROME P450 88A3 (EC 1.14...).
CYP88A3 OR YUP8H12.23.
                                                                           Theologis A., Osborne B.I., Vysotskaia V.S., Federspie Toriuni M., Yu G., Oji O., Araujo R., Chung E., Dewar Ecker J.R., Marziali A., Oefner P., Davis R.W.; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ database
                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001128; -. Pfam; PF00067; p450; 1. PRINTS; PR00385; P450; 1. PROSITE; PS00086; CYTOCHROME_P450; 1. Oxidoreductase; Monooxygenase; Membra BINDING 414 414 HEME (BY
                                                                                                                                         STRAIN=CV. COLUMBIA;
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Similarity 27.0%;
25; Conservative 9
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Swiss Institute
Bioinformatics
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                                                            TO THE CYTOCHROME P450 FAMILY.
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Pred. No. 8.7e-24;
4; Mismatches 210
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RESULT 7
C136_MYCTU STANDARD; PRT; 492 AA.

ID c136_MYCTU STANDARD; PRT; 492 AA.

AC p95099;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DT 01-OCT-2000 (Rel. 39, Created)
CE 01.14.--).

GN CYP136 OR RV3059 OR MTCY22D7.22C.

OS Mycobacterium tuberculosis.

OC Mycobacterium tuberculosis.

OC Actinomycetales; Corynebacterineae; Mycobacteridae;
Bacteria; Firmicutes; Actinobacteridae; Mycobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteridae;

OX NCBL_TaxLD=1773;
RP SEQUENCE FROM N.A.

RC STRAIN=H37RV;
RC STRAIN=H37RV;
RA COle S.T., Brosch R., Parkhill J., Garnier T., Churcher C.,
RA COLe S.T., Brosch R., Parkhill J., Garnier T., Churcher C.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.
RA Gordon S.V., Esqlmeier K., Gas S., Chillingworth T., Connor R.
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InterPro; IPR001128; -.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; 1.
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TRANSMEM 6 26 POTENTIAL.
BINDING 439 439 HEME (BY SIMILARITY).
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STRAIN=H37RY:
MEDLINE-98295987; PubMed-9634230;
MEDLINE-98295987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.,
Cole S.T., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.
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Pred. No. 9.3e
84; Mismatches
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.3e-24;
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R InterPro; IPR002397; -.

R InterPro; IPR002401; -.

R InterPro; IPR002401; -.

R PINTS; PR00359; BP450; 1.

R PRINTS; PR00359; BP450.

R PRINTS; PR00365; P4501.

R PRINTS; PR00463; EP450I.

R PRINTS; PR00465; EP450I.

R PRINTS; PR00465; CYTOCHROME_P450; 1.

PROSITE; PS00086; CYTOCHROME_P450; 1.

R PROSITE; PS00086; CYTOCHROME_P450; 1.

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"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete genome sequence.";
Nature 393:537-544(1998).
-i- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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  TVYPVDNLP
                                                           RHRYAFTPFGGGVHKCIGMVFDQLEIKTILHRLLRRYRLELSRP-DYQ----
                                                                                                              ASRESE I PEGGGLRSCVGKEFAKI -----LLKIFTVELARHCDWQLLNGPPTMKTSP
                                                                                                                                                                          TPVQWAMRQTVRDTELLGYYLPKGTNVIAYPGMNHRLPEIWTDPLTFDPERFTEPRNEHK
                                                                                                                                                                                                        PPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVADIFTNKEEFNPDRFIVPHPE-D
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CYTOCHROME P450 88A1 (EC 1.14.-.-) (DWAR
CYP88A1 OR D3.
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"The maize Dwarf3 gene encodes a cytochrome P450-mediated early step in Gibberellin biosynthesis.";
Plant Cell 7:1307-1317(1995).
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Andropogoneae; Zea.
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TISSUE SPECIFICITY: EXPRESSED IN ROOTS, DEVELOPING
VEGETATIVE MERISTEM, AND SUSPENSION CULTURE CELLS.
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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KSKGLLCKSNQDNKLDMETLEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPK
                          MDRLIEAQDERGRHLDDDEIIDVLVMYLNAGHESSGHITMWATVFLQENPDMFARAKAEQ
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                                                                                   RSYTELNYGMRAMAINLP-GFAYRGALRARRRLVA-VLQGVLDERRAARAKGVSGGGVDM
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57906 MW;
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POTENTIAL.
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Pred. No. 6.1e-18;
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                                                                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isbor send an email to license@isb-sib.ch).
                                                         EMBL;
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Mammalia; Eutheria;
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                                                      D55681; BAA09529.1; -. AB004096; BAA20354.1; - AB004087; BAA20354.1; J
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122:1114-1121(1997)
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BAA20354.1; JOINED BAA20354.1; JOINED BAA20354.1; JOINED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scarafia L.E.,
                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                            There are no
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                     CP84_ARATH STANDARD; PRT; 520 AA. 0,42600; Q.42600; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 10-OCT-2000.(Rel. 40, Last annotation update) CYTOCHROME P450 84A1 (FERULATE-5-HYDROXILASE) CYE84A1 OR FAHI OR AT4G56220 OR F23E13.110. Arabidopsis thallana (Mouse-ear Cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase; Monooxygenase; Electron transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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 Magnoliophyta;
              Eukaryota; Viridiplantae; Embryophyta;
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AB004091;
AB004092;
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AB004095; BAA20354.1;
U17697; AAA87074.1; -
                                                                                                                                                                                                                                                                                                            DNKLDMETLEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDT
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BAA20354.1;
BAA20354.1;
BAA20354.1;
eudicotyledons;
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  eudicots;
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              Tracheophyta;
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 Spermatophyta;
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RA MOOljman P., Klein Lankhorst K., Kose M., Lamberth S., Van den Daele H.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA De Keyser M., Rogers J., Cronin A., Lenard N., McLay K., Mayes R.,
RA Clark L., Doggett J., Hall S., Kay M., Lenard N., McLay K., Mayes R.,
RA Dose S., de Haan M., Maarse A., Schaefer M., Meeller Auer S.,
RA Dose S., de Haan M., Maarse A., Schaefer M., Grimm M., Loehnert T. H.,
RA Dose S., de Haan M., Maarse A., Schaefer M., Grawandi E.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Percz-Percz A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Frishman D., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Minx P., Bentley D., Fulton B., Miller N., Gerco T., Kemp K.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Minx P., Sepith J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Minx P., Sepith J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Massenst J., Schutz K., Johnson A., Shah R.,
RA Chan E., Marta M., Martiensen R., McCombie W.R.;
Ra Chan D., Shah R.,
Ra Chan B., Miller N., Groy B., Rodriguez M., Habedwa A., Hameed A., Lodhi 
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Pohl T., Duest
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MEDLINE=20083488; PubMed=10617198;
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                                                                                                                                                MEDLINE=99097044; PubMed=9880351; Ruegger M., Meyer K., Cusumano J.C., Chapple The regulation of ferulate-5-hydroxylase expenses of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the regulation of the re
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Institute
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REMBL; AL022141; CAA18128.1; -.

REMBL; AF068574; AADL1580.1; -.

REMBL; AL161589; CAB80293.1; -.

RINTERPOO, IPRO01128; -.

REMBL; PRO0035; P450; 1.

REMBL; PRO0385; P450; 1.

REMBL; PRO0086; CYTOCHROME_P450; 1.

REMBL; PRO0086; CYTOCHROME_P450; 1.

REMBL; AL161589; MONOXYGENASE; MEMBE (BY SIMILARITY).

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                            Eukaryota;
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Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
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Pred. No. 2.1e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001128;
InterPro; IPR002403;
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-I- PATHWAY: CHOLESTEROL BIOSYNTHESIS.
-I- SUBCELLULAR LOCATION: MICROSOMAL (POTENTIAL).
-I- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KOJIMA M., MOTOZUMI T., HAMASIMA N., OKAMOTO T.;
"Cloning of a pig lanosterol 14-demethylase CNNA.";
"Cloning to pig lanosterol 14-demethylase CNNA.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: CATALYSES C14-DEMETHYLATION OF LANOSTEROL;
                                                                                                                                                                                                                                                                                                                                                                                                       194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134
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SWVERLDFNPDRYLQDNPASGEKFAYVPFGAGRHRCIGENFAYVQIKTIWSTMLRLYEFD
                                            IFTNKEEFNPDRFIVPHPEDASRFSFIPFGGGLRSCVGKEFAKILLKIFTVELARHCDWQ
                                                                                            YDQLKDLNLLDRCIKETLRLRPPIMTMMRMAKTPQTVAGYTIPPGHQVCVSPTVNQRLKD
                                                                                                                           METLEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVIYSICDTHDVAD
: |: | : | | | | | | | | : | : |
                                                                                                                                                                                               DDEVAGMLIGLLLAGQHTSSTTSAWMGFFLARDKTLQEKCYLEQKT----VCGEDLP-PLT
                                                                                                                                                                                                                                               MQALKQSSTELLFGGHETTASAATSLITYLGLYPHVLQKVREEIKSKGLLCKSNQDNKLD
                                                                                                                                                                                                                                                                                              WLPLPSFRR----RDRAHREIKNIFYKAIQKRRQSEEK--IDDILQTLLDSTYKDGRPLT
                                                                                                                                                                                                                                                                                                                                                DVPFSGLYRGVKARNLIHARIEENIRAKIRRLQATEPDGGCKDALQLLIEHSWERGERLD
                                                                                                                                                                                                                                                                                                                                                                                               L--FEALSELIILTASHCL------HGKEIRSQLNEKVAQLYADLDGGFSHAAWLLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLVYPEVKRLMFRIAMRILLGCEPGPAGGGEDEQQLVEAFEEMTRNL---FS-----LPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTTPVFGKGVAYDVPNPVFLEQKKMLKSGLNIAHFRQHVSIIEKETKEYFQSWGESGERN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVRTILGAGCLSNLHDSSHKQRKKVIMQAFSREALQCYVLVIAEEVSSCLEQWLSCGERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATAFGKSPIEFLENAYEKYGPVFSFTMVGKTFTYLLGSDAAALLFNSKNEDLNAEDVYSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLQMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVH--WPA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLSSLLLACAFTL-ILVYLFRQAIGHL------APLPAGAKSPPYIFSPIPFLGH 73
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23.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 332; DB 1;
Pred. No. 4.4e-16;
7; Mismatches 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEME (BY SIMILARITY 0302949CE461AFD6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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Y SIMILARITY).
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474 467

LIDGYFPTVNYTTMIHTPENPVIRY LLNGP-PTMKTSPTVYPVDNLPARF

490

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RESULT 12
C4D8_DROME
                                                                                                                                                                                                                                                                                                                                                         RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Laid M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Laid M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Laid M., Mattel B., McIntosh T.C., McLeod M.P., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Sylies B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
RT Telegrane sequence of Drosophila melanogaster.";
RT Grence 287.7187.71001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams M.D., Celniker S.E., HOIT K.A., L.V., Adams M.D., Celniker S.E., Li P. W., Hoskins R.A., Galle R.F., Amanatides P.G., Scherer S.E., Li P. W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Aghayani A., An H.-J., Andrews Pfannkoch C., Baldwin D., Abril J.F., Aghayani A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C4D8_DROME STANDARD; PRT; 505 AA. 09VS79; Q24127; 01-OCT-2000 (Rel. 40, Created) 01-OCT-2000 (Rel. 40, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) 01-OCT-2000 (Rel. 40, Last annotation update) CYTOCHROME P450 4D8 (EC 1.14...-) (CYPIVD8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ballew R.M., Basu A., Baxendale J., Baylancurvy, Bolshakov S., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dapi Z., Mays A.D., Dew I., Dietz S.M., de Pablos B., Delcher A., Deng Z., Mays A.D., Daw I., Dietz S.M., Davies P., Davies M., Dugan-Rocha S., Dunkov B.C., Dun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                     ffrench-Constant R.H., Feyereisen R.;

"Cytochrome P450 gene clusters in Drosophila melanogaster.";

MOI. Gen. Genet. 251:290-297(1996).

-i- FUNCTION: MAY BE INVOLVED IN THE METABOLISM OF INSECT HORMONES

IN THE BREAKDOWN OF SYNTHETIC INSECTICIDES (BY SIMILARITY).

-i- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
                                                                                                                                                                                              Dunkov B.C., Rodriguez-Arnaiz R., Pittendrigh
                                                                                                                                                                                                                                                              SEQUENCE OF 315-442 FROM N.A. STRAIN=HAAG-79;
                                                                                                                                                                                                                          MEDLINE=96262181; PubMed=8676871;
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   FLAVOPROTEIN +
   H(2)0
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B.
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RESULT 13
C132_DROME
ID C132_DI
AC Q9VGB4.
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Best Local
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; Monooxygenase; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U34329; AAA80663.1; HSSP; P14779; 1BU7.
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                                                                                                                                                                                                                            KLDMETLEQLKYIGCVIKETLRLNPPVPGGFRVALKTFEL----NGYQIPKGWNVIYS
                                                                                                                                                                                                                                                                                                                                                                                                                              LSDGKVWHQRRKIITPTFHFSILEQFVEVFDQQSNICVQRLAQKANGNTF---DVYRSIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSSHK---QRKKVIMQAFSREALQCYVLVIAEEVSSCLEQWLSCGERGLLVYPEVKRLMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLLVVLLFGAG---WIIH-LGQADRRRKVANLPGPICPPLIGAMQLMLRLNPKTFIKVGR
                                                                                    MLAKIVR--EYELL
                                                                                                                FTVELARHCDWQLL
                                                                                                                                                            ICDTHDVADIFTNKEEFNPDRFIVPHPEDASR---FSFIPFGGGLRSCVGKEFAKILLKI
                                                                                                                                                                                                 PVSIRDLGELKYMECVIKESLRMYPPVPIVGRKLQTDFKYTHSVHGDGV-IPAGSEIIIG
                                                                                                                                                                                                                                                       PLINDEIREEVDTFMFEGHDTTTSALSFCLHELSRHPEVQAKMLEEIVQ----VLGTDRSR
                                                                                                                                                                                                                                                                                     RLDMQALKQSSTELLEGGHETTASAATSLITYLGLYPHVLQKVREEIKSKGLLCKSNQDN
                                                                                                                                                                                                                                                                                                                   WRQTQLIRTMQEFTIKVIEKRRQALEDQQSKLMDTADEDVGSKRRMALLDVLLMSTVDGR
                                                                                                                                                                                                                                                                                                                                           AR--NLIHARIEENIRAKIRRLQATE------PDGGCKDALQLL--IEHSWERGE
                                                                                                                                                                                                                                                                                                                                                                          AAALDIIAETAMGTKIYAQANESTPYAEAVNECTALLSWRFMSVYLQVELLFTLTHPHLK
                                                                                                                                                                                                                                                                                                                                                                                                     RIAMRILLGCEPGPA--GGGEDEQQLVEAFEEMTRNL-----FSLPIDVPFSGLYRGVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYYLKFGHLQRVWIFNRLLIMSGDAELNEQLLSSQEHLVK----HPVYKVLGQWLGNGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R---KYGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVHWPASVRTILGAGCLSNLH\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE003558; AAF50549.1; -.
                                                                                                                                          IFGVHRQPETFPNPDEFIPERH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00086; CYTOCHROME_P450; 1.
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505 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 327.5; DB 1
Pred. No. 9.2e-16;
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R -> C (IN REF. 2).
; 7BAA5271ED46093F CRC64;
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MBL outstation -
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C132_DROME Q9VGB4;

STANDARD;

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RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams N.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F., RA Adams M.D., Celniker S.E., Holt R.A., W. Hoskins R.A., Galle R.F., RA Adams M.D., Cheniker S.E., Holt R.A., W. Hoskins R.A., Galle R.F., RA Adams M.D., Cheniker S.E., Li P.W., Hoskins R.A., Galle R.F., RA Adams M.C., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Charley S., Daller R.G., Champe M., Chent R.A., Rank H.-J., Andrews Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ra Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Ra Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherty J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Ra Hostin D., Houston K.A., Bouck J., Brokstein P., Brottier P., Ra Burtis M.J., Evangelista C.C., Ferriaz C., Ferriera S., Fleischmann W., Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Glodek B., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K., Ra Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Ra Kimmel B.E., Kodira C.D., Kraft C., Kravitz J., Moshreti A., Ra McIntol S.M., Murphy B., Murphy L., Murphy D.M., Nelson D.L., Ra Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Ra Keinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Ra Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Ra Reinert K., Remington K., Stapleton M., Strong R., Wan S., Wan S., Tan G., Stapleton M., Stupski M.P., Smith T., Ra Perci J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Remington M., Strong R., Sun E., Ra Allians S.M., Moodage T., Wo
                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
PRINTS;
                                                                            FlyBase; FBgn0038006;
InterPro; IPR001128;
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PROBABLE CYTOCHROME P450 313A2 (EC 1.14.-.-) (CYPCCCXIIIA2).
CYP313A2 OR CG10094.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: MEMBRANE-BOUND.
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                                          PF00067
                                                                                                                                                                  AE003695;
                                  p450;
                                                                                                                                                             AAF54769.2;
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                                                                                                                                                                                                                                                                                                                                                  C4D2_DROME STANDARD; PRT; 501 AA. Q27589; Q27589; Q47588 O46053; O18651; O18674; Q9W514; 15-DEC-1998 (Rel. 37, Created) 01-OCT-2000 (Rel. 40, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) CYTOCHROME P450 4D2 (EC 1.14.-.-) (CYPIVD2). CYPOCHROME P450 4D2 (EC 1.14.-.-) (CYPIVD2). CYP4D2 OR EG:152A3.4 OR CG3466. Drosophila melanogaster (Fruit fly). Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse Pterygota; Neoptera; Endoptera; Diptera; Brachycera;
SEQUENCE FROM N.A STRAIN-OREGON-R;
                                                         [2]
                                                                                 melanogaster.
DNA Cell Biol
                                                                                                                                  *Cluster of cytochrome F
                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=OREGON-R;
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                                                                                                                                                                                            MEDLINE=94296569; PubMed=8024706;
                                                                                                                                                                                                                                                                                                                                         Ephydroidea;
                            SEQUENCE FROM
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BINDING 438 438 HEME (BY STMILARTTY).
SEQUENCE 493 AA; 56651 MW; 808769F4D0627262 CRC64;
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                                                                                 Biol.
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                                                                              13:663-668(1994)
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                                                                                                                                  P450 genes
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EME (BY SIMILARITY).
808769F4D0627262 CRC64;
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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rimert K., Remington K., Sanders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
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RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
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RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
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RT "The genome sequence of Drosophila melanogaster.";
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Addams N.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Hander R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
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A Ballew R.M., Basu A., Baxendale J., Bayakataroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Brottier P.,
Brottier P., Bayakataroglu L., Beasley E.M.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
A Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
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A Burtis K.C., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,
A Posler C., Gabrellata C.C., Ferraz C., Ferriera S., Fleischmann W.,
A Posler C., Gabrellata C.C., Ferraz C., Ferraz C., Ferraz C., Gabrat W.M., Glasser K.,
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Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,

Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu H
Dreano S., Gloux S., Lelaure V., Mottler S., Galibert F., Borkova
Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,

Papagjannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,

Modolell J., Peter A., Schottler P., Werner M., Mourkioti F.,

Beinert N., Dowe G., Schafer U., Jackle H., Bucheton A.,

Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,

McMillan P.J., Salles C., Tait E.A., Valenti P., Saunder R.D.,

Glover D.M.,
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                                                                                                                                                                                                                                    Phillips K.S., Begun D.J., Aquadro C.F.;

"Evidence for non-neutral evolution around the cytochrome p450 gcluster on the Drosophila melanogaster x chromosome.";

Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: INVOLVED IN THE METABOLISM OF INSECT HORMONES AND

THE BREAKDOWN OF SYNTHETIC INSECTICIDES (BY SIMILARITY).
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SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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EMBL; AB003423; AAR45741.1; --
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EMBL; AF017018; AAB71180.1; --
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Z23005; CAA80549.1;
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                                                                                                                                                        the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                          TESTIS, OVARY, ADRENAL, PROSTRATE, LIVER, KIDNEY, -i- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96404948; pubMed=8809088;
Rozman D., Stroemstedt M., Waterman M.R.;
"The three human cytochrome P450 lanosterol 14 alpha-demethylase (CYP51) genes reside on chromosomes 3, 7, and 13: structure of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company 
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"The ubiquitously expressed human CYP51 encodes demethylase, a cytochrome P450 whose expression
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97131516; PubMed=8975714;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96201125; PubMed=8619637;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     retrotransposed pseudogenes, association with a line-1 element, evolution of the human CYP51 family."; h. Blochem. Blophys. 333:466-474(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HFELLPLGPEP 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIFTNKEEFNPDRF--IVP--HPEDASRFSFIPFGGGLRSCVGKEFAKILLKIFTVELAR
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Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00086; CYTOCHROME_P450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00067;
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InterPro; IPR002403;
Pfam; PF00067; p450;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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U51684, AAC50951.1;
U51685, AAC50951.1;
U51686, AAC50951.1;
U51687, AAC50951.1;
U51688, AAC50951.1;
U51689, AAC50951.1;
U51689, AAC50951.1;
U51689, AAC50951.1;
FDLIDGYFPTVNYTTMIHTPENPVIRY
                   WQLLNGP-PTMKTSPTVYPVDNLPARF
                                           KDSWVERLDFNPDRYLQDNPASGEKFAYVPFGAGRHRCIGENFAYVQIKTIWSTMLRLYE
                                                                   ADIFTNKEEFNPDRFIVPHPEDASRFSFIPFGGGLRSCVGKEFAKILLKIFTVELARHCD
                                                                                         LTYDQLKDLNLLDRCIKETLRLRPPIMIMMRMARTPQTVAGYTIPPGHQVCVSPTVNQRL
                                                                                                       LTDDEVAGMLIGLLLAGQHTSSTTSAWMGFFLARDKTLQKKCYLEQKT--
                                                                                                                                                             LDMQALKQSSTELLFGGHETTASAATSLITYLGLYPHYLQKVREEIKSKGLLCKSNQDNK
                                                                                                                                                                                     GWLPLPSFRR----RDRAHREIKDIFYKAIQKRRQSQEK---IDDILQTLLDATYKDGRP
                                                                                                                                                                                                            IDVPFSGLYRGVKARNLIHARIEENI-RAKIRRLQATEPDGGCKDALQLLIEHSWERGER
                                                                                                                                                                                                                                   N--VFEALSELIILTASHCL-----HGKEIRSQLNEKVAQLYADLDGGFSHAAWLLP
                                                                                                                                                                                                                                                          GLLVYPEVKRLMFRIAMRILLGCEPGPAGGGEDEQQLVEAFEEMTRNL---FS-----LP
                                                                                                                                                                                                                                                                                  RLTTPVFGKGVAYDVPNPVFLEQKKMLKSGLNIAHFKQHVSIIEKETKEYFESWGESGEK
                                                                                                                                                                                                                                                                                                         ASVRTILGAGCLSNLHDSSHKQRKKVIMQAFSREALQCYVLVIAEEVSSCLEQWLSCGER
                                                                                                                                                                                                                                                                                                                                HAIAFGKSPIEFLENAYEKYGPVFSFTMVGKTFTYLLGSDAAALLFNSKNEDLNAEDVYS
                                                                                                                                                                                                                                                                                                                                                       ETLQMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVH--WP
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R -> T (IN REF. 4).

K -> R (IN REF. 4).
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Pred. No. 1
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9b_ba3:MTCY22D7
9b_p12:AF318501
9b_p11:AB018112
9b_p12:AF212991
9b_p12:AF212991
9b_p72:AC0077002
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gb_p12:ATCYP450R
gb_p14:SLU54770
                                                                      9b_p13:ATT18B16
9b_p12:ATCHRTV50
9b_p14:ZMU32579
9b_p12:AF139532
9b_r01:AF166266
9b_p12:AF214009
9b_p12:AF214008
9b_p12:AF214008
9b_r02:RATCP14DM
9b_r02:RATCP14DM
9b_r02:RATCP14DM
9b_r02:RATCP14DM
9b_r02:RATCP14DM
9b_r03:ATU38416
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gb_ro1:AF115769
gb_pr4:AF005418
gb_ov:AF199462
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gb_p12:AF279252
gb_p11:AB008097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM of: US-09-668-482-32 to: GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                       gb_ba3:MXTAH
gb_pl1:AB020744
gb_pl2:AF326277
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Search time (sec): 5019.990000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database sequences: 1344157
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gb_ov:AF185266
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gb_pr5:AF252297
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gb_ov:AF057566
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-DB--GenEmbl -CFMT-fastap -SUFFIX-rge -GAPOP-12.000 -GAPEXT-4.000
-MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000 -GAPOP-4.500
-GAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500 -FGAPOP-6.000
-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELEXT-7.000
-DELEXT-7.000 -START-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-PC+ -THR_MAX=100 -THR_MIN-0
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN-200000000 -USER-US9668482_eCGN1_1_8677 -NCPU-6
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i AF252297 Homo sapiens cytochro
(64 i D64003 Synechocystis sp. PCC
i AF185266 Gallus gallus CYP26 (C
i AF318211 Taxus cuspidata 5-alf
i AC006931 Arabidopsis thaliar
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! Y12657 M.mu
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1 i AC007002 Homo sapiens BAC cl
i AJ232955 Myxococcus xanthus cy
i AB020744 Arabidopsis thaliana
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(AF115769 Mus musculus cytochrc
(AF005418 Homo sapiens retinoid
(AF199462 Gallus gallus retinoid
7 (AL358613 Homo sapiens chromo
7 (AF057566 Xenopus laevis retino
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U32579 Zea mays DWARF3 (Gwarf3

AF139532 Liquidambar styracifi

AF16266 Mus musculus lanoster

AF214009 Brassica napus cytoch

AF214007 Brassica napus cytoch

AF214008 Brassica napus cytoch

AF214008 Brassica napus cytoch

D55681 Rattus sp. mRNA for cyt

U17697 Rattus norvegicus lanos

AR085702 Sequence 1 from pater
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AF318501 Arabidopsis thaliana
  AF150881 Lycopersicon esculen
AB009988 Sus scrofa mRNA for
! AL022121 Mycobacterium tube
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gb_pr10:HSU23942
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Fujii,H., Sato,T., Kaneko,S., Gotoh,O., Fujii-Kuriyama,
Osawa,K., Kato,S. and Hamada,H.
Metabolic inactivation of retinoic acid by a novel P450
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M.musculus mRNA for P450RA protein.
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PPGTMGFPFFGETLQMVLQRKKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILL
GBHRLVSVHWPASVRTILGAGCLSNLHDSSHKQRKKVIMQAFSREALQCYVLVIAEEMY
SSCLEQWLSCGERGLLVYPEVKRLMFRIAMRILLGGEPGPAGGEDEOQUKDAFEEMY
RNLFSLPIDVPFSGLYRGVKARNLIHARIEENIRAKIRRLQATEPDGGCKDALQLLIE
HSWERGERLDMQALKQSSTELLFGGHETTASAATSLITYLGLYPHYLQKVREEIKSKG
LLCKSNQDNKLDMETLEGLKYIGGHETTASAATSLITYLGLYPHYLQKVREEIKSKG
LLCKSNQDNKLDMETLEGLKYIGGVIKETLARDPVPGGFRVALKTFELNGYOIPKGW
NVIYSICDTHDVADIFTMKEEFNPDRFIVPHEDASRFSFIPFGGGLRSCVGKEFAKI
LLKIFTVELARHCDWQLLNGPPTMKTSPTVYPVDNLPARFTYFQGDI"

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/db_xref="taxon:10090"
/cell_line="P19"
57. .1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="P450RA protein"
/protein_id="CAA73206.1"
/db_xref="GI:2765214"
/db_xref="SWISS-PROT:055127"
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AB056457 Mus musculus Cyp4v
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Paine,C.T., Paine,M.L. and Snead,M.L.
Identification of amelogenin and tuftelin-interacting proteins using the yeast two-hybrid system Connect. Tissue Res. 38, 257-267 (1998)
                                                                                                                  Submitted (21-DEC-1998) CCMB, 2250 Alcazar Street, CSA103,
                                                                                                                                                                                                                                                                                                                               Mus musculus cytochrome
P450RA mRNA, complete co
                                                                                                                                            Paine, C.T., Paine, M.L. Direct Submission
                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                    house mouse.
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retinoic acid
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                                                                                                                Angeles,
            protein
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Ratio: 5.249
Percent Similarity: 100.000
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TTGCTGGGAGAGCACCGGTTGGTGTCGGTGCACTGGCCCGCGTCGGTGCG
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rGluProAspGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG
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alignment_block:
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                                                    PheProPhePheGlyGluThrLeuGlnMetValLeuGlnArgArgLysPh 67
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                                                                                                                                                                                               ATGGGGCTCCCGGCGCTGCTGGCCAGTGCGCTCTGCACCTTCGTGCTGCC
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Ratio: 5.033
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Homo sapiens retinoic acid hydroxylase mRNA, complete cds.
AF005418
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White, J.A., Beckett-Jones, B.,
Jones, G. and Petkovich, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (26-MAY-1997) Cancer Research Labs, (Botterell Hall, Rm 355, Kingston, Ont K7L 3N6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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1 (bases 1 to 1743)
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1039
               351 GluGlnLeuLysTyrIleGlyCysValIleLysGluThrLeuArgLeuAs
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JOURNAL
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AUTHORS
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                                                                                                                                                                                                   Submitted (28-OCT-1999) Max Planck Institute for Experimental Endocrinology, Feodor-Lynen Strasse 7, Hannover 30625, German Location/Qualifiers
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1 (bases 1 to 1479)
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2 (bases 1 to 1479)
Swindell, E.C., Thaller, C.,
Jessell, T.M. and Eichele, G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATCCGCAACCTCTTCTCCCCTCCCCATCGATGTGCCTTTCAGTGGGCTCT
            AL358613 166337 bp DNA HTG
Homo sapiens chromosome 10 clone RP11-348J12,
PROGRESS ***, 14 unordered pieces.
                                                                                                                                                                                                                                   1476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 161818 bases at least Q40 Consensus quality: 163255 bases at least Q30 Consensus quality: 163257 bases at least Q20 Tooset Side (1627).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert size: 165037; sum-of-contigs
Insert size: 176845; 5.5% error; agarose-fp
Quality coverage: 5.93x in Q20 bases; sum-of-
coverage: 5.81x in Q20 bases; agarose-fp
                                                                                                                                                                                                74613 83831 contig of 9221 bp in length 83834 83933; gap of 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 b
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On Apr 17, 2001 this sequence version replaced gi:13625010.
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CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
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* consists of 14 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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32410 32509: gap of 100 bp
32510 52913: contig of 20404 bp in length
52914 53013: gap of 100 bp
53014 55817: contig of 2804 bp in length
55918 55917: gap of 100 bp
55918 55917: gap of 100 bp
74513 74612: gap of 18595 bp in length
74513 74612: gap of 100 bp
74613 83833: contig of 9221 bp in length
74613 83833: contig of 9221 bp in length
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158410 166337: cont
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                                      /db_xref="taxon:9606"
                                                                /organism="Homo sapiens"
                                                                                                                                Location/Qualifiers
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51 PheProPhePheGl 	34 erSerArgAspAı ::: 55014 GCGGCCGCGACCO	17 OLGULGULGUPHG	1 MetGlyLeuProAla + + - - - - -	Align seg 1/1 to: AL3	alignment_block: US-09-668-482-32 x AL3	alignment_scores: Quality: 1 Ratio: Percent Similarity:	BASE COUNT 46344 a ORIGIN	v C f	misc_feature 1	misc_feature 1	• `	misc_feature 1	c_feature	misc_feature 1	misc_feature 1	misc_feature 9	misc_feature 8	misc_feature 8	Fi /	misc_feature 7	misc_feature 5	misc_feature 5 // f		misc_feature 3	0.16	misc_feature 1	
PheGlyGluThrLeuGlnMetValLeu.Gln	ArgSerCysAlaLeuProLeuProProGlyThrMetGly 50 	oLeuLeuPheLeuAlaAlaLeuLysLeuTrpAspLeuTyrCysValS 34 	OAlaLeuLeuAlaSerAlaLeuCysThrPheValLeuPr 17 	358613 from: 1 to: 166337	.358613	939.50 Length: 1166 4.007 Gaps: 13 41.509 Percent Identity: 39.623	77 c 34990	t_chain:3 nd:SP6 side:right"	ent_chain:3)166337 ."assembly_	37200158309 note="assembly_	note="as	assembly_fragment:02 .137099	"assembly_fragment:02028 132462	"assembly_tragment:01309" 129702	nt_chain:2" 105295	ragment		8393487001 /note="assembly_fragment:00938	108	t_chain:2" .83833		5301458817 /note="assembly_fragment:01466 fragment chain:2"	<pre>note="assembly_iragment:010/3 fragment_chain:1" fragment_chain:1"</pre>	side:left" .52913	In:1	o fra	lone lih="RPCT-11

56013	TPLEUSERCYSCLYGLUAYGLYFUEULEUVALTYPPTOGLUVALLYSAYG	167 55964
3		
167 55963	TyrValleuVall1leAlaGluGluValSerSerCysLeuGluGLnTTyrValleuVall1le::: :::	152 55914
Ú	NA	55864
151		151
55863	CCGANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	55814
151		151
151 55813	eMetGlnAlaPheSerArgGluAlaLeuGlnCys	140 55764
55763	GGGCGGATGGAGGCTTTTAACGCTGTCCCCTCCTCGGGACTCAGGTGAT	55714
140	Valll	139
55713	${\tt TGTGTCTGGCAGGACTGGGGGGTGTCTGGAAGGGGGACGGCGGTAGACGAGA}$	55664
138		138
55663	AGGACCCTCTGCCAGCTCCAGGTTAGCTATACCCAGCTCGGAGAGTGCCA	55614
138		138
55613	GAATTCCGGCTGATGGATGCTAGGCGCGGGCTAGCAGCTTGAGGTGGGCT	55564
138		138
55563	GGGGGCAGGAGGCGACGGCTGGACAGGGAAGGGGGACCCCCATTTATGAGCG	55514
138		138
138 55513	GlyCysLeuSerAsnLeuHisAspSerSerHisLysGlnArgLys.Lys. 	123 55464
122 55463	rgLeuValSerValHisTrpProAlaSerValArgThrIleLeuGlyAla 	106 55414
106 55413	ArgValMetGlyAlaAspAsnValArgArgIleLeuLeuGlyGluHisA 	89 55364
89 55363	ArgLysTyrGlyPheIleTyrLysThrHisLeuPheGlyArgProThrVa 	73 55314
72 55313	ArgArgLysPheLeuGlnMetLysArg	64 55264
55263	CAGGGCTGGCGGAGCGCGCGCGCTCCCCGGCGCCCCCTCATGCCCACTTC	55214
63		63
55213	GCTGAAGTCGGGGTAGGCGCCCCCGGGAGGCATGCTATTGCGGCTAGGAG	55164
63		63
55163	TGGGGCGGGACAGGCTGCTTCCCCGGAGCCCGGCGCGCGC	55114
63		63

18	roGlyP	
200	CATCCTACTGGGCTGCGAACCCCA lnGlnLenValGlnalabheGlnd	_ ი
56064	OALaGLYGLYGLYASPGluASPGluGlnLeuValGluAlaPheGluGluM ::::::	217 56113
217 56114	etThrArgAsnLeuPheSerLeuProIleAspValProPheSerGlyLeu TGACCCGCAATCTCTTCTCGCTGCCCATCGACGTGCCCTTCAGCGGGCTG	233 56163
234 56164	Tyrarg Tyrarg	235 56213
236 56214	GCGTCTGCTCACCGCCGCGCGCGCTCTCTGCGCTCAGGGCATGAAGGCGCGG	240 56263
241 56264	AsnLeuileHisAlaArgIleGluGluAsnIleArgAlaLysIleArgAr	257 56313
257 56314	gLeuGlnAlaThrGluProAspGlyGlyCysLysAspAlaLeuGlnLeuL ::: :	274 56363
27 4 56364	euIleGluHisSerTrpGluArgGlyGluArgLeuAspMetGln	288 56413
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56414	TGCGGAGTTTGGTCCCCTGGCTTTC	56463
288		288
56464	CCTGGGGCCCCCAAAGCGCGCGCCTGGGGCCCAGCTT	56513
28		288
, i	CGGCTCAGACTACAGCTATGGAATCCCGAAGGAAG	56563
56564	CACCCGGTCAGGAGAGCTGCGGAAGGGGCTGCGGCGGAACTGGGAGCATC	288 56613
288		288
56614	TTTCCAGGTTTCAAAGGGAAAGTTGGAATTTGC	56663
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56664	AACCTTGCGATTTTAATAAAACTAAGACTTTAACTCAGG	56713
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56714	CGTACTCGCCTTACTGCTCCAGCTGAACT	56763
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56764	TTTGTTTAAAGATATTGCTTTCCTTGACTTTCTG	56813
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56814	AAACATTTAGCCCTTCTAGTCTTCCCTCCAGAACTCTCAGTTCGATTCTG	56863
288		288
64	TGTCAAACCGCAGGCAGACTTG	56913
289	AlaLeuLysGlnSerSerThrGluLeuLeuPheGlyGl	301

20.4		384
57813		57764
384		374
373 57763	lyCysValIleLysGluThrLeuArgLeuAsnProProValProGlyGly :	357 57714
357 57713	nGlnAspAsnLysLeuAspMetGluThrLeuGluGlnLeuLysTyrIleG 	340 57664
340 57663	Gly.LeuLeuCysLysSerAs	334 57614
57613	TTAAGCCCTGTTTACGTCTGCTGGGCTGATTTTATTGGAGCACAAAATAA	57564
333		333
57563	TCCCCCTCCCAGTCTCCCCATCATGGGGCCCCTTTGGGTTTAGTCTCCAC	57514
333		333
57513	TTGTAAATAGATAGTGGATTTGGGCAGGCAAATGGCCATTAGCTGCTGTT	57464
333		333
57463	TTTTTGGGGGAACTTGGTCCTTCTAACTGGTGAGCAGCATTCTCCTGGGA	57414
333		333
57413	GTGAATAGCTGATTAGTGTGGGTGGTGGTGGTGAGTGTGGGGTGGGGGTT	57364
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57363	TCAGATAGGTTCCACTTTCTTGAATTGGTGTGTCCAAGGGCATACATA	57314
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57313	GACCTTGTATTCCTACCCCTCCTCCACCTTTTGCTGAACCGTGGAGATTC	57264
333		333
57263	${\tt TGAATAAACAGGATGGAGTCTTGAGCTGTGAGCCCACTTGGGCAGGGTTT}$	57214
333		333
57213	GAAAGTGCAAGGCCCAGGGCTGCGTGGGCCAGTGGGCAGAATTAGCTTTG	57164
333		333
57163	CCCTAGCCAACTTCCGAATAAGTCAGTGTGCTGCCTTCATGGAGTATTTT	57114
333		333
57113	GGGAGACTGGGTCTGGGGGTGTCCTTATTAGCTTAGGAAATTCAGCTGCT	57064
333		333
333 57063	euTyrProHisValLeuGlnLysValArgGluGluTleLysSerLys 	318 57014
318 57013	yHisGluThrThrAlaSerAlaAlaThrSerLeuIleThrTyrLeuGlyL 	301 56964
56963		56914

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MEDLINE
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AUTHORS
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LOCUS AF057566
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                                                                                                                                                                                                                         acid signalling
EMBO J. 17 (24), 7361-7372 (1998)
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AF057566
                                                                      Goettingen,
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                                                                                                                                                                                                                                                                     Hollemann,T., Chen,Y., Grunz,H. and Pieler,T Regionalized metabolic activity establishes
                                                                                                                                                                                                                                                                                                                       Xenopodinae; Xenopus.

1 (bases 1 to 1479)
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                        African clawed frog. Xenopus laevis
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Location/Qualifiers
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                       nLeuLeuAsnGlyProProThrMetLysThrSerProThrValTyrProV 483
                                                                                   IleLeuLeuLysIlePheThrValGluLeuAlaArgHisCysAspTrpGl 466
                                                                                                                                                          leProPheGlyGlyGlyLeuArgSerCysValGlyLysGluPheAlaLys 449
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 GCTCCTGAACGGATCCCCCGCCATGACAACCTCCCCGATTATCTGTCCTG
                                                                 ATCCTTCTCAAGGTGTTCGTGGTGGAATTGTGTCGTAATTGCGACTGGGA 1382
                                                                                                                                      TCCCTTTCGGAGTGAGTGAGTGCTGCATCGCAAAGAATTTGCTAAA 1332
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                                   ATGGGGCTGTACACCCTTATGGTCACCTTTCTCTGCACCATCGTGCTACC
oLeuLeuPheLeuAlaAlaLeuLysLeuTrpAspLeuTyrCysValS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi
Cypriniformes; Cyprinidae; Rasborinae; Danio.

1 (bases 1 to 1479)
Pactor To Rackett Tones, B., Bonasoro, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (28-AUG-1996) Cancer Research Labs,
Botterell Hall, Kingston, ON K7L 3N6, Canada
Location/Qualifiers
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J. Biol. Chem. 271 (47), 29922-29927 (1996)
97094702
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FSLPIDVPFSGLYRGLARNFIHSK IEENIRKKIQDDDNENEQKYKDALQLILTENSRS
SDEPFSLQAMKEAATELLFGGHETTASTATSLVMFLGLNTEVVQKVREEVQEKVEMGM
TTPGKGLSMELLDQLKYTGCVLKETLAINPPVPGGFRVALKTFELNGYQIPKGMNVIY
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FLVELTQHCNWILSNGPPTMKTGPTIYPVDNLPTKFTSYVRN"
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/db_xref="GI:1680716"
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/note="all-trans-retinoic acid 4-hydroxylase"
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KEYWORDS
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Homo Sapiens cytochrome P450 retinoid metabolizing protein P450RAI-2 mRNA, complete cds.
                                                                                                                                                                                    1 (bases 1 to 4445)
White,J.A., Ramshaw,H., Taimi,M., Stangle,W., Zhang,A.,
Everingham,S., Creighton,S., Tam,S.P., Jones,G. and Petkovich,M.
Edentification of the human cytochrome P450, P450RAI-2, which is predominantly expressed in the adult cerebellum and is responsible for all-trans-retinoic acid metabolism
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6403-6408 (2000)
                                                                                                                    2 (bases 1 to 4445)
White, J.A., Ramshaw, H., Taimi, M., Stangle, W., Zhang, A.,
Everingham, S., Creighton, S., Tam, S.-P., Jones, G. and Petkovich, M.
                                                                   Submitted (04-APR-2000) Cytochroma Inc., Bioscience Complex, Suite 2424, Kingston,
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                        Direct Submission
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                   Location/Qualifiers
1. .4445
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                                                                      Kingston,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1467
                                                                        116 Barrie Street,
, ONT K7L 3N6, Canada
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BASE COUNT ORIGIN

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Percent Similarity: 74.545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AF252297 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 GTCGCGGAGGGAGAAGTATGGCAACGTGTTCAAGACGCATTTGTTGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 nMetLysArgLysTyrGlyPheIleTyrLysThrHisLeuPheGlyA 86 : :::|||:::|||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 PhePheGlyGluThrLeuGlnMetValLeuGlnArgArgLysPheLeuGl 69
:::::|||||||| :: ::||||||
172 CTCATCGGAGAGACCGGCCACTGGCTGCTGCAGGGTTCTGGCTTCCAGTC 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 rgAspArgSerCysAlaLeuProLeuProProGlyThrMetGlyPhePro 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 uLeuPheLeuAlaAlaLeuLysLeuTrpAspLeuTyrCysValSerSerA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCACCCCGAG...GCCATCAACGTGTACCAGGAGGCGCAGAAGCTGACCT
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                                                                                                                                                                                                                     rgLysLysVallleMetGlnAlaPheSerArgGluAlaLeuGlnCysTyr 152
:::::|||||||::: |||
AGCGCAAGGTCTTCTCCAAGATCTTCAGCCACGAGGCCCTGGAGAGTTAC 471
                                                                                                                                                                                                                                                                                                                                     GCTGGGCCCCAACACGGTGTCCAATTCCATTGGCGACATCCACCGCAACA 421
                                                                                                                                                                                                                                                                                                                                                                         rCysGlyGluArgGlyLeuLeuValTyrProGluValLysArgLeuMetP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGCTGGCCGTGTCGCAGCTGTGGCAGCTGCGCTGGGCCGCCACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGACAAGAGCTGCAAGCTGCCCATCCCCAAGGGATCCATGGGCTTCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {	t LKVLAVELASTSRFELATRTFPRITLVPVLHPVDGLSVKFFGLDSNQNEILPETEAML}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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172

122

72

136

372 119

522 169 472 153 422

479 hrValTyrProValAspAsnLeuProAlaArgPhe 490

479 1435	3 sAspTrpGlnLeuLeuAsnGlyProProThrMetLysThrSerProT 4 :::::: ::: ::: :::	46 138
463 1385	7 PheAlaLysIleLeuLeuLysIlePheThrValGluLeuAlaArgHisCy (::: ::::::	44 133
446 1335	0 heSerPheIleProPheGlyGlyGlyLeuArgSerCysValGlyLysGlu	43 128
430 1285	4 eAsnProAspArgPheIleValProHisProGluAspAlaSerArgP	41 123
414 1235	8 IleCysAspThrHisAspValAlaAspIlePheThrAsnLysGlugluPh	39 118
397 1185	1 heGluLeuAsnGlyTyrGlnIleProLysGlyTrpAsnValIleTyrSer	38 113
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364 1085	8 GluThrLeuGluGlnLeuLysTyrIleGlyCysValIleLysGluThrLe :::: ::: :::	34 103
347 1035	5 euLeuCysLysSerAsnGlnAspAsnLysLeuAspMet ::: ::::: ::::: 2 TCCTGCACAGTGGCGGCTGCCCCTGCGAGGGCACACTGCGCCCTG	99 3
335 991	8 uTyrProHisValLeuGlnLysValArgGluGluIleLysSerLysGlyL::: ::: ::: ::: ::: ::: :::	31 94
318 941	2 HisGluThrThrAlaSerAlaAlaThrSerLeuIleThrTyrLeuGlyLe ::: 2 TATGCCACCACGGCCAGCGCCAGCACCTCATCATCATGCAGCTGCTGAA	30 89
301 891	5 euAspMetGlnAlaLeuLysGlnSerSerThrGluLeuLeuPheGlyGly :: ::::::: ::: ::::: 2 TGACCATGCAGGAGCTGAAGGACCGGAACCCTGGAGCTGATCTTTGCGGCC	28 84
285 841	8 sAspAlaLeuGlnLeuLeuIleGluHisSerTrpGluArgGlyGluArgL :::	26 79
268 791	52 ArgAlaLysIleArgArgLeuGlnAlaThrGluProAspGlyGlyCysLy ::::: ::: :::	25 75
251 753 .	35 rgGlyValLysAlaArgAsnLeuIleHisAlaArgIleGluGluAsnIle 	23 70
235 703	18 rargasnLeuPheSerLeuProIleAspValProPheSerGlyLeuTyrA : ::: ::: :::	21 65
218 653	02 GlyGlyGlyGluAspGluGlnGlnLeuValGluAlaPheGluGluMetTh :::	20 61
201	6 heArgIleAlaMetArgIleLeuLeuGlyCysGluProGlyF ::: ::: ::: 9 TCCGCATGGCCATCCGGGTGCTGCTGGGCTTCAGCATCCCT	18 56

JOURNAL MEDLINE REFERENCE JOURNAL MEDLINE REFERENCE SOURCE DEFINITION seq_documentation_block: seq_name: gb_ba3:SYCSLLE VERSION ACCESSION COMMENT REFERENCE FEATURES AUTHORS TITLE TITLE ORGANISM TITLE AUTHORS AUTHORS JOURNAL 1436 TCCTGCACCCGTGGATGGCCTCAGCGTCAAGTTC 1470 CDS source biosynthesis protein C; molybdopterin (MPT) converting factor, subunit 2; molybdopterin biosynthesis MoeA; oligopeptide transport system permease protein; peptidyl-tRNA hydrolase; phosphoribosyl formylglycinamidine cyclo-ligase; photosystem II p680 chlorophyll A apoprotein; polyA polymerase; endonuclease; replicative DNA helicase; succinate dehydrogenase iron-sulfur protein; tRNA-Cys; tRNA-fMet(exon1); tRNA-fMet(exon2); ycf34. Synechocystis sp. (strain:PCC6803) DNA. synthetase; acyl-CoA desaturase 1; alanine racémase; aspartate 1-decarboxylase; cyanate lyase; cytochrome p450; dTDP-glucose 4,6-dehydratase; elongation factor EF-G; endo-1,4-beta-glucanase; ferredoxin-nitrite reductase; ferredoxin-thioredoxin reductase, catalytic chain; ferrochelatase; flavoprotein; low affinity sulfate transporter; methionine aminopeptidase; methyltransferase; molybdenum cofactor biosynthesis protein A; molybdenum cofactor Okumura, S., Shimpo, S., Takeucni, C., Maug, A., Market, C., Marke Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome DNA Res. 2 (4), 153-166 (1995) 7-keto-8-aminopelargonic acid synthetase; KdtB; Mg-protoporphyrin IX monomethyl ester oxidative cyclase 66 kD subunit; MoxR protein NADH dehydrogenase subunit 5; MoxR; PleD; acetyl-coenzyme A dehydrogenase); 30S ribosomal protein S18; 50S ribosomal protein L33; 6-aminohexanoate-cyclic dimer hydrolase; D64003.1 GI:1001200 tRNA-fMet; 2-ketoacid dehydrogenase (malate dehydrogenase, lactate D64003 AB001339 D64003.1 GI:10 Synechocystis sp. Kaneko,T., Sato,S., Kotani,H., Tanaka,A., Asamizu,E., Nakamur. Miyajima,N., Hirosawa,M., Sugiura,M., Sasamoto,S., Kimura,T., Hosouchi,T., Matsuno,A., Muraki,A., Nakazaki,N., Naruo,K., Okumura,S., Shimpo,S., Takeuchi,C., Wada,T., Watanabe,A., Tabata, Kazusa DNA Research Institute, Gene Structure 2; 1532-3 Yanauchino, Kisarazu, Chiba 292, Japan (E-mail:tabata@kazusa.or.jp, Tel:0438-52-3933, Fax:0438-52-3934) 1 (bases 1 to 113064) Kaneko, T., Tanaka, A., Sato, S., Kotani, H., Potential protein coding regions were assigned on the basis of similarity search of the ORFs and GeneMark analysis. Submitted (30-AUG-1995) to the DDBJ/EMBL/GenBank databases. Satoshi Tabata,S. Direct Submission Sugiura, M. and Tabata, S. Bacteria; Cyanobacteria; Chroococcales; Synechocystis. (bases 1 to 11364) (bases 1 to 113064) (bases 1 to 113064) complement(1. .3960) /note="ORF_ID:s110178" /organism="Synechocystis /strain="PCC6803" /product="hypothetical protein" /protein_id="BAA10440.1" /db_xref="GI:1001201" /db_xref="taxon:1143" ocation/Qualifiers transl_table=11/ 113064 PCC6803 DNA complete genome, sp." Sequence determination of the Sazuka, T., Miyajima, N., T 13-FEB-1999 22/27, 2755703-2868766. Nakamura,Y., protein;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSLSOLRDKGTIEACAELERLIQELPHLPWLKETLTYAQQNMRRETWRPFKPDKLLEF
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EAPRTLDNFSTDIWKRWTPIILSVPNSFIDSNPRKNCKKLVSLSYHHSDDEFLTTLLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVIQEVLDTGLFSSRGLHRMGWAHQTYAEFFAAWYLTQRNIDLSKIKTLLYSSADSTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="ORF_ID:ssr1513"
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CAUCHT | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | ALL | A
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/note="ORF_ID:s110886"
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30 LeuTyrCysValSerSerArgAspArgSerCysAlaLeuProLeuProPr
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ISQWGSLRYAANTAMLAAVYSDGLTDPTGKYAQLAQDTVDYILGSNPRNASYNVGYGN
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RGKYSDSIPEVRNYYNSWSGYEDELAYGAAWLSRAVNSAGGDGSAYLQKALNIYNSDI
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VEQVTVVSRTGLATPQGPAGQITDGHQSRPGNGLTPIGGGEFSGGAGGHGSGHDHGDH
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RDGROOITFGGQSGALQAGLSLDLTGGYHDAGDHKKFGLPLASTLTTLAWGGVEFTD
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FNPAVDRLDFGLVSWELGLGARNSNTYYVRSHEYGVQERIENFNPATMKLSFLYYGT
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AAHQVVSQTVLVLFMVPLAMSYAATVRVGQWFGQQHWPQIRQAALVSIGLAVLFMLTA
GIALLAYPQQIIGLYLDLNDPANGEALNVGISIMKIAAFGLVLDGLQRTANGVLQGLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFPQQPHHRAASGVGWDGFRNGLPNEHILFGALVGGPTAANDFSYNDSRDDYISNEVA
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QARPIMLIVIAATLFNILGNYGLGFGKWGFPALGITGLAIASISAHWIMFLSLLVYML
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/transl_table=11
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                                                                                                                            GTCTATTGTTGGGACAACATTCTGACATTCGAGAAAGGGTCAGACAGGAA 63008
                                                          IleLysSerLysGlyLeuLeuCysLysSerAsnGlnAspAsnLysLeuAs
                                                                                                                                                                                                                                                     GCTATTGTTTGCCGGACATGAAACTTTAACTTCCGCATTATCTTCTTTTT
                                                                                                                                                                                                                                                                                                                                                                              GATAATAACCAACCGTTATCTTTGCCGGAGCTGAAGGATCAAATTTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                     GluArgGlyGluArgLeuAspMetGlnAlaLeuLysGlnSerSerThrGl
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                                                                                                                                                                                   leThrTyrLeuGlyLeuTyrProHisValLeuGlnLysValArgGluGlu
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AAAACCCGTTTATTTGGCAAAAATGTCATTTTTATTTCTGGGGCATTAGC
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.AAATTGCAGTTAAGCCAAGAGCTGAC 63040
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LOCUS AF185266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauría: Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (09-SEP-1999) Cell and Molecular Biology, Tulane
Submitted (09-SEP-1999) Cell and Molecular Biology, Tulane
University, 2000 Stern Hall 6400 Freret St., New Orleans, LA 70118,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chicken.
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Martinez-Ceballos, E. and Burdsal, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archosauria; Aves; Neognathae; Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                           /codon_start=2
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                                                                                                                                                       note-"contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CYP26) mRNA,
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VERSION
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ORIGIN
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LOCUS AF318211
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                                                                                                      FEATURES
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PUBMED
                                                                                                                                                                                                                                                            AUTHORS
TITLE
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                                                                                                                                                                        AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAATGAAAACCAGCCCCACT 322
                                                                                                                                                                                                           CONTRELEGATION 1494)

1 (bases 1 to 1494)

1 (bases 1 to 1494)

Schoendorf,A., Rithner,C.D., Williams,R.M. and Croteau,R.B.

Schoendorf,A., Rithner,C.D., Williams,R.M. and Croteau,R.B.

Molecular cloning of a cytochrome P450 taxane 10beta-hydroxylase

Molecular cloning of a cytochrome P450 taxane 10beta-hydroxylase

CDNA from Taxus and functional expression in yeast

CDNA from Taxus and functional expression in yeast

Natl Acad. Sci. U.S.A. 98 (4), 1501-1506 (2001)
                                                                                                                                                                                                                                                                                                                                Taxus cuspidata
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                      Washington State University, Pullman, Location/Qualifiers
                                                                                                                                                       Schoendorf, A. and Croteau, R. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Taxus cuspidata
                                                                                                                                                                                                                                                                                                               Coniferopsida; Coniferales; Taxaceae; Taxus.
                                                                                                                                                                                                                                                                                                                                                                     Taxus cuspidata.
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5.173
97.196
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alignment_scores:
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Ratio:
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US-09-668-482-32 x AF318211
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278 CCCTAATTGGGCATCCCACAGTTGTACTCTGCGGGCCTGCGGGAAACAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 uPheLeuAlaAlaLeuLysLeuTrpAspLeuTyrCysValSerSerArgA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuGlnCysTyrValLeuVallleAlaGluGluValSerSerCysLeu..
                                                                                                                                                                                                                                                     erHisLysGlnArgLysLysValIleMetGlnAlaPheSerArgGluAla 148
                                                                                                                                                                                                                                                                                                                                                                                       TTAGTTCTTTCGAACGAGGACAAGCTGGTAGAGATGGAAGGGCCCAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                              ArgIleLeuLeuGlyGluHisArgLeuValSerValHisTrpProAlaSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ### ATCGGGGAGACCATACAATTATTGCGGACACTCCGATCAGAAACACCTCA
TAAGAGGGCTTATCTTCTCCATTGCAAGCACCCTGTTTTTC.....
                                    alLysArgLeuMetPheArgIleAlaMetArgIleLeuLeuGlyCysGlu 197
                                                                           TGAAAAATGGAAG.....GGTAAAGATGAAGTGAAGGTGCTTCCTTTGG
                                                                                                                                                      TTACAAAATTATCTGGGTAGAATGAGTTCAGAAATAGGACACCATTTCAA
                                                                                                                                                                                                                                 ATCATCGCATCTTACGCACTGCACTTGCTCGGTTTTTGGGGCGCTCAAGCT
                                                                                                                                                                                                                                                                                                              TTTCATGAAACTGATTGGGGAAGATTCCATTGTTGCTAAAAAGAGGCGAGG
                                                                                                                                                                                                                                                                                                                                              {\tt rValArgThrIleLeuGlyAlaGlyCysLeuSerAsnLeuHisAspSerS}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .LysPheLeuGlnMetLysArgArgLysTyrGlyPheIleTyrLysThrH 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCACCGATCCTCTGTTAAACTTCCCCCTGGAAAGTTAGGTTTTCCTCTC
                                                                                                             .GluGlnTrpLeuSerCysGlyGluArgGlyLeuLeuValTyrProGluV
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/protein_id="AAK00946.1"
/db_xref="GI:12656592"
/translation="MOSFIFILKSIGTKFGQLESSPAILSITLAPILAIILLLIFRYNH
RSSVKLPPGKLGFPLIGETIQLLRTLRSETPQKKFDDRLKKFGPVYMTSLIGHPTVVL
CGPAGNKLVLSNEDKLJEMEGPKSFMKLIGEDSIVAKRGEDHRILRTALARFLGAQAL
QNYLGRMSSEIGHHFNEKWKGKDEVKVLPLFVRGLIFSIASTLFPDVNDGHQQKQLHHL
LETILVGSLSVPLDFPGTRYRKGLQARLKLDEILSSLIKRRRRDLRSGLASDQDLLS
VLLTFRDEKGNSLTDQGILDNFSAMFHASYDTTVAPMALIFKLLYSNPEYHEKVFQEQ
LEIIGKKEGGEDISWKDLKSMKYTMQAVQESLRNYPPVTGFGGGLRTCPGWEFSK
GWRVLCSPYTTHLREEYFPEPEPEFRFSRFEDEGRHVTPYTVPFGGGLRTCPGWEFSK
IEILLFVHHFVKNFSSYIPVDDNEKVLSDPLPPLPANGFSIKLFPRS"
29 a 315 c 314 g 436 t
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Gaps: 11
Percent Identity: 27.510
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA On Dec 17, 1999 this sequence version replaced gi:4512656.

The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D., Fujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E., Feldblyum,T.V., Buell,C.R., Ketchum,K.n., Lee,J.J., Ronning,C.M., Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., VanAken,S.E., Umayam,L., Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H., Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D., Mierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and Venter, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
                                                                                                                                                                                                                                                     F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC006931.5
                                                                                This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identified by repeatmasker (Arian Smit,
http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              predicted by tRNAscan-SE (Sean Eddy,
http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prediction programs including GRAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes were identified by a combination of three methods: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter, J.C.
Address all correspondence to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    We thank the CSHL/WashU/ABI consortium for sequencing BAC clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://www.tigr.org/tdb/at/at.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lin, X
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    at@tigr.org
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                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="F7D19.33; predicted by genscan"
complement(join(7700. .7818,7906. .8112,8195. .8348,
8844. .8989,9294. .9396))
/gene"At2942670"
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(2761. .2943,3035. .3164,3258. 3450. .3489,3570. .3646,3732. .3954))
//gene="At2942660"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(<2761. .2943,3035. .31
3450. .3489,3570. .3646,3732. .>3954))
/gene="At2g42660"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2132. .>116205)
/note="Sequence from clone F7D19"
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/db_xref="G1:659642"
/db_xref="G1:659642"
/translation="kgryspkyvDdavkalvkegneksrtekpolleedgefylvval
/ktanslation="kgryspkyvDdavkalvkegneksrtekpolleedgefylvval
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fkvyklsklksbygsfeskrklcdsydmefesdriviblkeltigkfeoskripvatus
lkhmmwredlekakcokamfymrigscosikvaklsmesddivenvtatuknovdvbls
lkhmmwredlekakcokamfymrigscosikvaklsmesddivenvtatuknovdvbls
kkhmmwredlekakcokamfymrigscosikvaklsmesddivenvtatuknovdvbls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="(TA)n"
5756. .5806
/rpt_family="(GA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="(GA)n"
4087. .4204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KTKKKNGKIHEVRYMDSNVSETLGDDEFDRSVGEDEVADDLNASGDKKKRKKMSSSKS
AVSGKPDIVKSKNGQKSKKLKKDIDESGGGFKAKTKRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(<1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(<7700. .>9396)
/gene="At2g42670"
/note="F7D19.33; predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(<2761. .>3954)
/gene="At2g42660"
/note="F7D19.34; predicted
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GGNIHCFKAITHCAILDILAPPYSSEHDRHCTYFRKSRREDLPGELEVDGEVVTDVTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8844 . .8989,9294 ..>9396))
/gene="At2g42670"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (join (<7700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MAGRSSPGKCSTWLDLNREETVEKNNEEESSVEDEDQITNNVRQ
YIRSNMPRLRWTPDLHLSFVRAVQRLGGPDRATPKLVLEMMNLKGLSIAHVKSHLQMY
RSKKLEPSSRPGFGAFMSGQRSYLMDMIDSRCIPHSDLRHAYNSKTVPSRVLNQDAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAD21740.1"
/db_xref="GI:4512686"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="At2g42650"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="At2g42650"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="At2g42650"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar="Columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Arabidopsis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                      LEEFQPPDDFVIRRIPYRGPVIRT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSGGGIQLPEFGNCRQKPTDDINTMLSLSLLSTSSEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {	t r}{	t 
                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAD21739.1"
/db_xref="GI:4512685"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1/
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        .10809,11165. .11248,11522. .11604,11693. .11994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .2131)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 predicted by genscan"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone
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alignment_block:
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                                                                                                                                                                     Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                        US-09-668-482-32 x AC006931
                                                                67490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
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           60
                                                                                                          44 LeuProProGlyThrMetGlyPheProPhePheGlyGluThrLeuGlnMe
tValLeuGlnArgArgLys....
                                                        CTTCTTCCTGGAGAAATGGGGCTTCCATGGATTGGTGAAACAATGGATTT
                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
                                                                                                                                                                     AC006931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAD21736.1"
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/db_xref="GI:4512682"
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QSVARASLSRQHEDSLSFGLPPISTGSMSDTDDVPDGATLTAHFLYQLALKMELKLE
IFSLGDQSKNVGKILIDMSSYYDVARKKRSAGLLDVDRTDLITFCGHBGSLEDRIFS
SLFRAERFSSQAQLKQGYPSIMRPSLDVQVPLGELLNEEPSKIRDSGLPGIEAFLRG
WDSYTSAPQNVGLFNECDKKSTTNWTELLNGSLVATECFRGTPYLEAMIDRKTKDGSV
UVKKWLQEALBRENISVNVRARPGYATKPELQAMIKALSQQQSSLLKNKGIIQLGAAT
                                                                                                                                                                                                                                                                                                    460.00
1.655
52.852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNLKFLNGLTEELEGRLNRLKSEETKEIPSDDQLDIDALDDDPWGKWGDEEEEEVDNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAALDESQSAKWDTFSSAEMMLNVSAGDTSQGLAAQISDLINKSAVAELQAKKNEKPD
SSSRGLLSFRDALLLTIVGYILAGENFPTSGSGGPFSWQEEHFLKEAIVDAVLENPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOIN (<14160. .14207,14422. .14565,14779. .14890,15255. ... 15513. .15664,15832. .17364,17446. .17514,17602. .17786) /gene="At2g42700" / 17786 / 17786 / 17786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product"putative lipase"
/protein_id="AAD21737.1"
/protein_id="AAD21737.1"
/db_xref="G1:4512683"
/translation="MAITTTSWEELLGSKNWDTILDPLDQSLRELILRCGDFCQATYD
AFVNDQNSKYCGASRYGKSSFFDKVMLENASDYEVVNFLYATARVSLPEGLLLGSQSR
AFVNDQNSKYCGASRYGKSSFFDKVMLENASDYEVVNFLYATARVSLPEGLLLGSQSR
DSWDRESNWFGYIAYTSDERSKALGRREIYIALRGTSRNYEWVNVLGARPTSADPLLH
                                                                                                                                                                                                                                                                                                                                                                                                                                        {	t KADESYDDMQLKLDLRDRVDSLFRFLHKLSSLRTRNLPLREGSLASESSFPGEPSGNK}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPEQDGSGGVVEGTTFDSDSEDEEGCKVMLGWLTIYTSNHPESKFTKLSLRSQLLAKI
KELLLKYKDEKPSIVLTGHSLGATEAVLAAYDIAENGSSDDVPVTAIVFGCPQVGNKE
FRDEVMSHKNLKILHVRNTIDLLTRYPGGLLGYVDIGINFVIDTKKSPFLSDSRNPGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(12052. .12273,12362.
/gene="At2g42690"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(1194. .12273,12362. .>13378))
/gene="At2g42690"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(14160...14207,14422...14565,14779...14890,15255...1
15513...15664,15832...17364,17446...17514,17602...17730)
/gene="At2g42700"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WHNLQAMLHVVAGWNGKKGEFKLMVKRSIALVNKSCEFLKAECLVPGSWWVEKNKGLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(11994. .>13378)
/gene="At2g42690"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MAGIGPITQDWEPVVIRKKPANAAAKRDEKTVNAARRSGADIET
VRKFNAGTNKAASSGTSLNTKMLDDDTENLTHERVPTELKKAIMQARTDKKLTQSQLA
QIINEKPQVIQEYESGKAIPNQQII.SKLERALGAKLRGKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="F7D19.30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="At2g42700"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="F7D19.31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(10668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="At2g42680"
10610. .11994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAD21738.1"
/db_xref="GI:4512684"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="At2g42680"
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                                                                                                                                                                     from:
                                                                                                                                                                                                                                                                                                      Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10809,11165.
                                                                                                                                                                  to: 116205
                                                                                                                                                                                                                                                                                                                          Length:
     PheLeuGlnMetL
                                                                                                                                                                                                                                                                                                    526
14
26.046
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     71
                                                          67539
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67886
                                                    68327 CAAGGTAACAATCAACTGAATATCAGAATGTTCTCTTCCTATCAGCAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67540 CTACAAAGCTCAGAAAAGCAACAGAGTTTTTGAGGATTTTGTAAATCCAA 67589
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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Koncz,C., Mathur,J., Szekeres,M. and Altmann,T.
Nucleic acid molecules encoding cytochrome P450-type proteins
involved in the brassinosteroid synthesis in plants
Patent: US 5952545-A 1 14-SEP-1999;
Location/Qualifiers
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thale cress.
Arabidopsis thaliana
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                                                                                                  Cytochrome P450.
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174 GAGACTTTTCAGCTGATCGGAGCTTACAAAACAGAGAACCCTGAGCCTTT
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                                                                                 124 ACCGTCGGATGGGTCTGCCTCCGGGAAGCCTTGGTCTCCCTCTGATAGGA
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                                     GluThrLeuGlnMetVal.....LeuGlnArgArgLysPh
                                                                                                           erCysAlaLeuProLeuProProGlyThrMetGlyPheProPhePheGly
                                                                                                                                                                                                            uAlaAlaLeuLysLeuTrpAspLeuTyrCysValSerSerArgAspArgS 39
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Brassinosteroids rescue the deficiency of CYP90, a cytochrome P450 controlling cell elongation and de-etiolation in Arabidopsis Cell 85 (2), 171-182 (1996)
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SSRVLLMEEAKKITFELTVKQLMSFDPGEWSESLRKEYLLVIEGFFSLPLPLFESTTYR
KAIQARRKVABALTVVVMKRREEEEGAARKKOMLAALLAADDGFSDEEIVDFLVALL
VAGYETTSTIMTLAVKPLTETPLALAQLKEEHEKIRAMKSDYSLEWSDYKSMFFTQC
VNETLRVANIIGGVFRRAMTDVEIKGYKIPKGWKVFSSFRAVHLDPNHEVDARTFNP
WRWQSNSVTTGPSNVTTPFEGGGPRLCPGYELARVALSVFLHRLVTGFSWVPAEQDKLV
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374 c 374 g 4
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1.562
57.256
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/db_xref="GI:853719"
/db_xref="SWISS-PROT:042569"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phenotype"
/note="cytochrome P450"
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48. .1466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:3702"
/chromosome="5"
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/cultivar="columbia"
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374 TAACCTTTTGGGGAAACACTCTCTGCTTCTTATGAAAGGTTCTTTGCATA 423
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                                                    LeuAspMetGluThrLeuGluGlnLeuLysTyrIleGlyCysValIleLy 361
                                                                                                                                                                                luGluIleLysSerLysGlyLeuLeuCysLysSerAsnGlnAspAsnLys
                                                                                                                                                                                                                                                                                                                                                                           GTGGCTTTACTTGTCGCCGGTTATGAAACAACCTCCACGATCATGACTCT
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CTTGAATGGAGTGATTACAAGTCAATGCCATTCACACAATGTGTGGTTAA
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LOCUS SLU54770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roGluAspAlaSerArgPheSerPheIleProPheGlyGlyGlyLeuArg
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U54770.1
                                                                                                                                                                                                                                                                                                                      Bishop,G.J., Harrison,K. and Jones,J.D.
The tomato Dwarf gene isolated by heterologous transposon tagging encodes the first member of a new cytochrome P450 family PCACT Cell 8 (6), 959-969 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Solanum lycopersicum
                                                                                                                                                                                                          Submitted (11-APR-1996) Gerard Bishop, Sainsbury Innes Centre, Colney Lane, Norwich, Norfolk, NR4
                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                  Bishop, G.
                                                                                                                                                                                                                                                                                                        96266705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tomato
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                                                                                                                               /organism="Lycopersicon
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                   /gene="dwarf"
/codon_start=1
                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:1421740
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                                                                         /gene="dwarf"
                                                                                                               'db_xref="taxon:4081"
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7UH, UK
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    Quality:
    Ratio:
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US-09-668-482-32 x SLU54770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   422 ACCAACTITIGCCTAAAATTGAGAGTTTATGAGATCCCACTTAACCAAT 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 ysTyrValLeu...ValIleAlaGluGluValSerSerCysLeuGluGln 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 sGlnArgLysLysValIleMetGlnAlaPheSerArgGluAlaLeuGlnC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 GATATTTTAGGAAAATGTAATATTGCAGCTGTCAATGGTTCAGCTCACAA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 ThrileLeuGlyAlaGlyCysLeuSerAsnLeuHisAspSerSerHisLy 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 euLeuGlyGluHisArgLeuValSerValHisTrpProAlaSerValArg 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122
563 CTTTAGCT......CAAGAATTCATGTCTGAATTTTTCAAT 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 TrpLeuSerCysGlyGluArgGlyLeuLeuValTyrProGluValLysAr 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 TAGTGAATGAAGCGAAAGGACTGGTCCCAGGATACCCACAGTCTATGATA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 TGGTTGTCCAACAATTGTTTCAATGGATTCAGAACTGAACAGATATATAC 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 ATGAAAAACCAAAGAGCCAGATATGGGAGTTTTTTAAATCACACATACT 221
                                                                                   200 roAlaGlyGlyGlyGluAspGluGlnGlnLeuValGluAlaPheGluGlu 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 eGlyArgProThrValArgValMetGlyAlaAspAsnValArgArgIleL 101 :||| ||| ||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40
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                                                                                                                                                                                      GATGGCATTTCTATCATCGTTGAAGCAAATTGCTGGTATTGAATCTACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCACTTTTTGGTGAAACTACTGAGTTTCTTAAACTTGGTCCAAGTTTC 171
                                                                                                                                                                                                                                                                                         gLeuMetPheArgIleAlaMetArgIleLeuLeuGlyCysGluProGlyP 200
                                                                                                                                                                                                                                                                                                                                                                                            TGG.....GATAATAAAGTTATTGACATTCAAGAGAAAACCAATAA
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LETSRLATIVNGVLRKTTODMEINGYILPKGWRLYVYTRELNYDPRLYDPYSEMPWR
WMDKSLEHDNSELVFGGGTRQCPGKELGVAEISTFLHYFVTKYRWEEIGGDKLMKFPR
VEAPNGLRIRVSAH"

242 c 268 g 415 t
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/db_xref="GI:142174
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Gaps: 10
Percent Identity: 26.998
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217	tThrArgAsnLeuPheSerLeuProIleAspValProPhe	233
598	CACTACCTATCAATCT	547
233	yrArgGlyValLysAlaArgAsnLeuIleHisAl	246
648	 GAAAATTATTG	597
246	leGluGluAsnIleArgAlaLysIleArgArgLeuG	262
869	TCATAGAAGAG AGAAGAGCTTCAAAGGAAATTCAA 7	732
263	LeuGlnLeuLleGluHisS	279
733	CATGATATGCTTGGTTACCTGATGAATGAGGAAGC 7	167
279	rgGlyGluArgLeuAspMetGlnAlaLeuLysGlnSerSer	96
768	AACACGATTCAAATTAACAGATGATGATGATGATTTAATTATAACT. 8	316
296	LeuPheGlyGlyHisGluThrThrAlaSerAlaAl	312
817	CTGTTTCCA	364
313	leThrTyrLeuGlyLeuTyrProHisValLeuGlnLysValArgGluG	329
865	GTGAAATATCTTCATGATCATCCAAAAGTTCTTGAAGAACTTAGAAAAGA	114
329	lyLeuLeuCysLysSerAsnGlnAspAsnLysLeu	346
915	ACACATGGCTATTAGAGAAAAAAAACCTGAGGATCCTATCG)58
346	lluGlnLeuLysTyrIleGlyCysValIleLysG	362
959	ATTACAACGATTACAGGTCAATGCGGTTCACACGAGCTGTGATTTTAGAG	800
363	;gLeuAsnProProValProGlyGlyPheArgValAlaLeuL	379
.009	CTCCAGGTTAGCAACAATAGTAAATGGGGTTTTGAGAAAAAA	.058
379	ThrPheGluLeuAsnGlyTyrGlnIleProLysGlyTrpAs	96
.059	GTATATCATTCCTAAAGGATGGAGAAT	108
396	spThrHisAspValAlaAspIlePheThrAsnLysGlu 4	112
.109	TATATACAAGGGAGTTGAATTACGATCCAAGACTTTATCCTGATCCATAT 1	.158
413	uPheAsnProAspArgPheIleValProHis	29
.159	TCGTTCAATCCATGGAGATGGATAAGAGCCTGGAACACCAAAAC 1	.206
429	erPheIleProPheGlyGlyGlyLeuArgSerCysValGlyLy	46
207	TGGTATTTGGAGGTGGTACTA	252
446	uPheAlaLysIleLeuLeuLysIlePheThrValGluLeuAl	62
253	AACTTGGTGTAGCAGAAATTTCCACATTTCTTCATTACTTCGTAACAAAA 1	302
463	CysAspTrpGlnLeuLeuAsnGlyProProThrMetLys 475	
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Database sequences: 730101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search information block: Query: US-09-668-482-32
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-Q=/cgn2_1/USPf0_spc1/USQ9668482/runat_05112001_13354_10917/app_query.fasta_1.1680
-DB-M_Geneseq_0601 -QFMT=fastap -SUFFIX=rng -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPEXT=4.000 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -GAPEXT=7.000 -YGAPEXT=0.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPEXT=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-TRANS=human40.cdi -LIST=45 -DOCALIGN=20 -THR_SCORE=pct
-TRANS=human40.cdi -LIST=45 -DOCALIGN=20 -THR_SCORE=pct
-NORM=ext -MINLEN=0 -MAXLEN=200000000
-USER=USO9668482_@CGN1_1_352 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
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Quality:

Ratio:

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Identity:

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    AAV09252 standard; cDNA; 1725 BP.
                                                      This nucleotide sequence encoding an isoform of cytochrome P450RAI. Its expression is dependent on the presence of retinoic acid (RA). The retinoid regulated genes such as the inducible cytochrome P450RAI gene specifically metabolises a derivative of the RA. The cytochrome P450 gene in general produces enzymes involved in the oxidative metabolism of endogenous and exogenous compounds. The cytochrome P450 mucleotide sequence can be used to induce or suppress the expression of its protein. P450RAI is highly induced by RA in cell lines and tissues. This allows for development of a drug screen using promoters and uncleotide sequences to identify drugs which are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
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                                                                                                                                                                                                                                                                                                                                                 Identifying DNA encoding inducible or suppressible cytochrome I by screening for drugs which reduce the catabolism of retinoic useful in cancer chemotherapy and the treatment of acne and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996;
21-JUN-1996;
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Sequence 1725 BP; 408
                                       reducing the catabolism of RA.
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Location/Qualifiers 25..1518 /*tag= a

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alignment_scores:
Quality: 2612.00
Ratio: 5.256
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-668-482-32 x AAV12205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Retinoid metabolising protein - useful to develop products to treat, e.g. cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or ichthyosis
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21-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-DEC-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1725 BP; 408 A; 425 C; 475 G; 417 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes are also claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; Page 62-64; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAW44161.
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                                                                                                                                                                                                                                                                                                           75 GCTGCTGCTTCCTGGCGGCGCTCAAGCTCTGGGACCTGTACTGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                              25 ATGGGGCTCCCGGCCTGCTGGCCAGTGCGCTCTGCACCTTCGTGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetGlyLeuProAlaLeuLeuAlaSerAlaLeuCysThrPheValLeuPr 17
                                                                                                                                                                                                                                                                                                                                   OLeuLeuLeuPheLeuAlaAlaLeuLysLeuTrpAspLeuTyrCysValS 34
Jones G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0724466.
96US-0667546.
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Gaps: 0
Percent Identity: 100.000
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1174	nproprovalproglyglypheargyalalabeulysinrfnegulleua	367 1125
1 6	GluGlnLeuLySTyrIleGlyCysValIleLySGluThrLeuArgLeuA	351 1075
	lyLeuLeuCysLysSerAsnGlnAspAsnLysLeuAspMetGluThrLeu 	334 1025
334 1024	7 yLeuTyrProHisValLeuGlnLysValArgGluGluIleLysSerLysG 	317 975
317 974	GlyHisGluThrThrAlaSerAlaAlaThrSerLeuIleThrTyrLeuGl 	301 925
300 924	rgLeuAspMetGlnAlaLeuLysGlnSerSerThrGluLeuLeuPheGly 	284 875
284 874	SLYSASPALALEUGINLEULEUI1eGluHisSerTrpGluArgGlyGluA 	267 825
267 824	IleArgAlaLysIleArgArgLeuGlnAlaThrGluProAspGlyGlyCy 	251 775
250 774	yrArgGlyValLysAlaArgAsnLeuIleHisAlaArgIleGluGluAsn 	234 725
234 724	ThrargasnLeuPheSerLeuProIleAspValProPheSerGlyLeuT	217 675
217 674	AlaGlyGlyGlyGluAspGluGlnGlnLeuValGluAlaPheGluGluMe	201 625
200 624	euMetPheArgIleAlaMetArgIleLeuLeuGlyCysGluProGlyPro	184 575
184 574	PLeuSerCysGlyGluArgGlyLeuLeuValTyrProGluValLysArgL	167 525
167 524	CysTyrValLeuVallleAlaGluGluValSerSerCysLeuGluGlnTr :	151 475
150 474	ysGlnArgLysLysVallleMetGlnAlaPheSerArgGluAlaLeuGln 1 	134 425
134 424	gThrileLeuGlyAlaGlyCysLeuScrAsnLeuHisAspScrScrHisL 1	117 375
117 374	LeuLeuGlyGluHisArgLeuValSerValHisTrpProAlaSerValAr 1	101 325
100	heGlyArgProThrValArgValMetGlyAlaAspAsnValArgArgIle 1	84 275

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seq_documentation_block:
ID AAV09247 standard; cI
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AC AAV09247;
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AC AAV09247;
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DT 07-JUL-1998 (first e
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PD 31-DEC-1997: 97WO-C
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PD 31-OCT-1996; 96US-(
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PP 23-JUN-1996; 96US-(
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PP 23-JUN-1996; 96US-(
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PP 21-JUN-1996; 96US-(
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PP 21-JUN-1996; 96US-(
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PP 1 Petkovich PM;
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PP PSDB; AAW37734.
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PP PSDB; AAW37734.
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Identifying DNA encod
PT Useful in Cancer chen
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PT Useful in Cancer chen
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PS Identifying DNA encod
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PS Example 4; Pages 56-5
XX
PS Example 4; Pages 56-5
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CC This nucleotide seque
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                                                                                                     Identifying DNA encoding inducible or suppressible cytochrome I by screening for drugs which reduce the catabolism of retinoic useful in cancer chemotherapy and the treatment of acne and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Retinoid regulated gene; cytochrome P450 gene; oxidative metabolism; P450RAI; retinoic acid; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGGATACCAGATCCCCAAGGGCTGGAATGTTATTTACAGTATCTGTGAC
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96US-0667546.
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                                         English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enzyme;
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sequence

encodes the human

cytochrome

P450RAI.

Its

 ${\tt AlaGlyGlyGluAspGluGlnGlnLeuValGluAlaPheGluGluMe}$

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alignment_scores:
Quality:
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     551
                                      184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression is dependent on the presence of retinoic acid (RA). The retinoid-regulated genes such as the inducible cytochrome P450RAI gene specifically metabolises a derivative of the RA. The cytochrome P450 gene in general produces enzymes involved in the oxidative metabolism of endogenous and exogenous compounds. The cytochrome P450 nucleotide sequence can be used to induce or suppress the expression of its protein. P450RAI is highly induced by RA in cell lines and tissues. This allows for development of a drug screen using promoters and nucleotide sequences to identify drugs which are useful for reducing the catabolism of RA.
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TCATGTTCCGAATCGCCATGCGCATCCTACTGGGCTGCGAACCCCAACTG
                                                                        GCTGAGCTGCGGCGAGCGCGCCTCCTGGTCTACCCCGAGGTGAAGCGCC
                                                                                           pLeuSerCysGlyGluArgGlyLeuLeuValTyrProGluValLysArgL
                                                                                                                                                                    CysTyrValLeuValIleAlaGluGluValSerSerCysLeuGluGlnTr
                                                                                                                                                                                                                                          ysGlnArgLysLysVall1eMetGlnAlaPheSerArgGluAlaLeuGln
                                                                                                                                                                                                                                                                                              CACCATTCTGGGATCTGGCTGCTCTAACCTGCACGACTCCTCGCACA
                                                                                                                                                                                                                                                                                                                   gThrIleLeuGlyAlaGlyCysLeuSerAsnLeuHisAspSerSerHisL
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                                                                                                                                                 TGCTACGTGCCGGTGATCACCGAGGAAGTGGGCAGCAGCCTGGAGCAGTG
                                                                                                                                                                                                                       AGCAGCGCAAGAAGGTGATTATGCGGGCCCTTCAGCCGCGAGGCACTCGAA
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Gaps:
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1151
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Seq_documentation_block:
ID AAV12204 standard; cDNA; 1494 BP
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AAV12204;
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PT 22-JUN-1998 (first entry)
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Retinoid metabolising protein; P
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KW actinic keratosis; oral leukoplat
KW retinoic acid; human; inhibitor;
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KW acute promyelocytic leukaemia; s
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us-09-668-482-32 x AAV12204
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                                                                                                Ratio:
Percent Similarity:
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                                                                                                                                                                    Quality:
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| CACCATTCTGGGATCTGGCTGCCTCTAACCTGCACGACTCCTCGCACA
GlyHisGluThrThrAlaSerAlaAlaThrSerLeuIleThrTyrLeuGl
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                                                                                                                                             CysTyrValLeuValIleAlaGluGluValSerSerCysLeuGluGlnTr
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XX BDT 31-OCT-2000 (first e
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XX Human; PSEC64; neuron
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                                                                                                                                                                                                                                                                                                                                                                                                                   Human PSEC64 encoding nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTAAATGGACCTCCTACAATGAAAACCAGTCCCACCGTGTATCCTGTGG
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                                                                                                                                                                                                                                                                                                                                                                        neuron
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                                                                                                                                                            /product= "PSEC64"
/note= "protein re
                                                                                                                                                                                                            /*tag= a
                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                   growth;
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98JP-0329989

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alignment_scores:
Quality: 2425.00
Ratio: 4.990
Percent Similarity: 97.787
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US-09-668-482-32 x AAA60752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AAA60752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a human protein, designated PSEC64, which is related to neuron growth. The PSEC64 protein and its gene can be used for the development of a preventive agent for use in the treatment of diseases in which nerves are involved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 8-10; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A protein related to the growth of neuron and a gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-468126/41.
P-PSDB; AAB12489.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2124 BP; 509 A; 510 C; 547 G; 558 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HERI-) HERIKKUSU KENKYUSHO KK
                                                                                                                                                                                       446
                                                                                                                                                                                                                                                                                          246 CCTGCAGATGAAGCGCAGGAAATACGGCTTCATCTACAAGACGCATCTGT
                                                                                                                                                                                                                                                                                                                                         196 TTCCCCTTCTTTGGGGAAACCTTGCAGATGGTACTGCAGCGGAGGAAGTT
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              167
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                                                                                                                                                                                                                                                     84 heGlyArgProThrValArgValMetGlyAlaAspAsnValArgArgIle 100
                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                       S1 PheProPhePheGlyGluThrLeuGlnMetValLeuGlnArgArgLysPh
                                                                                                                                                                                                                                                                                                                                                                                                                                           34 erSerArgAspArgSerCysAlaLeuProLeuProProGlyThrMetGly
                                                                                      CysTyrValLeuValIleAlaGluGluValSerSerCysLeuGluGlnTr 167
                                                                                                                                                                                                                                                                                                                                                                                            GCGGCCGCGACCGCAGTTGTGCCCTCCCATTGCCCCCCGGGACTATGGGC
                                       TGCTACGTGCCGGTGATCACCGAGGAAGTGGGCAGCAGCCTGGAGCAGTG
                                                                                                                                                                                                                                         TCGGGCGCCCACCGTACGGGTGATGGGCGCGCGCACAATGTGCGGCGCATC
PLeuSerCysGlyGluArgGlyLeuLeuValTyrProGluValLysArgL 184
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Percent Identity: 93.763
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Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   497
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1494	ULGUASNGLYPTOPTOTINMETLYSTINTSETPTOTINT VALITY EFFOVALA	467 1445
70 44 (IlePheThrValGluLeuAlaArgHisCysAspTrpGlnL 	451 1395
450	roPheGlyGlyGlyLeuArgSerCysValGlyLysGluPheAlaLysIle	434
1394		1345
434	PATGPheIleValProHisProGluAspAlaSerArgPheSerPheIleP	417
1344	::::::	1295
417	ThrHisAspValAlaAspIlePheThrAsnLysGluGluPheAsnProAs	401
1294	:::	1245
400	snGlyTyrGlnIleProLysGlyTrpAsnValIleTyrSerIleCysAsp	384
1244		1195
384	nProProValProGlyGlyPheArgValAlaLeuLySThrPheGluLeuA	367
1194		1145
367	GluGlnLeuLysTyrIleGlyCysValIleLysGluThrLeuArgLeuAs	351
1144		1095
350	lyLeuLeuCysLysSerAsnGlnAspAsnLysLeuAspMetGluThrLeu	334
1094		1045
334	YLEUTYFPTOHISVALLEUGLNLYSVALATGGLUGLUILELYSSETLYSG	317
1044		995
317	GlyHisGluThrThrAlaSerAlaAlaThrSerLeuIleThrTyrLeuGl	301
994		945
300	rgLeuAspMetGlnAlaLeuLysGlnSerSerThrGluLeuLeuPheGly	284
944		895
28 4	SLYSASPAlaLeuGlnLeuLeuIleGluHisSerTrpGluArgGlyGluA	267
89 4		845
267 844	IleArgAlaLysIleArgArgLeuGlnAlaThrGluProAspGlyGlyGy	251 795
250 794	yrArgGlyValLysAlaArgAsnLeuIleHisAlaArgIleGluGluAsn :	234 745
234 744	ThrargasnLeupheSerLeuproIleAspValProPheSerGlyLeuT :	217 695
217 694	AlaGlyGlyGlyGluAspGluGlnGlnLeuValGluAlaPheGluGluMe:	201 646
200 645	euMetPheArgIleAlaMetArgIleLeuLeuGlyCysGluProGlyPro :	184 596
ف د	GCCTCCTGGTCTACCCCGAGGTGAAGCGCC	

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alignment_scores:
                                                                                                                                   This sequence comprises a genomic clone of a novel mouse retinoid metabolising protein designated mp450RAI. A cDNA clone (see AAV12205) that includes a coding sequence for the full-length mp450RAI protein (see AAW414161) is also provided. The encoded protein is a retinoid oxidase that has the ability to hydroxylate retinoic acid at the 4 position of the beta-ionone ring and is inducible in epithelial cells exposed to retinoic acid. Zebrafish, the man and mouse P450RAI cDNA clones (see AAV12203-05) are claimed. They can be used in the recombinant production of p450RAI. Antisense sequences can be used in a claimed method for inhibiting retinoic acid hydroxylation for the treatment of cancer, actinic keratosis, oral leukoplakia, secondary tumours of the head and/or neck, non-small cell lung carcinomas, basal cell carcinomas, acute promyelocytic leukaemia, skin cancer, and premalignancy associated with actinic keratosis, acne, psoriasis and/or ichthyosis. Promoter wy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV12216
         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Retinoid metabolising protein - useful to develop products to treat, e.g. cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  actinic keratosis; oral leukoplakia; head tumour; neck tumour non-small cell lung carcinoma; basal cell carcinoma; acute promyelocytic leukaemia; skin cancer; acne; psoriasis; ichthyosis; therapy; diagnosis; screening; cytochrome P450; o
                                                                                                               Sequence 4164 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 69-70; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g. cance ichthyosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-077178/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996;
21-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid; mouse; inhibitor; antisense; cancer; actinic keratosis; oral leukoplakia; head tumour; neck tu
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         Quality: 1853.00
Ratio: 4.240
milarity: 41.778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jones G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0724466.
96US-0667546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-CA00440
                                                                                                            997 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Petkovich
                                                                                                               975
Length: 1046
Gaps: 10
Percent Identity: 41.396
                                                                                                            C; 1071 G; 1121 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PM, White JA;
                                                                                                            0 other;
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alignment_block: US-09-668-482-32 x AAV12216

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Align seg 1/1 to: AAV12216 from: 1 to: 4164
234 TyrArg
                                                                                                          781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            etThrArgAsnLeuPheSerLeuProIleAspValProPheSerGlyLeu
                                                                                                                        oAlaGlyGlyGlyGluAspGluGlnGlnLeuValGluAlaPheGluGluM
                                                                                                                                                                                    LeuMetPheArgIleAlaMetArgIleLeuLeuGlyCysGluProGlyPr
                                                                                                                                                                                                                                              rpLeuSerCysGlyGluArgGlyLeuLeuValTyrProGluValLysArg
                                                                                                                                                                                                                                                                                         GTGCTACGTGCCCGTGATCGCTGAGGAAGTCAGCAGTTGTCTGGAGCAGT
                                                                                                                                                                                                                                                                                                         nCysTyrValLeuValIleAlaGluGluValSerSerCysLeuGluGlnT|||||||||
                                                                                                                                                                                                                                                                                                                                                   CTGGGGGGTGCTCAGGTGATTATGCAGGCCTTCAGCCGCGAGGCACTCCA
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                                                                                                                                                                    CTCATGTTCCGCATCGCCATGCGCATCCTGCTGGGCTGCGAGCCGGGTCC
                                                                                                                                                                                                                               GGCTAAGCTGCGGCGAGCGCGGCCTCCTGGTCTACCCCGAGGTGAAGCGC
                                                                                                                                                                                                                                                                                                                                                                                                               CGAAGGGGGGGGGCTGAGGGAAAGTAGAGGATTGTAACACTCTCTGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGTTCAGGCAAAATAGAATGCGGGGGGGGGGGCTAGTCCTATGTGGTGGG
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236	881	TACCGGGTAAGGGCGGTTTGCGGAGTCGGAGTAGGGGAACGCAAGCTCGG	930
241 ASDILEUII-BAILANT ILEGALIGATE ILEGAL	ω ω	CATCGCTCACCGCCACGCTCTCTCCGCGCTCAGGGCGTGAAGGCGCGG	44 00
991 AACCTTATACACGCGCCATGAGGACAACATTCGCGCCAAGATCCGCCG 1036 257 GLUGLILLILLILLILLILLILLILLILLILLILLILLILLIL	41	nLeuIleHisAlaArgIleGluGluAsnIleArgAlaLysIleArgAr	57
	57	euGlnAlaThrGluProAspGlyGlyCysLysAspAlaLeuGlnLeuL	74
	ا تت	TITITITITITITITITITITITITITITITITITITI	80
288	8	IleGluHisSerTrpGluArgGlyGluArgLeuAspMetGln 	88 13
131 AGCAATTTCAAAAGGTGCCCAAGGGCCGGGGAGTGCCTCTGACTTTCCAGA 1180 288 181 CACACTTTCTGGGGTCTCCAAAGCCCTGTCAAGGCCCCAGCTACTTCCAA 1230 288 281 GTGGGCGGCATGCTAGGGTCTAGAGCCCTGTCAAAGCCCTGTGGGTCGTGACCC 1280 288 281 CTTCACGGAGCCAAACAACCATTCAAGAGAACATAACAT	æ		æ
288	·ω	CAATTTCAAAAGGTGCCAAGGGCCGGGGAGTGCCTCTGACTTTCCAGA	18
181 CACACTTTCTGGGGTCTCCAAAGCCCTGTCAAGGCCCCAGCTACTTCCAA 1230 288	8		00
288	œ	ACACTTTCTGGGGTCTCCAAAGCCCCTGTCAAGGCCCCAGCTACTTCCAA	23
231 GTGGGCGGCGATGCTAGGTCTAGAGCTTTCAACCTGTGGGTCGTGACCC 1280 288	8		œ
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281 CTTCACGGAGCCAAACCACCTTTCAGAAGGGTCGCCTAAGAGCATCTGC 139 288	8		æ
288 288 331 ATATCCGATATTTACATCAAGAAACATAACAGTAGCAAAATTACCGTTAT 138 288 288 431 AACCGTATTAAAGGGTGGCATTGGTCTAGAGAGGTGGCAACACGAGG 143 288 288 431 AACCGTATTAAAGGGTGGCATTGGTCTAGAGGGTGTGTGGAAGGGGTGGC 148 288 288 288 288 289 288 280 288 281 TGAGCAATGGGGAAGATCCCAAAGTTCAAAGGGCAAGGCTCATCACAA 153 288 288 289 288 281 TGTTTAAACCGGAAGAGCAGGATTTAAGGGAGTTTTGCGTTTTGTGG 158 288 288 289 288 280 288 281 TCTTTGACTTAGGTCAGGTCTTTGTAACAGTGCTATAAACTGCACTCAGA 288 288 288 289 288 280 288 281 TCTTTGAGTTCAGGTTTTTATCCTTAGGCACTAAACAATCTGCACACTCACA 288 288 289 288 280 288 281 TCTGTATAAACTTCCGTTTTGTTATCCTTAGGCACTAAACAAAC	28	TTCACGGAGCCAAACAACCCTTTCAGAAGGGTCGCCTAAGAGCATCTGC	ω
331 ATATCCGATATTTACATCAAGAAACATAACAGTAGCAAAATTACCGTTAT 1381 288	00		8
288	ω	ATCCGATATTTACATCAAGAAACATAACAGTAGCAAAATTACCGTTAT	38
288	æ		8
288 288 431 AACCGTATTAAAAGGGTGGCATTGGTCTAGAGAGCTGTGGAAAGGGGGTGGC 148 288 288 481 TGAGCAATGGGAAGATCCCAAAGTTCAAAGGGCAAGGCTCATCTACAAA 153 288 288 531 GGTTAAAGCGGAAGAGCAGGATTAAGGGATTTTGCGTTTTGTTGTGTGTG	38	AAGTAGCAACAAAGATAATTTTATCGTTGGGGGTCACCACAACACGAGG	43
431 AACCGTATTAAAGGGTGGCATTGGTCTAGAGAGCTGTGGAAGGGGGTGGC	8		8
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288	48	GAGCAATGGGGAAGATCCCAAAGTTCAAAGGGCAAGGCTCATCTACA	5
288	8		œ
288	ω̈	GTTAAAGCGGAAGAGCAGGATTAAGGGAGTTTTGCGTTTTTGTTTG	58
581 TCTTTGACTTTCTATGAACAAAACGGATTTTACCCTTGAAGTCTTCCGTG 163 288	8		œ
288	æ	${ t TTTGACTTTCTATGAACAAAACGGATTTTACCCTTGAAGTCTTCCGT$	63
631 CAATATTCTCAGGTCAGGTCTTTGTAACAGTGCTATAAACTGCACTCAGA 168 289AlaLeuLysGlnSerSerThr 295 289AlaLeuLysGlnSerSerThr 295 281 TCTGTATAAACTTCCGTTTTTATCCTTAGGCACTAAAACAATCGTCAACA 173 295 GluLeuLeuPheGlyGlyHisGluThrThrAlaSerAlaAlaThrSerLe 312 296 GluLeuTeuPheGlyGlyHisGluThrThrAlaSerAlaAlaThrSerLe 312 297 GluLeuTeuPheGlyGlyHisGluThrThrAlaSerAlaAlaThrSerLe 312 298 GluLeuLeuPheGlyGlyHisGluThlHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	8		8
289AlaLeuLysGlnSerSerThr 295 681 TCTGTATAAACTTCCGTTTTTATCCTTAGGCACTAAAACAATCGTCAACA 173 296 GluLeuLeuPheGlyGlyHisGluThrThrAlaSerAlaAlaThrSerLe 312 11111111111111111111111111111111111	63	AATATTCTCAGGTCAGGTCTTTGTAACAGTGCTATAAACTGCACTCAG	89
681 TCTGTATAAACTTCCGTTTTTATCCTTAGGCACTAAAACAATCGTCAACA 173 296 GluLeuLeuPheGlyGlyHisGluThrThrAlaSerAlaClATTCGTCAACA 12	œ	AlaLeuLysGlnSerSerTh	9
96 GluLeuLeuPheGlyGlyHiSGluThrThrAlaSerAlaAlaThrSerLe 312	68	CTGTATAAACTTCCGTTTTTATCCTTAGGCACTAAAACAATCGTCAAC	73
11 GNOCLOCIALISTICION DE CONTROLLO DE CONTROLLO CONTROLL	و د	1 1 1 1 1 1 1 1 1 1	12 78
81 GATCACTTACCTAGGACTCTACCCACATGTCCTCCAGAAAGTTCGAGAAG 183		TleThrTvrLenGlvLenTvrProHisValLenGlnLvsValArgGl	29
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2730	${\tt TTGACAGTGTCCTGCCTCTATGGTACTGGGAACCAATTTGCTCTCTCT$	2681
382		382
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382		382
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382		382
382 2580	ASnProProValProGlyGlyPheArgValAlaLeuLySThrPheGlu	367 2531
366 2530	euGluGlnLeuLysTyrIleGlyCysVallleLysGluThrLeuArgLeu 	350 2481
350 2480	.GlyLeuLeuCysLysSerAsnGlnAspAsnLysLeuAspMetGluThrL 	334 2431
2430	TTTTTGGAGTGCCCAGGGATCCATCACTCACTTTTTATCTGTTTCCATA	2381
333	Lys.	333
2380	CAGACGCCTTCAGGTTTAGTTAACAGGTGAGTCCTGCTGGGCTGACTTTT	2331
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1880		1831
332	IleLysSer	329

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FT CDS 97WO-C
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FH Rey 96US-0
XX
PP 31-DEC-1997; 97WO-C
XX
PP 23-JUN-1996; 96US-0
PR 21-JUN-1996; 96US-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Retinoid regulated gene; cytochrome P450 gene; ensoxidative metabolism; P450RAI; retinoic acid; RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytochrome zP450RAI cDNA sequence
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96US-0667546.
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/product= "Cytochrome zP450RAI"
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                                                                                                                                                           134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This nucleotide sequence encodes the cytochrome zP450RAI of the zebra fish. Its expression is dependent on the presence of retinoic acid (RA). The retinoid-regulated genes such as the inducible cytochrome P450RAI gene specifically metabolises a derivative of the RA. The cytochrome P450 gene in general produces enzymes involved in the oxidative metabolism of endogenous and exogenous compounds. The cytochrome P450 nucleotide sequence can be used to induce or suppress the expression of its protein. P450RAI is highly induced by RA in cell lines and tissues. This allows for development of a drug screen using promoters and nucleotide sequences to identify advanced to the cytochrome promoters and nucleotide sequences to identify
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1850 BP; 519 A;
                                                            CysTyrValLeuValIleAlaGluGluValSerSerCysLeuGluGlnTr
                                                                                                                                                                                                                                                                                          LeuLeuGlyGluHisArgLeuValSerValHisTrpProAlaSerValAr
                                      CACTACATTCCCGTGATCCAGCAGGAGGTGAAGAGCGCCATACAGGAATG
                                                                                                              gThrIleLeuGlyAlaGlyCysLeuSerAsnLeuHisAspSerSerHisL 134
                                                                                                                                                       ysGlnArgLysLysValIleMetGlnAlaPheSerArgGluAlaLeuGln
                                                                                                                                                                                                                                                                        CTGCTGGGCGAACACAAGCTGGTGTCTGTTCAGTGGCCAGCATCAGTGAG
                                                                                                                                                                                                                                                                                                                                                                      heGlyArgProThrValArgValMetGlyAlaAspAsnValArgArgIle
                                                                                                                                                                                                                                                                                                                                                                                                                           TCTGCGCATGAAACGGCAGAAATACGGGTGCATCTACAAGACGCACCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 eLeuGlnMetLysArgArgLysTyrGlyPheIleTyrLysThrHisLeup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGCCGTTCATTGGAGAAACGCTCCAGCTGATCCTCCAGAGAAAGGAAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACGAGTCGATCCGAACTGCAGAAGTCCTCTACCGCCAGGTACCATGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OLeuLeuPheLeuAlaAlaLeuLysLeuTrpAspLeuTyrCysValS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MetGlyLeuProAlaLeuLeuAlaSerAlaLeuCysThrPheValLeuPr 17
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Ratio: 4.070
milarity: 85.887
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seq_documentation_block:
ID AAV12203 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid; zebrafish; inhibitor; antisense; cancer; actinic keratosis; oral leukoplakia; head tumour; neck tumour non-small cell lung carcinoma; basal cell carcinoma; acute promyelocytic leukaemia; skin cancer; acne; psoriasis; ichthyosis; therapy; diagnosis; screening; ss.
                                             transcripts present in first resure regenerating in the presence or absence of retinoic acid were compared using a differential display pCR technique, and an isolated clone (see AAV12213) was used to screen a D. rerio 6-18 hr embryo cDNA library. Human (see AAV12204) and mouse (see AAV12205) p450RAI clones have also been identified. The isolated clones can be used in the recombinant production of p450RAI proteins. Antisense nucleic acids can be used in a claimed method for inhibiting retinoic acid hydroxylation for the treatment of cancer, actinic keratosis, oral leukoplakia, secondary tumours of the head and/or neck, non-small cell lung carcinomas, basal cell carcinomas, acute promyelocytic leukaemia, skin cancer, and premalignancy associated with actinic keratosis, acne, psoriasis and/or ichthyosis. Promoter sequences (see AAV12206-08) are also
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                                                                                                                                                                                                                                                                         This cDNA clone codes for a novel zebrafish retinoid metabolising protein (see AAW44159) designated zP450RAI. The encoded protein is retinoid oxidase that has the ability to hydroxylate retinoic acid at the 4 position of the beta-ionone ring and is inducible in epithelial cells exposed to retinoic acid. To isolate the clone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996;
21-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                  Claim 15; Page 52-54; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Retinoid metabolising protein - useful to develop products to treat, e.g., cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
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                                                                                                                                                                                                                                                                                                                                                                      GluThrLeuGluGlnLeuLysTyrIleGlyCysValIleLysGluThrLe 364
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Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid; human; inhibitor; antisense; cancer; actinic keratosis; oral leukoplakia; head tumour; neck tumour;

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alignment_scores:
Quality:
Ratio:
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US-09-668-482-32 x AAV12214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metabolising protein designated hp450RAI. Another genomic clone (see AAV12215) is also provided, as well as a cDNA clone (see AAV12204) Ct that includes a coding sequence for the full-length hp450RAI crotein (see AAW4160). The encoded protein is a retinoid oxidase ct that has the ability to hydroxylate retinoic acid at the 4 position cof the beta-lonone ring and is inducible in epithelial cells exposed to retinoic acid. The hp450RAI gene has been localised to captain a caid. The hp450RAI gene has been localised to composed to retinoic acid. The hp450RAI gene has been localised to composed to retinoic acid. They can be used in the recombinant composed to production of p450RAI. Antisense nucleic acids can be used in a colaimed method for inhibiting retinoic acid hydroxylation for the treatment of cancer, actinic keratosis, oral leukoplakia, secondary composed cell carcinomas, acute promyelocytic leukaemia, skin cancer, cand premalignancy associated with actinic keratosis, acne, generals and/or ichthyosis. Promoter sequences (see AAV12206-08)
                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AAV12214
                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         non-small cell lung carcinoma; basal cell carcinoma; acute promyelocytic leukaemia; skin cancer; acne; psoriasis; ichthyosis; therapy; diagnosis; screening; cytochrome P450; ds.
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21-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Retinoid metabolising protein - useful to develop products to treat, e.g. cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-077178/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beckett BR, Jones G,
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                                                                                                                                  676 ATGGGGCTCCCGGCGCTGCTGCCCAGTGCGCTCTGCACCTTCGTGCTGCC 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2677 BP; 489 A; 775 C; 868 G; 511 T; 34 other;
51 PheProPhePheGlyGluThrLeuGlnMetValLeu.Gln..........
                                                                          34 erSerArgAspArgSerCysAlaLeuProLeuProProGlyThrMetGly 50
                                                                                                                                                                                                                                                   1 MetGlyLeuProAlaLeuLeuAlaSerAlaLeuCysThrPheValLeuPr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the P450RAI genes are also claimed
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96US-0667546.
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63		ω
926	GCTGAAGTCGGGGTAGGCGCCCCCGGGAGGCATGCTATTGCGGCTAGGAG 9	75
63		ω
976	AGGGCTGGCGGGAGCGCGGCGCTCCCCGGMKYMCSCTCAWGCSCRCWWK 1	025
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1 6		
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106 1176	rgLeuValSerValHisTrpProAlaSerValArgThrIleLeuGlyAla 1	225
123 1226	GlyCysLeuSerAsnLeuHisAspSerSerHisLysGlnArgLysLys. 1 	38 275
138	1	38
1276	GG	325
138	1	ω 60
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138	1	38
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138	1	.38
1426	GTGTCTGGCAGGACTGGGGGTGTCTGGAAGGGGACGGCGGTAGACGAGAG 1	475
139	valīle	40
1476	GGGCGGATGGAGGCTTTTAACGCTGTCCCCTCCTCGGGACTCAGGTGAT	Ü
141 1526	MetGlnAlaPheSerArgGluAlaLeuGlnCysTyrValLeuVallleAl	L57 L575
157 1576	aGluGluValSerSerCysLeuGluGlnTrpLeuSerCysGlyGluArgG 1	174 1625
174 1626	l lyLeuLeuValTyrProGluValLysArgLeuMetPheArgIleAlaMet 1 .	190 1675
191 1676	ArgileLeuLeuGlyCysGluProGlyProAlaGlyGlyGlyGlyAspGl 2 	207 1725
207	uGlnGlnLeuValGluAlaPheGluGluMetThrArgAsnLeuPheSerL 	224 1775

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGCAGGCAGACTTGTGAGAATGTGGGTCTCACTCTATTCTTAGGCACTA
                                                                                                                                                             GTCTTCCCTCCAGAACTCTCAGTTCGATTCTGAGTAATCCTTCTGTCAAA
                                                                                                                                                                                                                 AAGATATTGCTTTCCTTGACTTTCTGTCAGCAAAACATTTAGCCCTTCTA 2475
                                                                                                                                                                                                                                                                     TACTCGCCTTACTGCTCCAGCTGAACTAAAGGGACGTTGCATTTTGTTTA 2425
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                                                                                                                                                                                                                                           TTTAATAAAACTAAGACTTTAACTCAGGAGTTTCCGGTAGRGCGGGGTCG
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271
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                                                                                                                                                                                                                221
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                                                                                                                                            LeuLeuGlyGluHisArgLeuValSerValHisTrpProAlaSerValAr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ......TCCGCTCTCCTTCGATGG......
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                                                                                                 TTAAAGAACGAATCAAAAGGTTTGGTTCCTGGTTACCCACAATCGATGCT 320
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u 446	heSerPheIleProPheGlyGlyGlyLeuArgSerCysValGlyLysGlu	430
A 1207	CTTTAATCCATGGAGATGGATGAAGAAGAGCTTGGAGTCACAAA	1164
P 430	heAsnProAspArgPheIleValProHisProGluAspAlaSerAr	413
T 1163	TACACGAGGGAAATTAATTACGATGCAAATCTTTATGAAGACCCATTGAT	1114
1 413	cHisAspValAlaAspIlePheThrAsnLysGlu	397
r 396 A 1113	hrPheGluLeuAsnGlyTyrGlnIleProLysGlyTrpAsnValIleTyr:::: :::	380 1064
10	ACGATCGTTAATGGGGTCCTAAGGAAAACTACTCGT	
w	qLeuAsnProProValProGlyGlyPheArqValAlaLeuI	363
h 363 C 1013	MetGluThrLeuGluGlnLeuLysTyrIleGlyCysValIleLysGluTh ::: ::::::::: ::: CTTGAGGACGTGAAGTCAATGAAGTTCACTCGAGCTGTGATTTATGAGAC	347 964
T 963	::::::::::::::::::::::::::::::::::::::	919
p 346	uLeuCysLysSerAsnGlnAspAsnLysLeuAs	330
. 918	TAAGTACCTTCATGATCACCCAAAAGCTCTTCAAGAACTAAGAGCTGAG.	870
I 330	yrPr	313
1 313 T 869	LeuLeuPheGlyGlyHisGluThrThrAlaSerAlaAlaThrSerLeuII ::: ::::: ATTTTGTATTCGGGTTACGAAACTGTCTCTACGACCTCAATGATGGCTCT	297 820
G 819	ACCGAT	7
.u 296	luArgGlyGluArgLeuAspMetGlnAlaLeuLysGlnSerSerThrGl	280
7	TGGAGAAACATTCACAGACATGTTAGGTTACTTGATGAAGAAGGAAG	Ν
28	yGlyCysLysAspAlaLeuGlnLeuLeuIleGluHisSerTr	265
	GluAsnIleArgAlaLysIleArgArgLeuGlnAlaThrGluProAspC	249 676
. 675	ATTATCGTTGCGGAATCCAAGCAAGAAAT	647
lu 248	lyLeuTyrArgGlyValLysAlaArgAsnLeuIleHisAlaArgIleG ::	232
4	CAAGCTTGTTGGGACTTTATCCGTTCCGATTGATCTTCCGGGCAC	597
:G 232	${\tt uGluMetThrArgAsnLeuPheSerLeuProIleAspValProPheSe}$	215
Gl 215 TT 596	GlyProAlaGlyGlyGlyGluAspGluGlnGlnLeuValGluAlaPhe	562
		. (
л 19	ysArgLeuMetPheArgIleAlaMetArgIleLeuLeuGlyCysGluP ::::: AACATATGGCATTTTTATCTTCACTACACACAAAMTCGCTACAAACTTAAA	182
lL 182 : CA 511	6 nTrpLeuSerCysGlyGluArgGlyLeuLeuValTyrProGluValI	16 47
CA 470		421
A 42	GCTTATGAGAGGCTCGCTTCTGTCTCTCATAAGCTCGACCATGATGA	
. n	ysGinAigLysLysVallieMetGinAlaPheSerArgGiuAlaLeuG	JL

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seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT85306
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                      p450-type hydroxylase. The hydroxylase can be used to identify brassinosteroids or brassinosteroid inhibitors, useful to produce plants with modified physiological and/or phenotypic characteristics. The modified plants may show, e.g. stimulation of growth, increased cell elongation, increased wood production, accelerated seed germination at low temperatures, an increase in accelerated seed germination at low temperatures, an increase in dry weight, repressed anthocyanin production during growth in light and/or inhibited de-etiolation which is induced, e.g. by cytokinin, in the dark or an increase in stress tolerance. The hydroxylase or its coding sequence can also be used for the recombinant production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytochrome P450-type hydroxylase; identification; brassinosteroid; brassinosteroid inhibitor; modified plant; recombinant production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT85306 standard;
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                                                                                                                                                                                                                                                                                                                                              The present sequence encodes Arabidopsis thaliana cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Pages 44-46; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated plant cytochrome P450-type hydroxylase gene - used to identify substances acting as brassino-steroid(s) or brassinosteroid inhibitors for the production of modified plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-489649/45.
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compounds, e.g. teasterone.
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48..1467
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Sequence 1608 BP;

382 A;

374 C;

374 G;

478 Ť;

0 other;

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                               CysTyrValLeuVal...IleAlaGluGluValSerSerCysLeuGluGl 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGACTTTTCAGCTGATCGGAGCTTACAAAACAGAGAACCCTGAGCCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                GACCATCTCATGCTTGATATTGACCGGTTAGTCCGGTTTAATCTTGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gThrIleLeuGlyAlaGlyCysLeuSerAsnLeuHisAspSerSerHisL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGGTGAACCGACGATTTTCTCAGCTGACCCGGAAACGAACCGGTTTGTT
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GluAsnIleArgAlaLysIleArgArgLeuGlnAlaThrGluProAspGl 265
                                                                                euTyrArg...GlyValLysAlaArgAsnLeuIleHisAlaArgIleGlu
                                                                                                                                                                                                                   ProAlaGlyGlyGlyGluAspGluGlnGlnLeuValGluAlaPheGluGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACGTATGCACTCTCTCACCATGAGCTTTGCTAATTCTTCAATCATTAAA
                                                   CTTACCGCAAAGCCATCCAAGCGCGGAGG.....AAGGTGGCG
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Arabidopsis thaliana DNA fragment SEQ ID NO: 56467
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                                          18-OCT-2000
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                                                                                                                                                                                                                                                                                                         AGCAAGACAAGCTGGTTTTCCTTTCCAACTACAAGAACGCAGAAACGGTAC 1430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerCysValGlyLysGluPheAlaLysIleLeuLeuLysIlePheThrVa 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTCTAATGTG......TTCACACCGTTTGGTGGAGGGCCAAGG
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05-MAR-1999;
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Percent Identity: 26.640
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1019 CTTGAATGGAGTGATTACAAGTCAATGCCATTCACACAATGTGTGGTTAA 1068
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             361 sGluThrLeuArgLeuAsnProProValProGlyGlyPheArgValAlaL 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 uAlaAlaLeuLysLeuTrpAspLeuTyrCysValSerSerArgAspArgS 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LeuLeuAlaSerAlaLeuCysThrPheValLeuProLeuLeuLeuPheLe 22
                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGGTCCTCT......CGTGTTCTCCTCATGGAAGAAGCCAAAA 574
                                                                                                                                                                                                                                                                             ysGlnArgLysLysValIleMetGlnAlaPheSerArgGluAlaLeuGln 150
                                                                                                                                                                                                                                                                                                                                    TAACCTTTTGGGGAAACACTCTCTGCTTCTTATGAAAGGTTCTTTGCATA 436
                                                       nTrpLeuSerCysGlyGluArgGlyLeuLeuValTyrProGluValLysA 183
                                                                                                              GACCATCTCATGCTTGATATTGACCGGTTAGTCCGGTTTAATCTTGATTC
                                                                                                                                                      CysTyrValLeuVal...IleAlaGluGluValSerSerCysLeuGluGl 166
                                                                                                                                                                                                                         AACGTATGCACTCTCTCACCATGAGCTTTGCTAATTCTTCAATCATTAAA 486
                                                                                                                                                                                                                                                                                                                                                                             gThrIleLeuGlyAlaGlyCysLeuSerAsnLeuHisAspSerSerHisL 134
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Ratio:
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Gaps: 15
Percent Identity: 26.640
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1393	::: AGTTGG	13
474	${\tt GluLeuAlaArgHisCysAspTrpGlnLeuLeuAsnGlyProProTh}$	4
457 1358	41 SerCysValGlyLysGluPheAlaLysIleLeuLeuLysIlePheThrVa 4	4 13
440 1308	24 roGluAspAlaSerArgPheSerPheIleProPheGlyGlyGlyLeuArg	12
424 1270	411 sGluGluPheAsnProAspArgPheIleValProHisp 4 :::	12
411 1220	95 IleTyrSerIleCysAspThrHisAspValAlaAspIlePheThrAsnLy ::: ::: ::: :::	1 11
394 1170	78 eulysThrPheGluLeuAsnGlyTyrGlnIleProLysGlyTrpAsnVal::	11
378 1120	61 sGluThrLeuArgLeuAsnProProValProGlyGlyPheArgValAlaL :	3 10
361 1070	345 LeuAspMetGluThrLeuGluGlnLeuLysTyrIleGlyCysValIleLy :	10
344 102	28 luGluIleLysSerLysGlyLeuLeuCysLysSerAsnGlnAspAsnLys	φ ω
328 976	11 rLeuIleThrTyrLeuGlyLeuTyrProHisValLeuGlnLysValArgG ::: ::: ::: :::::::: 27 CGCCGTCAAATTTCTCACCGAGACTCCTTTAGCTCTTGCTCAACTCAAGG	φ ω
311 926	aSerAlaAlaThrSe :::: CACGATCATGACTCT	~
294 876	lnSerSer	~ · · ·
278 844	265 yGlyGysLysAspAlaLeuGlnLeuIeuIleGluHisS	-1 11
265 794	nAlaT ; ; ; ; ; ;	
248 744	233 euTyrArgGlyValLysAlaArgAsnLeuIleHisAlaArgIleGlu :::::: ::: 	
233 706	216 uMetThrargAsnLeuPheSerLeuProIleAspValProPheSerGlyL::::::::::::::::::::::::::::::::::::	
216 659	200 ProAlaGlyGlyGlyGluAspGluGlnGlnLeuValGluAlaPheGluGl	
199 621	183 rgLeumetPheArgIleAlametArgIleLeuLeuGlyCysGluProGly :::::	

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AAC35582 standard;
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09-MAR-1999;

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01-APR-1999;

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::: ::: ::: ||||::: ::: ||||:::
AGCAAGACAAGCTGGTTTCTTTCCAACTACAAGAACGCAGAAACGGTAC 1443
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US-09-668-482-32 x AAC35582
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Percent Similarity:
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99US-0161361.
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1.523
57.202
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                                                                                                                                                                                      0161405.
                                                                                                                                                                                                  -0161404
                             Length: 486
Gaps: 16
Percent Identity: 27.984
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Align seg 1/1 to: AAC35582 from: 1 to: 1667
279 rpGluArgGlyGluArgLeuAspMetGlnAlaLeuLysGlnSerSerThr :::||| ||| |||
                                                                                                                                                          248
                                                                                                                                                                                             731
                                                                                                                         763
                                                                                                                                                                                                                                                                                                                                                                       198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             458 GGCTAATGAGAGGCTCGTTGCTTTCTTTAATAAGCCCAACCATGATGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 LeuLeuGlyGluHisArgLeuValSerValHisTrpProAlaSerValAr 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluGluAsnIleArgAlaLysIleArgArgLeuGlnAlaThrGluProAs
                                                                                                                                                                                      erGlyLeuTyrArgGlyValLysAlaArgAsnLeuIleHisAlaArgIle
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                                                                                                                                                                                                                                                                                eGluGluMetThrArgAsnLeuPheSerLeuProIleAspValProPheS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CysTyrValLeuValIleAlaGluGluValSerSerCysLeuGluGlnTr 167
                                                 pGlyGly.....CysLysAspAlaLeuGlnLeuLeuIleGluHisSerT
                                                                                                                                                                                                                                                              CAAGCTTGTTGTGGGAACTCTA...TCGGTCCCGATCGATATCCCGGGAA
                                                                                                                                                                                                                                                                                                                                                                 ProGlyProAlaGlyGlyGlyGluAspGluGlnGlnLeuValGluAlaPh 214
                                                                                                                                                                                                                                                                                                                                                                                                    CCAAACATATGGCATTTTTATCATCGTTGTTACAAATAGCTGAGACTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTT...TGCGGTTGGGATGATCTTGAGACAGTTGATATCCAAGAAAAGA 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACCATCTCTTG......CCTAAGATTGATGATTTCATGAGAAACTA 548
                                                                                                                     TGATATTCTAGGGACATGCAACATAGCTGCGGTTCATGGCCCGAGCCACC
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1198 GTATACACAAGAGAGATTAACTATGATACATCT...CTTTATGAAGATCC 1244
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1436 CAAGAGTT 1443
                                                                                                                                                                                                                                                         445 LysGluPheAlaLysIleLeuLeuLysIlePheThrValGluLeuAlaAr 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                395 IleTyrSerIleCysAspThrHisAspValAlaAspIlePheThrAsnLy 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 AspMetGluThrLeuGluGlnLeuLysTyrIleGlyCysValIleLysGl 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         329 luIleLysSerLysGlyLeuLeuCysLysSerAsnGlnAspAsnLysLeu 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312 ulleThrTyrLeuGlyLeuTyrProHisValLeuGlnLysValArgGluG 329 ::: ||||||| :::||| :::|||:::||||:::|| 954 TCTTAAGTATCTCCATGATCATCATCATAAAGCTCTTGAAGAACTCAGAAGAG 1003
                                                    478 roThrVal 480
                                                                                                                                                              461 gHisCysAspTrpGlnLeuLeuAsnGlyProProThrMetLysThrSerP 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  411 sGluGluPheAsnProAspArgPheIleValProHisProGluAspAlaS 428
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Database sequences: 351203
Database length: 113238999
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Cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-882-164D-31 + 2612.00 5657.71

Cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-724-466B-5 + 2437.00 5277.52

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-TRANS=human40.cd1 -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
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-TRANS=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT=pfs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-668-482-32
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1644 1
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                                                                                                                                               erSerArgAspArgSerCysAlaLeuProLeuProProGlyThrMetGly
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-238-821B-10 + 237.50
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                                       alignment_block:
US-09-668-482-32 x US-08-882-164D-31
                                                                                                 Quality: 2612.00
Ratio: 5.256
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (416) 863-26
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REGISTRATION NUMBER: 36,424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: COMPUTER: MS-LOC OPERATING SYSTEM: MS-LOC SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,164D
TTTNG DATE: June 25, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1725 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Box 25
CITY: Toronto
STATE: Ontario
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ox 25, Commerce Court West
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""MRER: 08/724,466
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         lyLeuLeuCysLysSerAsnGlnAspAsnLysLeuAspMetGluThrLeu 350
                                        ACTCTACCCACATGTCCTCCAGAAAGTTCGAGAAGAGATAAAGAGCAAGG
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08724466B Patent No. 6063606 GENERAL INFORMATION:
                                    TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 5:
                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724
FILING DATE: October 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,54
FILING DATE: June 21, 1996
ATTORNEY_AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERRENCE_POCKET NUMBER: 5076
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                 STREET: Box 25, Commerce Co
CITY: Toronto
ZIP: M5L 1A9
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/
COMPUTER: COMPAQ, IBM PC CC
OPERATING SYSTEM: MS-DOS 5.
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                     SEQUENCE CHARACTERISTICS:
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-724-466B-5
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Quality: 2437.00
Ratio: 5.035
Percent Similarity: 97.384
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                          spAsnLeuProAlaArgPheThrTyrPheGlnGlyAspIle 497
                                                  TCTAAATGGACCTCCTACAATGAAAACCAGTCCCACCGTGTATCCTGTGG
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                                                                                   CTTCTCAAAATATTTACAGTGGAGCTGGCCAGGCATTGTGACTGGCAGCT
                                                                                                                                                                                                                                                     TCCCCCAGTTCCAGGAGGGTTTCGGGTTGCTCTGAAGACTTTTGAATTAA
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-882-164D-5
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seq_documentation_block:
; Sequence 5, Application US/08882164D;
; Patent No. 6306624
; GENERAL INFORMATION:
; APPLICANT: Beckett, Barbara R., Jon
; TITLE OF INVENTION: Retinoid Metabo
; NUMBER OF SEQUENCES: 43

GENERAL INFORMATION:
APPLICANT: PetKovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 43

Protein

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CORRESPONDENCE: COLOR COURT West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M51 1A9
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb
COMPUTER: COMPAQ, IBM PC COMPATIBLE: COMPAQ, IBM PC COMPATIBLE: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION NUMBER: US/08/882,164D
FILING DATE: June 25, 1997
PRIOR APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: OCOBET 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
TELEPHONE: (416) 863-434
TELEPHONE: (416) 863-2653
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1494 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPONINGY: linear
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Quality: 2437.00
Ratio: 5.035
Percent Similarity: 97.384
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                                                                                                                                                      201
                                                                      67
                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon STREET: Box 25, Commerce Court West
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps: 0
Percent Identity: 93.360
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                                                                                                                                                                                                                       200
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17	hrHisAspValAlaAspIlePheThrAsnLysGluGluPheAsnProAs	40
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384 1150	7 nProProValProGlyGlyPheArgValAlaLeuLysThrPheGluLeua 3	36'
367 1100	1 GluGlnLeuLysTyrIleGlyCysVallleLysGluThrLeuArgLeuAs :	35 105
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284 850	7 slysaspalaleuGlnLeuLeuIleGluHisSerTrpGluArgGlyGluA 	26 80
267 800	1 IleArgAlaLysIleArgArgLeuGlnAlaThrGluProAspGlyGlyGy	25 75
250 750	4 yrArgGlyValLysAlaArgAsnLeuIleHisAlaArgIleGluGluAsn :::	23 70
23 4 700	7 tThrargAsnLeuPheSerLeuProIleAspValProPheSerGlyLeuT	21 65
217 650	1 AlaGlyGlyGlyGluAspGluGlnGlnLeuValGluAlaPheGluGluMe 	20 60
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184 550	67 pLeuSerCysGlyGluArgGlyLeuLeuValTyrProGluValLysArgL 	16 50
167 500	51 CysTyrValLeuValIleAlaGluGluValSerSerCysLeuGluGlnTr 51 TGCTACGTGCCGGTGATCACCGAGGAAGTGGGCAGCAGCCTGGAGCAGTG	15 45
150 450	34 ysGlnArgLysLysVallleMetGlnAlaPheSerArgGluAlaLeuGln 	40
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TOPOLOGY:
US-08-882-164D-38
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                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6306624
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 38, Application US/08882164D
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/667,546

FILING DATE: June 21, 1996

APPLICATION NUMBER: 08/724,466

FILING DATE: October 1, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Hunt, John C.

REGISTRATION NUMBER: 36,424

REFERENCE/DOCKET NUMBER: 50767/00010
                                                                                                                                                                                                                                                            TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1451
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MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484
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                                                                                                                                                                                                                                                                                                                     TELEPHONE: (416) 863-4344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Box 25,
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                       LENGTH: 4164 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/
FILING DATE: June 25, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: Canada
ZIP: M5L 1A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                          Quality: 1853.00
                                                                          Ratio:
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                                                                                                                                                                                     linear
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                                                       4.240
41.778
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                                                       Percent Identity:
                                                                                        Length:
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Align seg 1/1 to:
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                etThrArgAsnLeuPheSerLeuProIleAspValProPheSerGlyLeu 233
                                                                         oAlaGlyGlyGlyGluAspGluGlnGlnLeuValGluAlaPheGluGluM
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                                                                                                                                                                                          rpLeuSerCysGlyGluArgGlyLeuLeuValTyrProGluValLysArg
                                                                                                                                                                                                                                    CGAAGGGGGGGGGCTGAGGGAAAGTAGAGGATTGTAACACTCTCTGCTC
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329 1830	312 ulleThrTyrLeuGlyLeuTyrProHisValLeuGlnLysValArgGluG	H.
312 1780	296 GluLeuLeuPheGlyGlyHisGluThrThrAlaSerAlaAlaThrSerLe 	
295 1730	1681 TCTGTATAAACTTCCGTTTTTATCCTTAGGCACTAAAACAATCGTCAACA	۳
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288	274 euIleGluHisSerTrpGluArgGlyGluArgLeuAspMetGln	
1080	ωι	\vdash
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257 1030	241 AsnleuileHisAlaArgIleGluGluAsnIleArgAlaLysIleArgAr 	
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    Patent No. 6063006
    GENERAL INFORMATION:
    AppLICANT: Petkovich
    AppLICANT: Beckett,
    TITLE OF INVENTION:
    NUMBER OF SEQUENCES:
    CORRESPONDENCE ADDRES
    ADDRESSEE: Blake,
    STREET: Box 25, CC
    CITY: TOTORTO
    ZIP: M5L 1A9
    COUNTRY: Canada
    COMPUTER READABLE FOR
    MEDIUM TYPE: Diske
    COMPUTER: COMPAQ,
    OPERATION SYSTEM:
    SOFTWARE: WORD PEI
    CURRENT APPLICATION DEPLICATION DEPLICATION DEPLICATION DEPLICATION DEPLICATION DEPLICATION DEPLICATION DEPLICATION DEPLICATION DAME:
    APPLICATION UNMBER
    PILING DATE: June
    ATTORNEY/AGENT INFORM
    NAME: HURT, John |
    REGISTRATION NUMBE
    REFERENCE/DOCKET N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-724-466B-3
            APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 50,424
REFERENCE/DOCKET NUMBER: 50767/0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEPAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Ca
                                                                                                                                                                                                                                                                        FILING DATE: October 1, 1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/724,466B
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Box 25, Commerce Court West
1850 base pairs
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alignment_scores:
Quality: 1734.00
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TOPOLOGY: linear
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erGlyLeuTyrArgGlyValLysAlaArgAsnLeuIleHisAlaArgIle
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Percent Identity: 67.742
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seq_documentation_block:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
"""" or SEQUENCES: 43
                                                                                                                Sequence 3, Application US/08882164D Patent No. 6306624
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ACCCAGTGGACAATCTCCCTACCAAATTCACTAGTTAT 1554
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alignment_block:
US-09-668-482-32 x
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION UNMER: US/08/882,16/
APPLICATION DATA:
PILING DATE: June 25, 1997
PRIOR APPLICATION DATA:
APPLICATION UNMER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REGISTRATION NUMBER: 36,424
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LENGTH: 1850 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Diskette, 3 1/2 inch, 1
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
                                                                                                          84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
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STREET: Box 25, Commerce
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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heGlyArgProThrValArgValMetGlyAlaAspAsnValArgArgIle
                                                                       TCGGGAACCCGACTGTCAGGGTGATGGGAGCTGATAATGTGAGGCAGATT
                                                                                                                                            TCTGCGCATGAAACGGCAGAAATACGGGTGCATCTACAAGACGCACCTCT
                                                                                                                                                               eLeuGlnMetLysArgArgLysTyrGlyPheIleTyrLysThrHisLeuP
                                                                                                                                                                                                                                                                                     GACGAGTCGAACTGCAGAAGTCCTCTACCGCCAGGTACCATGGGC
                                                                                                                                                                                                                                                                                                                                                             CGTTTTACTCTTTCTCGCCGCGGTGAAGTTGTGGGAGATGTTAATGATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 1734.00
Ratio: 4.070
milarity: 85.887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-882-164D-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/882,164D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 1850
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                                                                       387
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1017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 CysTyrValLeuVallleAlaGluGluValSerSerCysLeuGluGlnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         626 TGAAGAAACTCATGTTTCGGATAGCTATGAGAATCCTGCTTGGTTTTGAA 675
                                                                                                                                                                                                                                                                                                                                                              231 erGlyLeuTyrArgGlyValLysAlaArgAsnLeuIleHisAlaArgIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 eGluGluMetThrArgAsnLeuPheSerLeuProIleAspValProPheS 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            588 GCTGCAAAAAGACTCCTGC......GTGCTGGTTTATCCAGAAA 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gThrIleLeuGlyAlaGlyCysLeuSerAsnLeuHisAspSerSerHisL
|||||||||::: || |||||||:::|||
AACCATCCTGGGCTCTGACACCCTCTCCAATGTCCATGGAGTTCAACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProGlyProAlaGlyGlyGlyGluAspGluGlnGlnLeuValGluAlaPh 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pLeu......SerCysGlyGluArgGlyLeuLeuValTyrProGluV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ysGlnArgLysLysValIleMetGlnAlaPheSerArgGluAlaLeuGln 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluGluAsnIleArgAlaLysIleArgArgLeuGlnAlaThrGluProAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAGAGCAAATA.....AAGACGGACGAGCAAGAACTGGTGGAAGCTTT
                                                                                                                                                                                                                                                                                                          ysSerLysGlyLeuLeuCysLysSerAsnGlnAspAsnLysLeuAspMet 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rgGlyGluArgLeuAspMetGlnAlaLeuLysGlnSerSerThrGluLeu 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pGlyGlyCysLysAspAlaLeuGlnLeuLeuIleGluHisSerTrpGluA 281:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGGAAAACATCAGGAAGAAATTCAAGAT...GACGACAATGAAAACGA
                                                                                                                                                                                                                                   GluThrLeuGluGlnLeuLysTyrIleGlyCysValIleLysGluThrLe 364
                                                                                                                                                                                                                                                                                         AGGAGAAGGTTGAAATGGGCATGTATACACCTGGAAAGGGCTTGAGTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAGAAATACAAAGACGCCCTTCAGCTGTTGATCGAGAACAGCAGAAGAA 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IleCysAspThrHisAspValAlaAspIlePheThrAsnLysGluGluPh 414
                                                                 uArgLeuAsnProProValProGlyGlyPheArgValAlaLeuLysThrP 381
                                                                                                                                                                                                                  GAGCTGTTGGACCAGCTGAAGTACACTGGATGTGTGATTAAAGAGACTCT 1166
                                                                                                                                          TAGAATCAACCCTCCTGTTCCCGGAGGATTCAGAGTCGCACTCAAAACCT 1216
537
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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-882-164D-36
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alignment_block:
US-09-668-482-32 x US-08-882-164D-36
                                                                                                                                                                      alignment_scores:
    Quality:
    Ratio:
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                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATENL NO. CONTROL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/882,16
PETLING DATE: June 25, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: OCTOBER 1, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: OCTOBER 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: HUNT, JOHN C.
REGISTRATION NUMBER: 36,424
REGISTRATION NUMBER: 36,424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (416) 863-2653 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: COMPAQ, IBN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   464 pTrpGlnLeuLeuAsnGlyProProThrMetLysThrSerProThrValT 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 yrProValAspAsnLeuProAlaArgPheThrTyrPhe 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 2677 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage COMPUTER: COMPAQ, IBM PC compatible OPERATING SYSTEM: MS-DOS 5.1 SOFTWARE: WORD PERFECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Box 2:
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eAsnProAspArgPheIleValProHisProGluAspAlaSerArgPheS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAGCCGGAGAGATTCATGAGCAAAGGTCTGGAGGACGGGTCCAGGTTTA 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGGATTCTCTCAAACGGACCCCCGACAATGAAAACAGGCCCGACTATTT 1516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCCAGTGGACAATCTCCCTACCAAATTCACTAGTTAT 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCAAAGTGTTACTCAAGATCTTTTTAGTTGAGTTAACGCAGCATTGCAA 1466
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M5L 1A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ontario
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Box 25, Commerce Court West
                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                         1251.00
4.075
45.889
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                                                                                                                                      Percent Identity:
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                                                                                                                                      43.797
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Align s	seg 1/1 to: US-08-882-164D-36 from: 1 to: 2677
1 676	MetGlyLeuProAlaLeuLeuAlaSerAlaLeuCysThrPheValLeuPr 17
17 726	OLeuLeuPheLeuAlaAlaLeuLySLeuTrpAspLeuTyrCysValS 34
34 776	erSerArgAspArgSerCysAlaLeuProLeuProProglyTI :::
51 826	PheProPhePheGlyGluThrLeuGlnMetValLeu.Gln6
63	
876	TGGGGCGGGACAGGCTGCTTCCCCGGAGCCCGGCGCGCGC
63	
926	CTGAAGTCGGGGTAGGCGCCCCCGGGAGGCATGCTATTGCGGCTAGG
63	
976	GGGCTGGCGGAGCGCGGCGCTCCCCGGMKYMCSCTCAWGCSCRCWW
1026	:ArgArgLysPheLeuGlnMetLysArg
73	lisLeuPheGlyArgProThrVa 89
89 1126	SnValArgArgIleLeuLeuGlyGluHisA 10
106 1176	rgLeuValSerValHisTrpProAlaSerValArgThrIleLeuGlyAla 122
123 1226	GlyCysLeuSerAsnLeuHisAspSerSerHisLysGlnArgLysLys 138
138	
1276	GGGCAGGAGGCGACGGCTGGACAGGGAGGGGGACCCCATTTATGAG
13	:
1326	AATTCCGGCTGATGGATGCTAGGCGCGGCTAGCAGCTTGAGGTGGGCT 13
7	ACCCTCTGCCAGCTCCAGGTTAGCTTTCCCAGC
138	
1426	TGTCTGGCAGGACTGGGGGTGTCTGGAAGGGGACGGCGGTAGACGAGA
139	ValIl
٠ ٧	GGCGGATGGAGGCTTTTAACGCTGTCCCCTCCTCGGGACTCAGGTGATT 15
141	ArgGluAlaLeuGlnCysTyrValLe

26 AAGATATTGCTTTCCTTGACTTTCTGTCAGCAAAACATTTAGCCCTTCTA 2475	242
38 288	28
6 TACTCGCCTTACTGCTCCAGCTGAACTAAAGGGACGTTGCATTTTGTTTA 2425	237
38 288	28
26 TTTAATAAAACTAAGACTTTAACTCAGGAGTTTCCGGTAGRGCGGGGTCG 2375	232
38 288	28
76 TCAAAGGGAAAGTTGGAATTTGCAAAAATGTTAATAAAGAACCTTGCGAT 2325	227
38 288	28
26 GGAAGGGGCTGCGGMGGAAACTGGGAGCATCCCCTAGCCTTTAMCAGGTT 2275	222
88 288	28
76 CAGCTATGGAATCCCGAAGGAAGGCTGAGACACCCGGTCAGGAGAGCTGC 2225	217
88 288	28
26 AGCGCGCGCCTGGGGGCCCAGCTTTCTGGAGTGGGCGGCCGGC	212
88 288	28
76 GCGGAGTTTGGTCCCCTGGCTTTCCAAGGCGCTGTTCCTGGGGGCCCCCAA 2125	207
88 288	28
o composeriscamansaciscisciscascisiisaicsascactcsi 1 raglygluaraleuaspmetsin	28
4 pGlyGlyCysLysAspAlaLeuGlnLeuLeuIleGluHisSerTrpGluA 281	o N
6 GAGC	
8 GluGluAsnIleArgAlaLysIleA	24
36Gly.ValLysAlaArgAsnLeuIleHisAlaArgIle 247	187
26 GEGCTGCEGACTAGEGEGCGCGGEACCTGGGCGTCTGCTCACCGCCGCGCG 1875	182
35 235	23
	177
<pre>4 euProIleAspValProPheSerGlyLeuTyrArg.</pre>	22
107 uGlnGlnLeuValGluAlaPheGluGluMetThrArgAsnLeuPheSerL 224	20 17:
91 ArgIleLeuLeuGlyCysGluProGlyProAlaGlyGlyGlyGlyGluAspG1 207 	16
	16:
74 lyLeuLeuValTyrProGluValLysArqLeuMetPheArqIleAlaMet 190	
174 157 AGIUGIUVAISerSerCysLeuGIUGINTrpLeuSerCysGIyGIUArgG 174 157	1 15
26 A	15

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seq_documentation_block:
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                                                                 alignment_block:
                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                          TOPOLOGY:
US-08-724-466B-11
                                          US-09-668-482-32 x US-08-724-466B-11
                                                                                                         Percent Similarity:
Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/724,466B
FILING DATE: October 1, 1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: 08/667,546
FILING DATE: June 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 50767/00004
REFERENCE/DOCKET NUMBER: 50767/00004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3 1/2 inch, 1 COMPUTER: COMPAQ, IBM PC compatible OPERATING SYSTEM: MS-DOS 5.1 SOFTWARE: WORD PERFECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Toronto
ZIP: M5L 1A9
COUNTRY: Canada
                                                                                                                                                                                                                                                                           LENGTH: 351 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysGlnSerSerThrGluLeuLeuPheGlyGlyHisGluThrThrAlaSe
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                                                                                                                              Quality:
Ratio:
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to: US-08-724-466B-11
                                                                                                                                                                                                                                                                linear
                                                                                                         604.00
5.207
99.145
                                                                                       oaps: 0
Percent Identity: 97.436
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    from:
                                                                                                                                                    Length:
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    to:
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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-882-164D-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
APPLICANT: Beckett, Barbara Retinoid Metabolizing Protein
                                                                                                                                                          APPLICATION NUMBER: US/08/882,16
FILING DATE: June 25, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION UMBER: 08/724,466
FILING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
TELEPHONE: (416) 863-465
TELEFAX: (416) 863-265
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362
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|151 GACATGGAAATTTTGGAACAACTTAAATACATCGGGTGTGTTATTAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 GluLeuLeuPheGlyGlyHisGluThrThrAlaSerAlaAlaThrSerLe
                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: Canada ZIP: M5L 1A9
COMPUTER READABLE FORM:
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                                                                                  REFERENCE/DOCKET NUMBER: 50 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 GATCACTTACCTGGGGCTCTACCCACATGTTCTCCAGAAAGTGCGAGAAG
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CITY: Toronto
STATE: Ontario
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                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette, ,, MEDIUM TYPE: Diskette, ,, Compatible COMPUTER: COMPAQ, IBM PC compatible COMPUTER: MS-DOS 5.1
                                                                                                                                                                                                                                                                                                                                                      COMPUTER: COMPAQ
OPERATING SYSTEM:
SOFTWARE: WORD PI
                                                                                                                            NAME: Hunt, John C. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrSerIleCysAspThrHisAspValAlaAspIlePheThrAsnLySG1 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGACTTTTGAATTAAATGGATACCAGATTCCCAAGGGCTGGAATGTTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Box 25, Commerce Court West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blake,
                                                               (416) 863-4344
                                           863-2653
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                                                                                                                                                                                                                                                                                                                     US/08/882,164D
                                                                                                                            36,424
                                                                                                          50767/00010
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: nucleic acid
; STRANDEDNESS: singl
; TOPOLOGY: linear
US-08-882-164D-11
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                                                                                                                                                                                                                                                                                                                                                Sequence 1 Patent No.
                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: KONCZ, CSABA
APPLICANT: MATHUR, JAIDEEP
APPLICANT: SZEKERES, MIKLOS
APPLICANT: ALTMANN, THOMAS
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                     TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING CYTOCHROME TITLE OF INVENTION: P450-TYPE PROTEINS INVOLVED IN THE BRASSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 A 351
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                                                                                                     ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP STREET: P.O. BOX 747 CITY: Falls Church STATE: Virginia COUNTRY: USA
                                                                                         COUNTRY: USA
ZIP: 22040-0747
                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TyrSerIleCysAspThrHisAspValAlaAspIlePheThrAsnLysG1 412
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5, 5952545
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                                                                                                                                                                                                                                                         ALTMANN, THOMAS
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99.145
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Percent Identity: 97.436
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 Version #1.30 (EPO)
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; NAME/KEY:
; LOCATION:
US-08-622-166A-1
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US-09-668-482-32 x US-08-622-166A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1608 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO ANTI-SENSE: NO
                                       117
                                                                             324
                                                                                                                101
                                                                                                                                                      274
                                                                                                                                                                                                                                                                                                  174 GAGACTTTTCAGCTGATCGGAGCTTACAAAACAGAGAACCCCTGAGCCCTTT 223
                                                                                                                                                                                                                           224 CATCGACGAGAGAGTAGCCCGGTACGGTTCGGTTTTCATGACGCATCTTT 273
                                                                                                                                                                                                                                                                                                                                                                             124 ACCGTCGGATGGGTCTGCCTCCGGGAAGCCTTGGTCTCCCTCTGATAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
ORGANISM: A. thaliana
                                                                                                                                                                                 84 heGlyArgProThrValArgValMetGlyAlaAspAsnValArgArgIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE
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                                                                                                                                                                                                                                                                                                                            56 GluThrLeuGlnMetVal......LeuGlnArgArgLysPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 CTCCTCTTCCATCGCCGCCGGCTTCCTCCTACTC..... 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 uAlaAlaLeuLysLeuTrpAspLeuTyrCysValSerSerArgAspArgS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                         eLeuGlnMetLysArgArgLysTyrGlyPheIleTyrLysThrHisLeuP
TAACCTTTTGGGGAAACACTCTCTGCTTCTTATGAAAGGTTCTTTGCATA 423
                                 gThrIleLeuGlyAlaGlyCysLeuSerAsnLeuHisAspSerSerHisL 134
                                                                         CTTCAGAACGAAGGGAAGCTTTTTGAGTGTTCTTATCCTGCTTCCATTTG 373
                                                                                                            LeuLeuGlyGluHisArgLeuValSerValHisTrpProAlaSerValAr 117
                                                                                                                                                  TTGGTGAACCGACGATTTTCTCAGCTGACCCGGAAACGAACCGGTTTGTT 323
                                                                                                                                                                                                                                                                                                                                                                                                                   erCysAlaLeuProLeuProProGlyThrMetGlyPheProPhePheGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
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ER: 0147-0153P
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Gaps: 15
Percent Identity: 26.640
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294	64 ArgArgLysPheLeuGInMeCLysArgArgNySTyrolyrnellelyLys 	
244	υī	
63	47 lyThrMetGlyPheProPhePheGlyGluThrLeuGlnMetValLeuGln	
47 194	30 uTyrCysValSerSerArgAspArgSerCysAlaLeuProLeuProProG	
30 160	14 PheValLeuProLeuLeuLeuPheLeuAlaAlaLeuLysLeuTrpAspLe	
	Align seg 1/1 to: US-08-991-677-3 from: 1 to: 1883	
	alignment_block: US-09-668-482-32 x US-08-991-677-3	
	alignment_scores: 358.50 Length: 506 Quality: 358.50 Length: 506 Gaps: 21 Percent Similarity: 54.150 Percent Identity: 26.680	
,	; NAME/KEY: CDS ; LOCATION: (74)(1606) US-08-991-677-3	
	2055	
	SEO	
	CUF	
osperms	; GENERAL INFORMATION: APPLICANT: Chiang, Vincent L APPLICANT: Carraway, Daniel T APPLICANT: Smeltzer, Richard H TITLE OF INVENTION: Production of Syringyl Lignin in Gymnospe	
	<pre>seq_documentation_block: Sequence 3, Application US/08991677A patent No. 6252135</pre>	
	<pre>seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-991-677-3</pre>	
	491 ThrTyrPhe 493 1431 CCGATCTTC 1439	
490 1430	474 etLysThrSerProThrValTyrProValAspAsnLeuProAlaArgPhe 4 ::: :::	
474 1380	457 IGluLeuAlaArgHisCysAspTrpGlnLeuLeuAsnGlyProProThrM 4	
457 1345	441 SerCysValGlyLysGluPheAlaLysIleLeuLeuLysIlePheThrVa 4	
1295	424 roGluAspAlaSerArgPheSerPheILeProPheGLyGLYGLYLEUAIG :::::::	

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1023
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341 nAspAsnLysLeuAspMetGluThrLeuGluGlnLeuLysTyrIleGlyC 358
                                                                                                                                                                                                                                                                                                                                                                            973 CAAAGCTATCATGGACGTAATGTTTGGAGGGACCGAAACGGTGGCGTCCG 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 GlyGluArgLeuAspMetGln...AlaLeuLys......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 lyGlyCysLysAspAlaLeuGlnLeuLeuIleGluHisSerTrpGluArg 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    823 CATCGACGATCATATACAGAAGGGGAGTAAAAACTCGGAGGAGGTTGATA 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 nIleArgAlaLysIleArgArg.....LeuGlnAlaThrGluProAspG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     723 ATATAGCTGATTTTATCCCTTGGCTCAAATGGGTTCCTCAGGGGATTAAC 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     673 CGAGTTCGTGGCCATACTGCAAGAGTTTTCGCAGCTGTTTGGTGCTTTTA 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     571 CAATATTGGGTCGACG......GTGAATATCGGCGAG......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             521 TGGGAGTCGGTCCGAGACGAGGTCGACTCGGCAGTACGAGTGGTCGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 Tyr.....ValLeuValIleAlaGl 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              471 TGCGTAAACTCTGCGTCATGAAATTATTTAGCCGGAAACGAGCCGAGTCG 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 lnArgLysLysValIleMetGlnAlaPheSerArgGluAlaLeuGlnCys 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 TGACCGAGCCGACATGGCCTTCGCTCACTACGGCCCGTTTTGGCGTCAGA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 AlaSerValArgThrIleLeuGlyAlaGlyCysLeuSerAsnLeu...Hi 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 CCTCAAGATGGGATTCTTACACATGGTGGCCGTTTCCACACCCGACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 alArgArgIleLeuLeuGlyGluHisArgLeuValSerValHisTrpPro 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCAGGCTCAACAAGGCACGAGGGGCGCTTGATGGGTTTATTGACAAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGATC.....TCGCATGAGGACCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCGAATCTGACGATCTTCAAAATTCCATCAAACTCACCAAAGACAACAT 972
                                                                            LysValArgGluGluIleLysSerLysGlyLeuLeuCysLysSerAsnGl 341
                                                                                                                                                                                                                                CGATTGAATGGGCCATGACGGAGCTGATGAAAAGCCCCAGAAGATCTAAAG 1072
                                                                                                                                                                                                                                                                                                laAlaThrSerLeuIleThrTyrLeuGlyLeuTyrProHisValLeuGln 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                        .GlnSerSerThrGluLeuLeuPheGlyGlyHisGluThrThrAlaSerA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ....LysAlaArgAsnLeuIleHisAlaArgIleGluGluAs 250
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alignment_block: us-09-668-482-32 \times us-09-091-432-1
                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Arabidopsis thaliana US-09-091-432-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-09-091-432-1
                                                                                                                                                                                                                                                                  alignment_scores:
                                                                      Align seg 1/1 to: US-09-091-432-1 from:
                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Microsoft Word 2.0C
SEQ ID NO 1
LENGTH: 1838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09091432 Patent No. 5981837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/091,432
CURRENT FILING DATE: 1998-06-18
EARLIER APPLICATION NUMBER: PCT/US96/20094
EARLIER FILING DATE: 1996-12-19
EARLIER APPLICATION NUMBER: US 60/009,119
EARLIER APPLICATION NUMBER: US 60/013,388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chapple, Clint
TITLE OF INVENTION: A Method For Regulation Of Plant Lignin Composition
FILE REFERENCE: 7024-325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1996-03-14 NUMBER OF SEQ ID NOS: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1455 CTGTGGCTCACCTTCACTGTTTCACGTGGGAGTTG......CCG 1495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     439 uArgSerCysValGlyLysGluPheAlaLysIleLeuLeuLysIlePheT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       456 hrValGluLeuAlaArgHisCys...AspTrpGlnLeuLeuAsnGlyPro 471
                       15 ValLeuProLeuLeuPheLeuAlaAlaLeuLysLeuTrpAspLeuTy 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGGTCTTGCCCCGGTATGCAACTCGGACTCTACGCGCTAGAGACG...A 1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluAsp.....AlaSerArgPheSerPheIleProPheGlyGlyGlyLe 439
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337.00
1.221
53.592
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25.825
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933	aaammacmcacmcacaccccccamccaaacmmacc	20
288	TrpGluArgGlyGluArgLeuAspMetGln	279
278 883		267 834
266 833	.ArgAlaLysIleArgArgLeuGlnAlaThrGluProAspGl ::: ::::: ::: ACATATGAAGAAGAAGGAGAATCAAAACGCTGTGGATGATGA	252 784
251 783	VallysalaargAsnLeuIleHisAlaargIleGluGluAsnIle	237 734
236 733	spValProPheSerGlyLeuTyrArgG::::	227 684
8 N	ualaPheGluGluMetThrArgAsnLeuPheSerI : ::::: ::::::::::::::::::::::::::::	212 634
212 633	CysGluProGlyProAlaGlyGlyGlyGluAspGluGlnGlnLeuValGl	196 605
195 604	MetPheArgIleAlaMetArgIleLeuLeuGly ::: ::: ::: ACTTACCGGGCAGCGTTTGGGTCAGCC	179 561
179 560	ysLeuGluGlnTrpLeuSerCysGlyGluArgGlyLeuLeuValTyrP ;;; ;; ;; ; ;; ; aCGTTGGTAAGCCTATAAACGTCGGGGAGCAAATTTTTG	162 520
162 519	IleAlaGluCluValSerSe	152 470
151 469	alIlemetGlnAlaPheSerArgGluAlaLeuGlnCys ::: ::::: :: grgrcArgAAGGrgrttaGCCGTAAAAGAGCTGAGTCA	
135 419	CATGGCTTTCGCTCACTACGGACCGTTTTGGAGACAGA	129 370
129 369	laGlyCysLeuSerAsnLeuHi ::::: :: GCTATAAGCTATCTGACTTA	114 341
113 340	HisArgLeuValSerValHisTrpPro ::: :: :CAAGACAGCGTCTTCTCGAACCGGCCT	97 291
97 290	spAsnV ::: ccgAgg	81 241
81 240	ELGUGInMETLYSATGATGLYSTYTG1YPhEIlGTYTLYSTh 	65 197
54 196	\textslyPheProPhePheGlyGluThrLeuGlnMetValL ::: ::: ::: ::: ;ACGAGGTTGGCCCATCATAGGCAACATGTTAATGATGGACC	48 147
18 146	ArgAspArgSerCysAlaLeuProLeuProProG 	31 107
106		80

ORGANISM: Mycobacterium tuberculosis FERATURE: OTHER INFORMATION: CDC 1551 OTHER INFORMATION: "n" bases at various positions throughout	FILE REFERENCE: 24366-20007.00 CUURRENT APPLICATION NUMBER: US/09/103,840A CUURRENT FILING DATE: 1998-06-24 NUMBER OF SEQ ID NOS: 2 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 2 LENGTH: 4403765 Type: DNA	PATENT NO. 0.243.26 GENERAL INFORMATION: APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R. APPLICANT: FRASER, Claire M. APPLICANT: FRASER, Claire M. APPLICANT: VENTER, John C. TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN TITLE OF INVENTION: TÜBERCULOSIS	<pre>seq_name: /cgn2_b/ptodatd///IIId/ob_cvmb.seq.05 03 103 0400 2 seq_documentation_block: ; Sequence 2, Application US/09103840A</pre>	euAsnGlyProProThrMetLysThrSer 477	451 euLeuLysIlePheThrValGluLeuAlaArgHisCys 463	434 opheGlyGlyGlyLeuArgSerCysValGlyLysGluPheAlaLysIleL 451 ::: ::: 1366 GTTCGGGTCGGGTCGTAGATCGTGCCCGGGTATGCAA	420 IleValProHisProGluAspAlaSerArgPheSerPheIlePr 434 ::: ::: ::: :::	403 spValAlaAspIlePheThrAsnLysGluGluPheAsnProAspArgPhe 419 1266 GCGACCCAACCTCTTGGACTGAACCCGGACACGTTTAGACCATCGAGGTTT 1315	386 rGlnIleProLysGlyTrpAsnValIleTyrSerIleCysAspThrHisA 403 : ::: ::: 1216 CTTCATTCCCAAGAAATCTCGTGTGATGATCAACGCGTTTGCCATAGGAC 1265	370 ValproglyGlyPheArgValAlaLeuLysThrPheGluLeuAsnGlyTy 386 ::: ::::::::::::::::::::::::::::::	353 euLysTyrIleGlyCysValIleLysGluThrLeuArgLeuAsnProPro 369	336 uCysLysSerAsnGlnAspAsnLysLeuAspMetGluThrLeuGluGlnL 353	321 HisValleuGlnLysValArgGluGluIleLysSerLysGlyLeuLe 336 ::: ::::: ::::: ::: ::: :	304 hrThralaSerAlaAlaThrSerLeuIleThrTyrLeuGlyLeuTyrPro 320 	934 TGACAATATCAAAGCAATCATGGACGTTATGTTTGGAGGAACGGAAA 983
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; OTHER INFORMATION: represent a, US-09-103-840A-2
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US-09-668-482-32 x US-09-103-840A-2/rev
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Percent Similarity:
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4120209GTCTGGCCTGCACGCGCCCGCGCCAACACCGAGATCGACGACGTCGTCAT 4120160
                                                                                                                                                   4120259CAGAGCAGTTGACCGTGCGCTACGCACTGCGTTCGGTTGGGCGCACTACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 MetArgIleLeuLeuGlyCysGluProGlyProAlaGlyGlyGlyGluAs 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 gLeuValSerValHisTrpProAlaSerValArgThrIleLeuGlyAlaG
                                                                                                                                                                                                                      223 erLeuProIleAspValProPheSer......GlyLeuTyrArg 235
                                                                                                                                                                                                                                                                                                                                                                              206 pGluGlnGlnLeuValGluAlaPheGluGluMetThrArgAsnLeuPheS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 eAlaGluGluValSerSerCysLeuGluGlnTrpLeuSerCysGlyGluA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 lyCysLeuSerAsnLeuHisAspSerSerHisLysGlnArgLysLysVal 139
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                                                                   GlyValLysAlaArgAsnLeuIleHisAlaArgIleGluGluAsnIleAr 252
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Gaps: 12
Percent Identity: 24.123
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APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, OWEN R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 1
LENGTH: 4411529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09103840A Patent No. 6294328
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; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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Quality:
Ratio:
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US-09-668-482-32 x US-09-103-840A-1/rev
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Ratio: 1.348
Percent Similarity: 53.509
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|| ::: ::: || || || || :::
4128199GTCCGTTTGCGATGTTGACGGTGGCGCGCTGATGCTGGATGTGATC 4128150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 IleMetGlnAlaPheSerArgGluAlaLeuGlnCysTyrValLeuValIl 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 lyCysLeuSerAsnLeuHisAspSerSerHisLysGlnArgLysLysVal 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 gLeuValSerValHisTrpProAlaSerValArgThrIleLeuGlyAlaG 123
                                                                                                                                                                                                                                                                                                                                                                            190 MetArgIleLeuLeuGlyCysGluProGlyProAlaGlyGlyGlyGluAs 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 eAlaGluGluValSerSerCysLeuGluGlnTrpLeuSerCysGlyGluA 173
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236 GlyValLysAlaArgAsnLeuIleHisAlaArgIleGluGluAsnIleAr 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 ArgValMetGlyAlaAspAsnValArgArgIleLeuLeuGlyGluHisAr 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 sTyrGlyPheIle..... 78
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                                                                                                                                            erLeuProIleAspValProPheSer..........GlyLeuTyrArg 235
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352	336 LeuCysLysSerAsnGlnAspAsnLysLeuAspMetGluThrLeuGluGl
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319 4127765	302 sGluThrThrAlaSerAlaAlaThrSerLeuIleThrTyrLeuGlyLeuT
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TYPE: DNA ORGANISM: Mycobacterium tuberculosis FEATURE: OTHER INFORMATION: CDC 1551 OTHER INFORMATION: "n" bases at various positions throughout the sequen OTHER INFORMATION: represent a, t, c or g S-09-103-840A-2
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79 TyrLysThrHisLeuPheGlyArgProTh 88
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:g 257 - 	244 isalaargIleGluGluAsnIleArgalaLysIleArgArg
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Query length: 497
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COMMENT
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                           104 GluHisArgLeuValSerValHisTrpProAlaSerValArgThrIleLe
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Ratio: 4.613
milarity: 94.333
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70 tLysArgArgLysTyrGlyPheIleTyrLysThrHisLeuPheGlyArgP
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                                                                          GAAGCGCAGGAAATACGGCTTCATCTACAAGACGCATCTGTTCGGGCGGC
                                                                                                                                                       TTTGGGTGAACT...AATTGTCTGACCAAGCGGAGGAAGTTCCTGCAGAT
                    roThrValArgValMetGlyAlaAspAsnValArgArgIleLeuLeuGly
CCACCGTACGGGTGATGGGGCGCGCAATGTGCGGGCGCATCTTGCTCGGA
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Contact: Genoscope
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AL539668 LTI_FL013_FBrn1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Organ: Fetal brain; Vector: pcMvSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMvSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliangelifetech.com URL: fliangelifetech.com URL: http://fulllength.invitrogen.com"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="CSODF036YG04"
/clone=lib="LTI_F1013"
/clone=lib="LTI_F1013"
/dev_stage="pooled tissue from week, 24 week and 26 week)"
/lab_host="PH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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Gaps: 1
Percent Identity: 89.000
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Primates;
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.9e-35
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BE506442 db83bl1.y1 Wellcome
BG486108 dad60f10.x1 Wellcom
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
                                                                                                          ACCESSION
VERSION
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Primates;
1 (bases 1 to 893)
Li,W.B., Gruber,C., Jessee,J.
                                                             Homo sapiens
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                                                                                                                          prime, mRNA sequence
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                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Contact: Genoscope
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//lab_host="DHIUB"
//lab_host="DHIUB"
//note="organ; brain; Vector: pCMVSPORT 6; 1st strand cDNA
/note="organ; brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: fliang@lifetech.com URL:
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/db_xref="taxon:9606"
/clone="CS0DM014YL13"
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REFERENCE
AUTHORS
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SOURCE
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AL532444 LTI_NFL001_NBC4 Homo
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1028)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                         Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope_cns.fr, Web : www
                                                                                                                                                                                                                                                                                                                     EST
                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                            prime, mRNA sequence.
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                                                                                                                   .1028
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                                                                                                                                            www.
                                                                                                                                            .genoscope.cns
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US-09-668-482-32 x AL532444/rev
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oAspArgPheIleValProHisProGluAspAlaSerArgPheSerPheI
                                          GATACTCATGATGTGGCAGAGATCTTCACCAACAAGGAAGAATTTAATCC
                                                                  AspThrHisAspValAlaAspIlePheThrAsnLysGluGluPheAsnPr 416
                                                                                                                           TAAATGGATACCAGATTCCCAAGGGCTGGAATGTTATCTACAGTATCTGT
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Ratio: 4.739
nilarity: 92.553
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alignment_scores:
Quality: 1001.00
Patio: 4.859
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LOCUS AL539667
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                                                                               US-09-668-482-32 x AL539667/rev
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Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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                                                                                                                                                                                                                                                                     fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
190 c 204 g 229 t 27 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Organism "Homo sapiens"
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Gaps:
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CS0DF036YG04 3
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SOURCE
ORGANISM
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KEYWORDS
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                AUTHORS
TITLE
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                                                                                                                                                              sequence.
AW513600
                                                                                                                                                                                           AW513600 618 bp mRNA EST xo47b06.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone similar to SW:CP26_HUMAN O43174 CYTOCHROME p450
          Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 618)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                Homo sapiens
                                                                                                                              AW513600.1
EST.
Tumor Gene Index
                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                 human.
                                                                                                                                             GI:7151678
             Genome Anatomy Project (CGAP),
                                                              Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                51 CTTCCCCTTCTTGGGGAAACCTTGCAGATGGTACTGCAGCGGAGGAAGT 100
SerSerArgAspArgSerCysAlaLeuProLeuProProGlyThrMetGl
                                                                      eLeuLeuGlyGluHisArgLeuValSerValHisTrpProAlaSerValA 117
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                                                                                                                                                                                                                                                                                                                                                              TCCTGCAGATGAAGCGCAGGAAATACGGCTTCATCTACAAGACGCATCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Emmert-Buck, M.D., Ph.D.
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Seq primer: -40UP from Gibco
High quality sequence stop: 440.
Location/Qualiflers
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"
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4.935
96.602
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2707091"
/clone_lib="NCI_CGAP_Utl"
/tissue_type="well-differentiated endometrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 c
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ORGANISM
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LOCUS BE236243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 537)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
                 Quality:
Ratio:
                                                                                                                                                                                                                                                                                                          BACKWARD: GTTTTCCCAGTCACGACG
Plate: 85 row: B column: 21
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                          and -minmatch 12 options.
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                               Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                                                                                                                                                                                                                                                                                              USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, US Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST discovery in swine Unpublished (2000)
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Mammalia; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa
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143959 MARC 1PIG S
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                                                                                                                                                                                                                                                                                                                                                               FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_
Library made from pooled tissue from day 11, 13
and 30 embryos."
163 c 174 g 104 t
                                                                                                                                                                                      /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                      /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
900.00
5.114
98.324
                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Gaps: 0
Percent Identity: 94.972
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Percent Similarity:

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KEYWORDS
SOURCE
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US-09-668-482-32 x BE236243
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                                                                                                                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      luGluValSerSerCysLeuGluGlnTrpLeuSerCysGlyGluArgGly 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lMetGlyAlaAspAsnValArgArgIleLeuLeuGlyGluHisArgLeuV 108
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                                                                                                                                                                                                                                                                                                                                                CATCCTGCTGGGCTGCGAGCCCCGGCTGGCGAGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGAAGTGGACAGTTGCCTGGAGCAGTGGCTGAGCTGCGGAGAGCGCGGC
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                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Muri 1 (bases 1 to 539)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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602045632F1 NCI_CGAP_Li9
            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-femail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
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EST.
                                                                                                                                                                                                                                                   mRNA sequence.
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  distribution: MGC
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Mus musculus cDNA
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GCTAAGCTGCGGC
                            pLeuSerCysGly 171
                                                        TGCTACGTGCCCGTGATCGCTGAGGAAGTCAGCAGTTGTCTGGAGCAGTG
                                                                                                                     AGCAGCGAAAGAAGGTGATTATGCAGGCCTTCAGCCGCGAGGCACTCCAG
                                                                                                                                                                                  CACCATCCTGGGCGGCTGCCTCCCAACCTGCACGATTCCTCGCACA
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Location/Qualifiers
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LOCUS BF533769
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eLeuGlnMetLysArgArgLysTyrGlyPheIleTyrLysThrHisLeuP 84
                                                                                                                                                             GCAGCCGCGATCGCAGCTGCGCCCTCCCCTTGCCCCCCGGTACCATGGGC 199
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Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9779 row: c column: 22
High quality sequence stop: 564.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
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BF533769
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                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
On Jun 22, 2000 this sequence version replaced gi
Other_ESTs: db61c05.x1
Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1810
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE189825 696 bp mRNA EST 07-AUG-2000 db61c05.y1 Wellcome CRC pSK egg Xenopus laevis cDNA clone IMAGE:3377480 5' similar to gb:gb|AF057566.1|AF057566 Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Pers, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        laevis retinoic acid converting enzyme (XENOPUS);, mRNA sequence.
BE189825
BE189825.2 GI:9729548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        African clawed frog. Xenopus laevis
                                                                                                                                                                                                                                     University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WashU Xenopus EST project, 1999
                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 696)
                                                                                                                                                                                                               quality sequence stop: 483.
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BASE COUNT ORIGIN

alignment_block:

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108

IMAGE: 692620

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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                      TGATGTATCCCGCCATCAAGCGACTGATGTTCCGCATTGCCATGAAGCTC
                                                                                                                                                                                                                                                                                                                                                                                         uValSerSerCysLeuGluGlnTrpLeuSerCysGlyGluArgGlyLeuL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaPheSerArgGluAlaLeuGlnCysTyrValLeuValIleAlaGluGl 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rValHisTrpProAlaSerValArgThrIleLeuGlyAlaGlyCysLeuS
                                                                                                   IleHisAlaArgIleGluGluAsnIleArgAlaLysIleArgArgLeuGl
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Note: This is a Xenopus Gene Collection (XGC) library."

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                                                                                                         alignment_block:
US-09-668-482-32 x AA239785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                 324 GlnLysValArgGluGluIleLysSerLysGlyLeuLeuCysLysSerAs 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
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                                                                                                                                                                Similarity:
CAGAAAGTTCGAGAAGAGATAAAGAGCAAGGGCTTACTTTGCAAGAGCAA
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                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
Contact: Marra M.Mouse EST Project
WashU-HHH Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 474)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T. Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA239785 474 bp mRNA EST 03-MAR-1997 mx800a03.rl Soares mouse NML Mus musculus cDNA clone IMAGE:692 similar to TR:G1001252 G1001252 HYPOTHETICAL 50.6 KD PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 461.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI:426180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
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Bonaldo."
99 c 118 g 122 t
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5.382
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Louis,

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502 209 455 193 405 176 358 159 308 143 258 126 208 109 158

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REFERENCE
AUTHORS
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LOCUS BF236872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9446 row: p column: 19
High quality sequence start: 2
High quality sequence stop: 545.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                          1 (bases 1 to 545)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                       602027980F1 NCI_CGAP_Li9
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                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                  house mouse
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/clone_lib="NCI_CGAP_Li9"
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                                                           /organism="Mus musculus"
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US-09-668-482-32 x BF236872
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 KEYWORDS
                                                                   DEFINITION
                                                                                seq_documentation_block:
LOCUS BF055367
                                                                                                                           seq_name:
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                                                                                                                                                                                                                                                                                                                                             ArgThrIleLeuGlyAlaGlyCysLeuSerAsnLeuHisAspSerSerHi 133
                                                                                                                                                                                                                                                                                                                                                                                      TCTTGCTGGGAGAGCACCGGTTGGTGTCGGTGCACTGGCCCGCGTCGGTG
                                                                                                                                                                                                                                                                                    CGCACCATCCTGGGCGCGGCTGCCTCTCCAACCTGCACGATTCCTCGCA
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                                                                                                                                                        TGGCTAAGCTGCGGC
                                                                                                                                                                                 TrpLeuSerCysGly 171
                                                                                                                           gb_est82:BF055367
## BF055367
BF055367.1
BF055367.1
                                                     BF055367 646 bp mRNA EST 16-OCT-2000 7j78f12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3392591 3' similar to SW:CP26_HUMAN 043174 CYTOCHROME P450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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                                         mRNA sequence
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/note="Organ: liver; Vector: pcMV-SPORT6; Site_1:
Site_2: Sall; Cloned unidirectionally. Primer: Oli
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 165 c 184 g 109 t
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4.820
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Percent Identity: 94.220
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                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: BF055367
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-668-482-32 x BF055367/rev
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                                                                                                                                                                                                                                                                                                                                                    350 LeuGluGlnLeuLysTyrIleGlyCysValIleLysGluThrLeuArgLe 366
                                                                                                                                                                                                                                                           593
                                                                                                                                                                                                                                                                            366 uAsnProProValProGlyGlyPheArgValAlaLeuLysThrPheGluL 383
                                                                                                                                                                                                                                                                                                                               643 TTGGCCCACCTTAAATACTTCGGGTGTGTTATAAAGGAGACCCTTNGACT
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                                                                                                                                                                                 543 AAAATGGATACCAGATTCCCAAGGGCTGGAATGTTATCTACAGTATCTGT
                                                                                                                                                                                                  383 euAsnGlyTyrGlnIleProLysGlyTrpAsnValIleTyrSerIleCys 399
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                                                                     416 oAspArgPheIleValProHisProGluAspAlaSerArgPheSerPheI 433
                                                                                                       ASPThrHisAspValAlaAspIlePheThrAsnLysGluGluPheAsnPr
leProPheGlyGlyLeuArgSerCysValGlyLysGluPheAlaLys 449
                                                                                                                                                                                                                                                         GAATCCCCCAGTTCCAGGAGGGTTTCGGGTGCTTCTGAAGACTTTTAATT
                                   TGACCGATTCATGCTGCCTCACCCAGAGGATGCATCCAGGTTCAGCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 646)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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Location/Qualifiers
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5.160
97.297
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129 c 120 g 194 t
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/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon;9606"
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Gaps: 0
Percent Identity: 91.216
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BASE COUNT
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LOCUS AW174347
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AW174347
AW174347.1 GI:6440295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: S.L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Other_ESTs: fi42a06.x1
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1 (base 1 to 720)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
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        172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence stop: 478.
insert. Size selection was performed to exclude fragments (1.5kb Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science) and kindly donated by Dr. Koichi Kawakami. Custom primers for sequencing: 5' end primer CTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA.
                                                                                                                                                                                             with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DrallI adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DralII sites of the pMEL8S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTGT). XhoI should be used to isolate the cDNA
                                                                                                                                                                                                                                                                                                      /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTT];
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Sugano Kawakami zebrafish DRA"
/sex="mixed (one male and one female, incl
unfertilized eggs)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="2640274"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="AB"
                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   'lab_host="DH10B (phage resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dr. Koichi Kawakami DNA
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     including
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707
                                                                                            214 eGluGluMetThrArgAsnLeuPheSerLeuProIleAspValProPheS 231 :|||:::||
                                                                                                                                                613
                                                                                                                                                                                                                                                                                                                                                                              475 CACTACATTCCCGTGATCCATCAGGAGGTGAAGAGCGCCATACAGGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                    151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 PheProPhePheGlyGluThrLeuGlnMetValLeuGlnArgArgLysPh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 GACGAGTCGATCCGAACTGCAGAAGTCCTCTACCGCCAGGTACCATGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 erSerArgAspArgSerCysAlaLeuProLeuProProGlyThrMetGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 OLeuLeuLeuPheLeuAlaAlaLeuLysLeuTrpAspLeuTyrCysValS 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 ATGGGGCTGTACACCCTTATGGTCACCGTTGTCTGTTCCATCGTGCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pLeu.....SerCysGlyGluArgGlyLeuLeuValTyrProGluV 181
                                                                                                                                                                                                                                                                                                                                                                                                CysTyrValLeuValIleAlaGluGluValSerSerCysLeuGluGlnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heGlyArgProThrValArgValMetGlyAlaAspAsnValArgArgIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eLeuGlnMetLysArgArgLysTyrGlyPheIleTyrLysThrHisLeuP
||||:::||||||||:::|||||||||||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACCATCCTGGGCTCTGACACCCTCTCCAATGTCCATGGAGTTCAACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGGGAACCCGACTGTCAGGGTGATGGGAGCTGATAATGTGAGGCAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGCGCATGAAACGGCAGAAATACGGGTGCATCCTCAAGACGCACCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGTTTTACTCTTTCTCGCCGCGGGGAAGTTGTGGGAAGATGTTAATGATCC 124
                                                                                                                                                                                                                                                                                                   GCTGCAAAAAGACTCCTGC......GTGCTGGTTTATCCAGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAACAAGAAAAAGGCCATTATGAGGGCGTTCTCTCGAGATGCTCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gThrIleLeuGlyAlaGlyCysLeuSerAsnLeuHisAspSerSerHisL 134
                     erGlyLeuTyrArg 235
                                                                                                                                                                                   ProGlyProAlaGlyGlyGlyGluAspGluGlnGlnLeuValGluAlaPh
TTGGTCTGTACAGG 720
                                                                        GGAGCGAATGATCAGCGACGTGGTCTGCTTGCCAATCCACGTTCCTTTCA
                                                                                                                                                 CCACAGCAAATA...
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Percent Identity: 62.185
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JOURNAL
US-09-668-482-32 x AW765767
                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WashU Xenopus BST project, 1999
Unpublished (1999)
Other_ESTS: da77a02.x1
Contact: Sandy Clifton, Ph.D.
                                                                                                                                                           Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       image.llnl.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berkeley)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Washington University Genome Sequencing Center
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4.209
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Align seg 1/1 to:

AW765767

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Danio Terio

Danio Terio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Rasborinae; Danio.

1 (bases 1 to 640)

Clark, M., Johnson, S. L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy

S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylia, T., Underwood

K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,

Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,

Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
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PheProPhePheGlyGluThrLeuGlnMetValLeuGlnArgArgLysPh
                                 GACGAGTCGATCCGAACTGCAGAAGTCCTCTACCGCCAGGTACCATGGGC
                                                      erSerArgAspArgSerCysAlaLeuProLeuProProGlyThrMetGly
                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Stephen L. Johnson washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Possible reversed clone: similarity on wrong strand Seq primer: T3 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          www.rzpd.de)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: zbrafish@watson.wustl.edu
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1998)
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/db_xref="taxon:7955"
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67	eLeuGlnMetLysArgArgLysTyrGlyPheIleTyrLysThrHisLeuP 84	
262	TCTGCGCATGAAACGGCAGAAATACGGGTGCATCTACAAGACGCACCTCT 311	_
84	heGlyArgProThrValArgValMetGlyAlaAspAsnValArgArgIle 100	U
312	TCGGGAACCCGACTGTCAGGGTGATGGGAGCTGATAATGTGAGGCAGATT 361	_
101	LeuLeuGlyGluHisArgLeuValSerValHisTrpProAlaSerValAr 117	7
362	CTGCTGGGCGAACACAAGCTGGTGTCTGTTCAGTGGCCAGCATCAGTGAG 411	_
117	AspSer	**
412	AACCATCCTGGGCTCTGACACCCTCTCCAATGTCCATGGAGTTCAACACA 461	_
134	ysGlnArgLysLysValIleMetGlnAlaPheSerArgGluAlaLeuGln 150	0
462	AAAACAAGAAAAAGGCCATTATGAGGGCGTTCTCTCGAGATGCTCTGGAG 511	_
151	ğ	7
512	CACTACATTCCCGTGATCCAGCAGGAGGTGAAGAGCGCCATACAGGAATG 561	_
167	SerCysGlyGluArgGly	-
562	GCTGCAAAAAGACTCCTGC	θ
181	alLysArgLeuMetPheArgIleAlaMetArgIleLeuLeu 194	
600	TGAAGAAACTCATGTTTCGGATAGCTATGAGAATCCTGCTT 640	

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